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OM nucleic - nucleic search, using sw model

Run on: May 15, 2004, 22:29:22 ; Search time 5963.83 Seconds
(without alignments)
17340.609 Million cell updates/sec

Title: US-10-067-449-10

Perfect score: 2386

Sequence: 1 tcgactctagaggtccctc.....ctggactttctccagttg 2386

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 seqs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

- 1: gb.ba.*
- 2: gb.htg.*
- 3: gb.in.*
- 4: gb.om.*
- 5: gb.ov.*
- 6: gb.pat.*
- 7: gb.ph.*
- 8: gb.pl.*
- 9: gb.pr.*
- 10: gb.ro.*
- 11: gb.sts.*
- 12: gb.sy.*
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- 14: gb.vi.*
- 15: em.ba.*
- 16: em.fun.*
- 17: em.hum.*
- 18: em.in.*
- 19: em.mu.*
- 20: em.om.*
- 21: em.or.*
- 22: em.ov.*
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- 40: em.htgo.mus.*
- 41: em.htgo.other.*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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1	2386	100.0	2386	6	AX573332	AX573332 Sequence
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3	1528.2	64.0	2482	10	RATIRGT	J04561 Rat insulin
4	1528.2	64.0	2506	10	RATGLUT4	D28561 Rat insulin
5	1526.6	64.0	2447	10	RATIRGTSM	M25862 Rat insulin
6	1490.4	62.5	2338	6	AX573334	AX573334 Sequence
7	1488.8	62.4	2338	6	AX573335	AX573335 Sequence
8	1416.6	62.3	2338	6	AX573336	AX573336 Sequence
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11	1378.2	57.8	2521	10	MUSGT2A	M23383 M.musculus
12	1241.8	52.0	1539	4	AF531753	AF531753 Equus cab
13	1229	51.5	7828	6	AX573331	AX573331 Sequence
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15	1214	50.9	2355	4	AX339876	AX339876 Oryctolag
16	1206.2	50.6	1544	4	AY458600	AY458600 Bos tauru
17	1191.8	49.9	2642	4	D63150	D63150 Bos tauru
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21	692.2	29.0	2894	5	AF247395	AF247395 Salmo tru
22	690.4	28.9	3137	5	AF502957	AF502957 Oncorhyn
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31	679	28.5	2856	6	AR281087	AR281087 Sequence
32	679	28.5	2856	6	AR437878	AR437878 Sequence
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45	600.6	25.2	2145	9	AK122999	AK122999 Homo sapi

ALIGNMENTS

RESULT 1	AX573332	AX573332	2386 bp	DNA	linear	PAT 29-NOV-2002
LOCUS	Sequence 10 from Patent WO02064784.					
DEFINITION	Sequence 10 from Patent WO02064784.					
ACCESSION	AX573332					
VERSION	AX573332.1	GI:26005218				
KEYWORDS	Rattus norvegicus (Norway rat)					
SOURCE	Rattus norvegicus					
ORGANISM	Rattus norvegicus					
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;					
	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;					
	Rattus.					
REFERENCE	1					
AUTHORS	Mueller,G., Koller,K.P., Boles,E., Wiczorke,R. and Dlugai,S.					
TITLE	Yeast strain of saccharomyces cerevisiae with functional expression					

of a glut transporter
JOURNAL Patent: WO 02064784-A 10 23-AUG-2002;
Aventis Pharma Deutschland GmbH (DE)
FEATURES Location/Qualifiers
source
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/mol_type="unassigned DNA"
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ORIGIN

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Best Local Similarity 100.0%; Pred. No. 0;
Matches 2386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB |||||
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DB |||||

QY 61 TAACTCAATAAAATTTTCGAAATCCTTTTCTTACGGTCTTTCTTCGGGAACCTAGATAG 120
DB |||||

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DB |||||

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DB |||||

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DB |||||

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QY 181 GTTTTGGCATGGCAACGAGGGCTGGAAATTAACGGTAGCGCGCTTAACGATAGTAA 240
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QY 241 TAGGCACCACTGCGGTGAGCAACAATAAGTCCGCATTTTATGTTTTTCAAAA 300
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RESULT 2
RNIRG LOCUS RNIRG 2086 bp mRNA linear ROD 12-SEP-1993
DEFINITION Rat mRNA for insulin-regulatable glucose transport (IRGT).
ACCESSION X14771
VERSION X14771.1 GI:56501
KEYWORDS glucose transport.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.

REFERENCE 1 (bases 1 to 2086)
AUTHORS James,D.E., Strube,M. and Mueckler,M.
TITLE Molecular cloning and characterization of an insulin-regulatable
glucose transporter
JOURNAL Nature 338 (6210), 83-87 (1989)
MEDLINE 89143771
PUBMED 2645527
COMMENT Data kindly reviewed (23-MAY-1990) by Mueckler M.
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QY 2015 GTCCCATCATCTC 2027
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Db |||||

RESULT 3
RATIRGT
LOCUS Rat insulin-responsive glucose transporter (GT) mRNA, complete cds.
DEFINITION
ACCESSION J04524
VERSION J04524.1 GI:204979
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Rattus.
REFERENCE 1 (bases 1 to 2482)
AUTHORS Charron,M.J., Brosius,F.C. III, Alper,S.L. and Lodish,H.P.
TITLE A glucose transport protein expressed predominately in insulin-responsive tissues
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 86 (8), 2535-2539 (1989)
MEDLINE 89202363
FUBMED 2649883
COMMENT Original source text: Rattus norvegicus (strain Sprague-Dawley) male soleus cDNA to mRNA.
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QY	1535	CCTGGCAGCATGTGTGGCTGTGCCATCTTGATGACGGTGGCTGTGCTGTGGAGCG	1594
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LOCUS			
DEFINITION			
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ACCESSION			
M25482			
VERSION			
M25482.1 GI:537942			
KEYWORDS			
glucose transporter protein.			
SOURCE			
Rattus norvegicus (Norway rat)			
ORGANISM			
Rattus norvegicus			
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;			
Rattus.			
REFERENCE			
1 (bases 1 to 2447)			
AUTHORS			
Birnbaum,M.J.			
TITLE			
Identification of a novel gene encoding an insulin-responsive			
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JOURNAL			
Cell 57 (2), 305-315 (1989)			
MEDLINE			
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PUBMED			
2649253			
COMMENT			
On Sep 14, 1994 this sequence version replaced gi:341356.			
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Qy	575	TCAGTTGGCTATAAACATTGGAGTCAATCAACGCCCCACAGAAAGTGATGAAACAGAGCTA	634
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Qy	875	GATACTCAATTTCCGGAACGGTTCCCTCATTTGGCGCCTACTCAGGGGTAAACATCAGGGTTGGT	934
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Qy	1175	GGAGGGGCTGCCCCGAAAGAGTCTAAAGCGCTGACAGGCTGGGCTGATGTGTCTGATGC	1234
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Db	993	GAGCCAGAGCTCTCAGGCATCAATGTGTTTTTCTACTATTTCACACAGCATCTTTGAGTT	1052
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QY	1955	CAGTACAGAACTTGAATATCTTAGGGCCAGATGAGAATGACTAATCGATTGAAGTGAGAC	2014
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DEFINITION	Sequence 12 from Patent WO02064784.		
ACCESSION	AX573334		
VERSION	AX573334.1	GI:26005220	
KEYWORDS	Rattus norvegicus (Norway rat)		
SOURCE	Rattus norvegicus		
ORGANISM	Rattus norvegicus		
REFERENCE	1		
AUTHORS	Mueller, G., Koller, K.P., Boles, E., Wieszorke, R. and Dlugai, S.		
TITLE	Yeast strain of saccharomycetes cerevisiae with functional expression of a glut transporter		
JOURNAL	Patent: WO 02064784-A 12 22-AUG-2002;		
	Aventis Pharma Deutschland GmbH (DE)		
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RESULT 7

AX573335
LOCUS AX573335 2338 bp DNA linear PAT 29-NOV-2002
DEFINITION Sequence 13 from Patent WO02064784.
ACCESSION AX573335
VERSION AX573335.1 GI:26005221
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
REFERENCE 1
AUTHORS Mueller, G., Koller, K.P., Boles, E., Wiczorke, R. and Dlugai, S.
TITLE Yeast strain of saccharomyces cerevisiae with functional expression of a glut transporter
JOURNAL Patent: WO 02064784-A 13 22-AUG-2002;
Aventis Pharma Deutschland GmbH (DE)
FEATURES
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Best Local Similarity 77.8%; Pred. No. 0;
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DEFINITION Sequence 14 from Patent W002064784.
ACCESSION AX573336
VERSION AX573336.1 GI:26005222
KEYWORDS Rattus norvegicus (Norway rat)
SOURCE Rattus norvegicus
ORGANISM Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1
AUTHORS Mueller,G., Koller,K.P., Boles,E., Wiczorke,R. and Dlugai,S.
TITLE Yeast strain of saccharomyces cerevisiae with functional expression
of a glut transporter
JOURNAL Patent: WO 02064784-A 14 22-AUG-2002;
Aventis Pharma Deutschland GmbH (DE)
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RESULT 9

BC014282

LOCUS

DEFINITION

BC014282

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

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TITLE

BC014282 2556 bp mRNA linear ROD 04-OCT-2003
Mus musculus solute carrier family 2 (facilitated glucose transporter), member 4, mRNA (CDNA clone MGC:13736 IMAGE:4207674), complete cds.

BC014282

BC014282.1 GI:15679950

MGC.

Mus musculus (house mouse)

Mus musculus

Mammalia; Eutheria; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

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Straussberg R.L., Collins, F.S., Wagner, L., Shennan, C.M., Schuler, G.D.,

Klausner, R.D., Zebner, B., Buetow, K.H., Schaefer, C.F., Bhat, N.K.,

Hopkins, R.F., Jordan, H., Moore, T., Max, S.I., Wang, J., Hsieh, F.,

Diatchenko, L., Marusina, K., Farmer, A.A., Rubin, G.M., Hong, L.,

Stapleton, M., Soares, M.B., Bonaldo, M.P., Casavant, T.L.,

Schetz, T.E., Brownstein, M.J., Udwin, T.B., Toshiki, S.,

Carninci, P., Prange, C., Raha, S.S., Loquellano, N.A., Peters, G.J.,

Abramson, R.D., Mullaly, S.J., Bosak, S.A., McSwan, P.J.,

McKernan, K.J., Malek, J.A., Gunaratne, P.H., Richards, S.,

Worley, K.C., Hale, S., Garcia, A.M., Gay, L.J., Hulyk, S.W.,

Villalón, D.K., Muzny, D.M., Sodergren, E.J., Lu, X., Gibbs, R.A.,

Fahey, J., Helton, E., Kettman, M., Madan, A., Rodriguez, S.,

Sanchez, J., Whiting, M., Madan, A., Young, A.C., Shevchenko, Y.,

Dufford, G.G., Blakesley, R.W., Touchman, J.W., Green, E.D.,

Bickson, M.C., Rodriguez, A.C., Grimwood, J., Schmutz, J., Myers, R.M.,

Butterfield, Y.S., Krzywinski, M.I., Skalska, U., Smal, D.E.,

Schnerf, A., Schein, J.E., Jones, S.J. and Marra, M.A.

Generation and initial analysis of more than 15,000 full-length

human and mouse cDNA sequences

Proc. Natl. Acad. Sci. U.S.A. 99 (26), 16899-16903 (2002)

22388257

12477932

2 (bases 1 to 2556)

Straussberg, R.

Direct Submission

Submitted (17-SEP-2001) National Institutes of Health, Mammalian

Gene Collection (MGC), Cancer Genomics Office, National Cancer

Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590,

USA

NIH-MGC Project URL: <http://mgc.nci.nih.gov>

Contact: MGC help desk

Email: cgabs-remail.nih.gov

Tissue Procurement: Jeffrey E. Green, M.D.

cDNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)

DNA Sequencing by: Institute for Systems Biology

<http://www.systemsbio.org>Contact: amadansystemsbiology.org

Anup Madan, Jessica Fahey, Erin Helton, Mark Kettman, Anuradha

Madan, Stephanie Rodriguez, Amy Sanchez and Michelle Whiting

Clone distribution: MGC clone distribution information can be found

through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>

Series: IRAC Plate: 18 Row: m Column: 11

This clone was selected for full length sequencing because it passed the following selection criteria: Hexamer frequency ORF analysis, similarity but not identity to protein.

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QY 1535 CCTGGCAGGATGTGTGGCTGTGCCATCTTATGACGGTGGCTCTGCTGCTCTGGAGCG 1594
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QY 1595 GGTTCATCCATGAGTTATGTGTCATGCTGGCCATATTTGGCTTTGTGGCTTCTTTGA 1654
DB 1307 GGTTCAGCCATGAGTATGTCTCATCGTGGCCATATTTGGCTTTGTGGCTTCTTTGA 1366
QY 1655 GATTGGTCTGGGCCCATCCCTGGTTTCATTTGCGCGAGCTCTTTCAGCAGCGGCCCCCG 1714
DB 1367 GATTGGGCCCTGGGCCCATTCCTCGTTTCATTTGGCAGAGCTCTTTCAGCAGCGGCCCCCG 1426
QY 1715 CCCAGCAGCATGGCTGTAGCTGGTTTCTCCAACTGGACCTGTAACTTTCATCGTTGGCAT 1774
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RESULT 11
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LOCUS M.musculus glucose transporter 2 mRNA, complete cds.
DEFINITION M23383 J04557
ACCESSION M23383.1 GI:193706
VERSION glucose transporter type 2.
KEYWORDS Mus musculus (house mouse)
SOURCE Mus musculus
ORGANISM Mus musculus
REFERENCE 1. (bases 1 to 2521)
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
Kaelstner, K.H., Christy, R.J., McLenithan, J.C., Braiterman, L.T.,
Cornelius, P., Pekala, P.H. and Lane, M.D.
TITLE Sequence, tissue distribution, and differential expression of mRNA
for a putative insulin-responsive glucose transporter in mouse
3T3-L1 adipocytes
JOURNAL Proc. Natl. Acad. Sci. U.S.A. 86 (9), 3150-3154 (1989)
MEDLINE 89240694
PUBMED 2654938
COMMENT Original source text: M.musculus adipocyte cell line 3T3-L1, cDNA
to mRNA.
Draft entry and computer-readable sequence for [1] kindly provided
by M. Lane, 28-MAR-1989.

FEATURES
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Query Match 57.8%; Score 1378.2; DB 10; Length 2521;
Best Local Similarity 94.1%; Pred. No. 0;
Matches 1457; Conservative 0; Mismatches 83; Indels 9; Gaps 2;

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Qy 1349 GCAGCTGAGCAGCAGCTCTCAGGCACTCAATGCTGTTTCTACTACTTCAACCGCATCTT 1408
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Qy 1409 TGAGTTAGCTGGGGTGGAAACGAGCAGCTACGCCACCATAGAGCTGGTGTGGTCAATAC 1468
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 DB 1518 CGTCTCTCTGCTGCTTCTTCACTTCTTCACTTCTTCAAGAGTGCCTGAACACAGAGCCG 1577
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 DB 1578 GACGTTTGACAGATCTCAGCTGCTTTCGACGAGACCTTCTCTTTAGAGCAGGAGT 1637
 QY 1949 GAAACCCAGTACAGACTTGAATCTTATAGGCCAGATGAGACTAA 1997
 DB 1638 GAAACCCAGTACAGACTTGAATCTTATAGGCCAGATGAGACTGA 1686

RESULT 12

AF531753
 LOCUS
 DEFINITION Equus caballus glucose transporter type 4 (GLUT4) mRNA, complete cds.

ACCESSION AF531753.1 GI:22347677

VERSION

KEYWORDS

SOURCE

ORGANISM

Equus caballus (horse)

Equus caballus

Mammalia; Eutheria; Perissodactyla; Equidae; Equus.

1 (bases 1 to 1539)

Jose-Cunilleras, E., Hayes, K.A., Toribio, R.E., Mathes, L.E. and Hinchcliff, K.W.

Equus caballus insulin-responsive glucose transporter, glucose transporter type 4 (GLUT4) mRNA

Unpublished

2 (bases 1 to 1539)

Jose-Cunilleras, E., Hayes, K.A., Toribio, R.E., Mathes, L.E. and Hinchcliff, K.W.

Direct Submission

Submitted (21-JUL-2002) Veterinary Clinical Sciences, The Ohio State University, 601 Vernon L. Tharp St, Columbus, OH 43210, USA

Location/Qualifiers

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/organism="Equus caballus"

/mol_type="mRNA"

/db_xref="taxon:9796"

/tissue_type="skeletal muscle"

1. .1539

/gene="GLUT4"

8. .1537

/gene="GLUT4"

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ORIGIN

Query Match 52.0%; Score 1241.8; DB 4; Length 1539;
 Best Local Similarity 87.9%; Pred. No. 1.3e-288;
 Matches 1351; Conservative 2; Mismatches 184; Indels 0; Gaps 0;

QY 461 AAGCAACNTAATCTCTGAATTCAGCAGATCGGCTCTGAGATGGGAAACCCCTCAGCA 520
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 DB 61 GCAGTGAATCTGGGACACTGGTCTCTCGCAGTATTTCTGTGTGCTTGGCTCCCTTCAGTT 120
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RESULT 14

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HUMIRGT LOCUS HUMIRGT
DEFINITION Human insulin-responsive glucose transporter (GLUT4) mRNA, complete cds.
ACCESSION M20747.1 GI:186552
VERSION M20747.1
KEYWORDS insulin-responsive glucose transporter.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 2128)
AUTHORS Fukumoto,H., Kayano,T., Buse,J.B., Edwards,Y., Pilch,P.F., Bell,G.I. and Seino,S.
TITLE Cloning and characterization of the major insulin-responsive glucose transporter expressed in human skeletal muscle and other insulin-responsive tissues
JOURNAL J. Biol. Chem. 264 (14), 7776-7779 (1989)
MEDLINE 89255193
PUBMED 2656669
COMMENT Original source text: Human jejunum and muscle, cDNA to mRNA, clones lambda-h-[JHT-3, AMT-6, FWT-1].
Draft entry and computer-readable sequence for [1] kindly provided by G.I.Bell. 19-APR-1989.
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Best Local Similarity 86.2%; Pred. No. 1.9e-285;
Matches 1359; Conservative 0; Mismatches 217; Indels 0; Gaps 0;
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QY 575 TCAGTTTGGCTATAACATTGGAGTCAATCAACGCCCCACAGAAAGTGAATGAACAGAGCTA 634
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QY 733 GGGCACTTGCAGCTGTGGCCACTGCTTCTTGGGCTCAGAGTGTCTGCTGCTCTCTGCA 792
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QY 853 CGAGGGGCTGCCGAAAGAGTCTGAAAGCGCTGACAGGCTGGGCGGATTTCTGAGT 912
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 Db |||||
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 ACCESSION AY339876
 VERSION AY339876.1 GI:37813341
 KEYWORDS Oryctolagus cuniculus (rabbit)
 SOURCE Oryctolagus cuniculus
 ORGANISM Oryctolagus cuniculus
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 REFERENCE 1 (bases 1 to 2355)
 AUTHORS Navarrete Santos,A., Kirstein,M. and Fischer,B.
 TITLE Two insulin-responsive glucose transporter isoforms and the insulin receptor are developmentally expressed in rabbit preimplantation embryos
 JOURNAL Unpublished
 REFERENCE 2 (bases 1 to 2355)
 AUTHORS Navarrete Santos,A., Kirstein,M. and Fischer,B.

Direct Submission
 Submitted (11-JUL-2003) Anatomy and Cell Biology, Martin Luther University Halle-Wittenberg, Gr. Steinstrasse 52, Halle (Saale), Sachsen-Anhalt 06097, Germany
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 CDS 1. 1530
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 QY 61 ACCGGAACCTCGTCTCGCGGTGTTCTCAGCCGTGCTTGGGTCCCTCAGTTTGGCTAC 120
 QY 588 AACATTGGAGTCATCAACGCCCCACAGAAAGTGAATGAACAGAGCTACAATCAACTTGG 647
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 QY 121 AACATTGGGTTCATCATGTGCCCCGACAGAGTGTGAGCAGAGAGCTACAATGAGACCTGG 180
 QY 648 CTGGGTAGGCGAGGTCTCTGGGGGACCGGATCTCCATCCCAAGGCAACCTCACTACCTTT 707
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 QY 181 CTCGGAGGCGAGGGGCCGAGGGACCGGCTCCATCCCGCCGCGGACCTCAACCACTC 240
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 QY 241 TGGGCCCTCTCTGTGGCCATCTTCTCGTGGGCGCATGATTTCTCTCTTCTCATCGGC 300
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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 15, 2004, 22:27:02 ; Search time 556.671 Seconds
(without alignments)
18208.601 Million cell updates/sec

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Scoring table: IDENTITY_NUC

Gapop 10.0 , Gapext 1.0

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Total number of hits satisfying chosen parameters: 6747726

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Post-processing: Minimum Match 0%
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Listing first 45 summaries

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8: Geneseqn2003bs:*
9: Geneseqn2003cs:*
10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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3	1488.8	62.4	2338	6 AAL49314	Aal49314 Rat Glut1
4	1485.6	62.3	2338	6 AAL49315	Aal49315 Rat Glut1
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10	679	28.5	2544	6 ABI99628	Abi99628 Mouse isc
11	679	28.5	2571	9 ADB53698	AdB53698 Primary r
12	679	28.5	2854	7 ABX74453	Abx74453 Human cDN
13	679	28.5	2856	3 AAC65871	Aac65871 Human lun
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15	679	28.5	2856	6 ABV77983	Abv77983 Hypoxia-r
16	679	28.5	2856	6 ABL49090	AbL49090 Human lun
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19	679	28.5	2856	7 ABX76166	Abx76166 Lung canc
20	679	28.5	2856	8 ADA28225	Ada28225 Human lun
21	679	28.5	2856	9 ADE53430	AdE53430 Human lun
22	679	28.5	2893	5 AAF98714	Aaf98714 Human lat
23	679	28.5	3366	6 ABZ35362	Abz35362 Human gen

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25	678.2	28.4	2778	7 ABT31931	Abt31931 Human bre
26	670.2	28.1	2613	6 ABS51821	Abs51821 Novel hum
27	667.4	28.0	2683	6 ABS51820	Abs51820 Novel hum
28	663	27.8	2349	6 ABK35243	Abk35243 Human cDN
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31	631.8	26.5	2850	2 AAZ24632	Aaz24632 Human lun
32	589	22.7	3046	6 ABS51824	Abs51824 Novel hum
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34	542.8	22.7	3915	6 ABK83953	Abk83953 Human cDN
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38	477.2	20.0	1527	9 ADC39215	AdC39215 Novel hum
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40	464.6	19.5	2126	6 ABQ76439	Abq76439 S. cerevi
41	456.2	19.1	3168	6 ABN95601	Abn95601 Gene #209
42	456.2	19.1	3168	6 ABS59538	Abs59538 Human cDN
43	456.2	19.1	3439	9 ADD29802	Add29802 Human tum
44	454.8	19.1	1943	2 AAT66496	Aat66496 Rat gluco
45	454.8	19.1	2573	7 ABT41856	Abt41856 Toxicity

ALIGNMENTS

RESULT 1

AAL49311

ID AAL49311 standard; DNA; 2386 BP.

XX AC AAL49311;

DT 07-NOV-2002 (first entry)

XX DE Rat Glut4 containing vector H2rg4g2.

XX KW Rat; Yeast; GLUT4; glut transporter; hexose; antidiabetic; anorectic;

XX OS Rattus norvegicus.

XX PN WO200264784-A2.

XX PD 22-AUG-2002.

XX PF 09-FEB-2002; 2002WO-EP001373.

XX PR 14-FEB-2001; 2001DE-01006718.

XX (AVET) AVENTIS PHARMA DEUT GMBH.

XX PI Mueller G, Koller K, Boles E, Wleczorke R, Dlugai S;

XX DR WPI; 2002-636632/68.

XX PT New strains of yeast, useful in screening for modulators of hexose

XX PT transport, potential antidiabetic and antioesity agents, lack native

XX PT hexose-transport function.

XX PS Claim 10; Page 36-37; 58pp; German.

XX CC The present invention relates to a strain of Saccharomyces cerevisiae
that cannot grow on a substrate containing hexose as the only source of
carbon but the ability to grow on such substrates is restored when the
GLUT4 gene is expressed. A strain transformed to express the GLUT1 or
GLUT4 genes can be used to identify compounds that increase/reduce hexose
transport by these proteins. These compounds, optionally after
development, are potential drugs for treating diabetes and obesity. The
present sequence is a vector containing the rat Glut4 coding sequence as
used in the invention

XX SQ Sequence 2386 BP; 560 A; 610 C; 542 G; 674 T; 0 U; 0 Other;

Query Match				100.0%; Score 2386; DB 6; Length 2386;			
Best Local Similarity				100.0%; Pred. No. 0;			
Matches 2386; Conservative 0; Mismatches 0; Indels 0; Gaps 0;							
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Qy	181	GTTTTTGCGATGGCAAGCGGCTGGAAAATTAACGGTACGCGCCTAAACGATAGTAA	240				
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Qy	301	CCTAGCAACCCACCAAACTTGTCATCGTTCCGGATTCAAAATGATATAAAAAGCGA	360				
Db	301	CCTAGCAACCCACCAAACTTGTCATCGTTCCGGATTCAAAATGATATAAAAAGCGA	360				
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Db	421	GATTTAAGAACACAAATTAATAAATTAAGAAAGCTTATAAGCAACAATATGTCGAAT	480				
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Db	601	TCAAAGCCCCACAGAAAGTGATGAACAGAGCTAACAATGCAACTTGGCTAGGCAAGG	660				
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Qy	841	TCAATGGGCTAGCCAAATGCGGGCTCTATGAGATACTCATTTCTCGGAGGGTCTCTCA	900				
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RESULT 2
AAL49313
ID AAL49313 standard; DNA; 2338 BP.
XX
AC AAL49313;
XX
DT 07-NOV-2002 (first entry)
DE Rat Glut1 containing vector H2rg1g2.
XX
KW Rat; yeast; GLUT4; glut transporter; hexose; antidiabetic; anorectic;
XX vector; ds.
XX
OS Rattus norvegicus.
XX
PN W0200264784-A2.
XX
PD 22-AUG-2002.
XX
PF 09-FEB-2002; 2002WO-EP001373.
XX
PR 14-FEB-2001; 2001DE-01006718.
XX
PA (AVET ) AVENTIS PHARMA DEUT GMBH.
XX
PI Mueller G, Koller K, Boles E, Wieczorke R, Dlugai S;
XX
DR WPI; 2002-636632/68.
XX
PT New strains of yeast, useful in screening for modulators of hexose
PT transport, potential antidiabetic and antiobesity agents, lack native
PT hexose-transport function.
XX
PS Example; Page 40-41; 58pp; German.
XX
CC The present invention relates to a strain of Saccharomyces cerevisiae
CC that cannot grow on a substrate containing hexose as the only source of
CC carbon but the ability to grow on such substrates is restored when the
CC GLUT4 gene is expressed. A strain transformed to express the GLUT1 or
CC GLUT4 genes can be used to identify compounds that increase/reduce hexose
CC transport by these proteins. These compounds, optionally after
CC development, are potential drugs for treating diabetes and obesity. The
CC present sequence is a vector containing the rat Glut1 coding sequence as
CC used in the invention
XX
SQ Sequence 2338 BP; 538 A; 611 C; 539 G; 650 T; 0 U; 0 Other;

Query Match 62.5%; Score 1490.4; DB 6; Length 2338;
Best Local Similarity 77.8%; Pred. No. 0;
Matches 1857; Conservative 0; Mismatches 481; Indels 48; Gaps 3;

Qy 1 TCAGCTCTAGAGGATCCCTTAAGCTAATCCTTTATGAATCCGCGAGAAACGGGGTCTTT 60
|||
61 TAACTCAATAAATATTTTCGAAATCCTTTTCTAGCGGTTTCTTCGGAACCTAGATAG 120
|||
61 TAACTCAATAAATATTTTCGAAATCCTTTTCTAGCGGTTTCTTCGGAACCTAGATAG 120
|||
121 GTGGCTCTTCCACCTGTTTTCATCATTTTGTAGTTTTCGCAAGCATATGGGTGCTTTTC 180
|||
121 GTGGCTCTTCCACCTGTTTTCATCATTTTGTAGTTTTCGCAAGCATATGGGTGCTTTTC 180
|||
181 GTTTTTCGCGATGCGAAGCGAGGCTCGAAAAATTAACGGTACCGCGCTAAACGATAGTAA 240
|||
181 GTTTTTCGCGATGCGAAGCGAGGCTCGAAAAATTAACGGTACCGCGCTAAACGATAGTAA 240
|||
241 TAGGCCACGCAACTGCGGTGGACGACAAATAAGTCGCCCATTTTTATGTTTCAAAA 300
|||
241 TAGGCCACGCAACTGCGGTGGACGACAAATAAGTCGCCCATTTTTATGTTTCAAAA 300
|||
301 CTAGCAACCCGCCAACCAACTTGTCTATCGTTCGGGATTCACAAATGATATAAAGCGGA 360
|||
301 CTAGCAACCCGCCAACCAACTTGTCTATCGTTCGGGATTCACAAATGATATAAAGCGGA 360
|||
361 TTACAATTTTACATTTCTAACCAGATTGAGATTTCTCTTTTCAATTTCTCTTATATTA 420
|||
361 TTACAATTTTACATTTCTAACCAGATTGAGATTTCTCTTTTCAATTTCTCTTATATTA 420
|||
421 GATTATAAGAAACAAACAAATTAATAATTAACAAAGACTTATAAAGCAACATATGCTGAAT 480
|||
421 GATTATAAGAAACAAACAAATTAATAATTAACAAAGACTTATAAAGCAACATATGCTGAAT 480
|||
481 TCAGCAAGATCGGCTCTGAAGATGGGGAACCCCTCAGCAGCGAGTGACTGGGACACTGG 540
|||
481 TCAGCAAGATCGGCTCTGAAGATGGGGAACCCCTCAGCAGCGAGTGACTGGGACACTGG 540
|||
541 TCCTTGTCTGATTTCTCAGCTGTGCTTGGCTCCCTTCAGTTTGGCTATATTAACATTTGAGTCA 600
|||
508 TGTGGCGTGGGAGGGGCGAGTGTCTCGGATCCCTGCGAGTTCCGCTATAAACCGGTTGCTCA 567
|||
601 TCAACGCCCCACAGAAAGTGAATGAACAGAGCTTACAACTGCAACTTGGCTGGTAGGCAGG 660
|||
568 TCAACGCCCCACAGAAAGTGAATGAAGAGTTTCTACATCAACATGAACACCGCTATG 627
|||
661 GTCTTGGGGACCGGACTCCATCCCAAGGCAACCTCAGTACCTTTTGGGCTCTCTCCG 720
|||
628 G-----AGAGTCCATCCATCCACCACTCACCACACTCTGCTCTCTCTCCG 675
|||
721 TGGCCATCTTCTGTGGGTGGCATGATTTCTCTCTCTCTCATTGGCATCATTTCTCAAT 780
|||
676 TGGCCATCTTCTGTGGGTGGCATGATTTCTCTCTCTCTCTCTGTTGTTTAAATC 735
|||
781 GGTGGGAAGGAAAGGGCTATCTCTGGCCCAACAAATGTCTTGGCTGTGCTGGGGGGCGCC 840
|||
736 GCTTTGGCAGGCGGAACCTCACTGATGATGAACCTGTTGGCTTGTGCTGCGGTGC 795
|||
841 TCATGGGCTAGCCAAATGCGCGGCTCTCTATGAGATATCTCATTCGCGAGCGTTCTCTCA 900
|||
796 TTATGGGTTTCTCCAAACTGGGCAAGTCTCTTGGATGCTGATCTCTGGGCGCTTCAATCA 855
|||
901 TTGGCGCTTACTCAGGCTTAAACATCAGGTTGGTGTCTATGATGCGGAGAAATCGCCC 960
|||
856 TTGGAGTGTACTGTGGCGCTGACCCCGGCTTGTGCCCCTATGATGTTGGGGAGGTGTAC 915
|||
961 CCACTCATCTTGGGGTGTCTTGGGAACACTCAACAAATTTGGGCATCGTCAATTTGGCATTC 1020
|||
916 CCACAGCTCTTGTGGAGGCGCTGGGACCTGACACAGCTGGGCACTGTTGGGATCC 975
|||
1021 TGGTTCGCCAGGTGTTGGGTTTGGAGTCTATGCTGGGCAAGTACCTCTGCGCAATGTC 1080
|||
976 TTATTGCCAGAGGTTTGGGCTTAGACTCTCATATGCGCAATGAGACTTGTGCGCTCTAC 1035
|||
1081 TTCTGCTATCAGAGTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1140
|||
1036 TGCTCAGTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1095
|||
```


QY 121 GTGGCTCTCCACTGTTTTCATCATTTTGTGTTTTCGCAAGCAATGCGTCCCTTTTC 180
DB 121 GTGGCTCTCCACTGTTTTCATCATTTTGTGTTTTCGCAAGCAATGCGTCCCTTTTC 180
QY 181 GTTTTTCGATGCGACGAGGCTGGAATAATTAACGGTACCGCCCTTAACCATAGTAA 240
DB 181 GTTTTTCGATGCGACGAGGCTGGAATAATTAACGGTACCGCCCTTAACCATAGTAA 240
QY 241 TAGGCCACGCAACTGGCGTGGAGGACCAACAATAAGTGGCCCATTTTATGTTTCAAAA 300
DB 241 TAGGCCACGCAACTGGCGTGGAGGACCAACAATAAGTGGCCCATTTTATGTTTCAAAA 300
QY 301 CTTAGCAACCCCAACCAACTGTTGATCGTTCGGGATTCACAAATGATATAAAGGCGA 360
DB 301 CTTAGCAACCCCAACCAACTGTTGATCGTTCGGGATTCACAAATGATATAAAGGCGA 360
QY 361 TTACAATTTACATTTCAACGAGATTTGAGATTTCTCTCTTCTCAATTTCTCTATATTA 420
DB 361 TTACAATTTACATTTCAACGAGATTTGAGATTTCTCTCTTCTCAATTTCTCTATATTA 420
QY 421 GATTATAAGAAACAAATAATTAATAAAGACTTTATAAAGCAACATAATGTCTGAAT 480
DB 421 GATTATAAGAAACAAATAATTAATAAAGACTTTATAAAGCAACATAATGTCTGAAT 480
QY 481 TCCAGCAGATCGGCTCTGAAGATGGGAAACCCCTCAGACGAGATGACTGGGACACTGG 540
DB 481 TCAGCAAGA-----AGGTGACGGGCGGCTTA 507
QY 541 TCCCTGCTGATTTCTCAGCTGCTGCTGGCTCCCTCAGTTTGGCTATAACATTTGGAGTCA 600
DB 508 TGTGGCGGTGGAGGGGAGTGTCTGGATCCCTGCGAGTTTGGCTATAAACCCGGTGTCA 567
QY 601 TCAACGCCCCCAGAGAGTGAATGAACAGAGCTACAAATGCAACTTGGCTGGTAGGCGAGG 660
DB 568 TCAACGCCCCCAGAGAGTGAATGAAGAGTGTCTACAAATCAACATGAACACCGCTATG 627
QY 661 GTCCTGGGGACCGGACTCCATCCCAACAGGACCTCTCACTACCTTTGGGCTCTCTCCG 720
DB 628 G-----AGAGTCCATCCCACTCCACCACTCAACCACTCTGGTCTCTCTCCA 675
QY 721 TGGCCATCTTCTGTGGGTGGATGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCAAT 780
DB 676 TGGCCATCTTCTGTGGGTGGATGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 735
QY 781 GGTGGGAAGAAAGGGCTATGTGGCCCAACAAATGTTGGCTGTGGTGGGGGGGGCCCC 840
DB 736 GCTTTGGCAGCGGAACTCATGCTGATGATGAACTGTTGGCTTGTGCTGCGGTGC 795
QY 841 TCATGGGCTTAGCCAAATGCGCGGCTCTCTATGAGATPACTATTCGGAAGGTTCCTCA 900
DB 796 TTATGGGTTTCTCCAACTGGGCAAGTCTTTGAGATGCTGATCTGGGCGGCTTCATCA 855
QY 901 TTGGCGCTTACTCAGGCTTAACATCAGGTTGCTGCTATGATGTTGGGGAATCGCCC 960
DB 856 TTGGAGTGATCTGGGCTTACCAACCGGCTTTGTGCCCATGATGTTGGGGAGGTGTAC 915
QY 961 CCACTCATCTTGGGGTGGCTTGGGAACACTCAACAAATTTGGCCATCGTCAATTTGGCATTC 1020
DB 916 CCACAGCTCTTGGGAGCCCTGGGACCCCTGCAACAGCTGGGCACTGTTGGGATCC 975
QY 1021 TGGTGGCCAGGTGTTGGGTTTGGAGTCTATGCTGGGCAAGCTACCTGTGGCCATGTC 1080
DB 976 TTATGGCCAGGTGTTGGGCTTAGACTCCATCATGAGCAATGAGCACTTGTGGGCTCTAC 1035
QY 1081 TTTGGGTATCACAGTACTCCCTGCTCTCTGAGCTGCTCTGTTGGCCCTCTGTCCTG 1140
DB 1036 TGCTCAGTGTCTCTCATCCAGGCTGCTACAGTGTATCTCTGTTGGCCCTCTGCGCTG 1095
QY 1141 AGAGCCCCCATCTCTCATCATCCGAACTGGAGGGGCTGCTGGGCAAGAGTCTAA 1200
DB 1096 AGAGCCCCCT 1155
QY 1201 AGCGCTGACAGGCTGGGCTGATGTGTCTGATGCACTGGCTGAGCTGAAGGATGAGAAC 1260

DB 1156 AAAAGCTTCGAGGGAAGAGAGGCTGCAACCGAGACCTGCGAGAGATGAAGAGAGGCTC 1215
QY 1261 GGAAGTTGAAAGAGAGAGGCTGCACTGCTCTGCTGAGCTCTCTGGGAGGAGCCGACCCACC 1320
DB 1216 GGCAGATGATGCGGAGAGAGAGGTCACCATCTTGGAGCTGTTCCGCTCAACCCGCTTACC 1275
QY 1321 GGCAGGCTCTGATTAATTTGAGTGGTCTGAGCTGAGCCAGCAGCTCTCAGGCAATCAATG 1380
DB 1276 GCCAGCCCATCTCTCATCGCGTGGTCTGAGCTGTCAGCTGTCAGCAGCTGTCGAGCATCAATG 1335
QY 1381 CTGTTTTTACTATTTCAACAGCATCTTTGAGTGTAGCTGGGTGGAAACAGCCAGCTTACG 1440
DB 1336 CTGTGTTTACTACTCAACAGCATCTTCGAGAAGGAGGCTGTCAGCAGCTGCTGTATG 1395
QY 1441 CCACCATAGAGCTGCTGTTGTTGCTCAATACGCTCTTCACTGTTGCTCTGGTCTCTTAGTAG 1500
DB 1396 CCACCATGCTGCTGGGTATGCTCAACAGGCTTCACTGTTGTTGCTCTGCTGTTCTGCTGG 1455
QY 1501 AGCAGCTGGGAGCAGGACACTCCATCTCTGGGCTGGCAGGCACTGTGTGGCTGTGCCA 1560
DB 1456 AGCAGCTGGGCTGGGACCTGCACTCTCACTGCTGCTGGCTGGCATGGGGCTGTGCTG 1515
QY 1561 TCTTGATGAGGCTGCTGCTGCTGCTGAGAGGGGTTCACTCACTGAGTATGTGTCCA 1620
DB 1516 TGCTCATGACCATCGCCCTGGCCCTGCTGAGCAGCTGCCCCGATGTCTCTATCTGAGTA 1575
QY 1621 TCGTGCCCATTTTGGCTTTTGGCTCTCTTTCAGATGCTGCTGCTGCTGCTGCTGCTGCT 1680
DB 1576 TCGTGCCCATTTTGGCTTTTGGCTCTCTTTCAGATGCTGCTGCTGCTGCTGCTGCTGCT 1635
QY 1681 TCAATTGTCGCGAGCTCTTTCAGCAGGCGCCCGCCAGCAGCAGCTGCTGTAGTGTGTT 1740
DB 1636 TCAATTGTCGCGAGCTGTTTCAGCAGGCGCGCCGACCTGCTGCTGCTGCTGCTGCTGCT 1695
QY 1741 TCTCAGCTGAGCTGTAATCTTTCATCTGTTGGCATGAGGTTTCCAGTATGTTGCGGATGCTA 1800
DB 1696 TCTCTAACTGGACCTCAAACTTCATCTGTCGCGCACTGTCTTCCAAATATGTGGAGCACTGT 1755
QY 1801 TGGGCTCCCTAGCTTCTCTTCTTATTTGCGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCT 1860
DB 1756 GTGGCCCCCTAGCTTCTTCTCATCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1815
QY 1861 TCTAAGAGTGTCTGAAACAGAGGCGGCACTTTGACAGAGCTCTGCGCCACCTTCCGAC 1920
DB 1816 ACTTCAAAGTCTCTGAGACCAAGGCGGACCTTTCATGAGATGCTTCCGGCTTCCGGC 1875
QY 1921 GGCACCTTCTCTTAGAGCAGGAGGTGAACCCAGTACAGAACTTTGAATATCTTAGGGC 1980
DB 1876 AGGGGGTGC---CAGCCAGAGCGCAAGACACTGAGGAGCTCTTCCACCTCTGGGG 1932
QY 1981 CAGATGAGAACTGAATAATCGATTTGAAGTGAGAGCTCCATCATCTCTCTTAATTTTCA 2040
DB 1933 CTGACTCCCAAGTGAATCGATTTGAAGTGAGAGCTCCATCATCTCTCTTAATTTTCA 1992
QY 2041 TGACTGACGTTTTTCTCTCAATTAATATCATAGTATTTGTTGAAAAAAGAAAAA 2100
DB 1993 TGACTGACGTTTTTCTCTCAATTAATATCATAGTATTTGTTGAAAAAAGAAAAA 2052
QY 2101 AATTTCCCTTATCAATGATATCTTACGATATATAAATTTCTTACCTAAACCTATTTAT 2160
DB 2053 AATTTCCCTTATCAATGATATCTTACGATATATAAATTTCTTACCTAAACCTATTTAT 2112
QY 2161 TGTGTACATATACAGATATTAATACATATAAAGCTTTTCTCTAAAAACAGAAAAA 2220
DB 2113 TGTGTACATATACAGATATTAATACATATAAAGCTTTTCTCTAAAAACAGAAAAA 2172
QY 2221 AAAAGAAAAAGTAAACATGCTCTGCCATCTTTGTTTCCGAGCAAAATTTAAAAACGCAA 2280
DB 2173 AAAAGAAAAAGTAAACATGCTCTGCCATCTTTGTTTCCGAGCAAAATTTAAAAACGCAA 2232
QY 2281 AATGAATTTGCTCCCTATGAATTTATTAAGGACCAATCACTACAGACTTATCTCTGGGGGT 2340

Db 2233 AATGAATTGTCCTATGAAATTAATAAGGACCAATCACCAGACTTATCTCTGGGGGT 2292
 Qy 2341 CCTCTAGAAATAAGCTAGGCTACCTGCTGACCTTCTTCAGTTG 2386
 Db 2293 CCTCTAGAAATAAGCTAGGCTACCTGCTGACCTTCTTCAGTTG 2338
 RESULT 4
 AAL49315
 ID AAL49315 standard; DNA; 2338 BP.
 AC AAL49315;
 XX AAL49315;
 XX 07-NOV-2002 (first entry)
 DT
 XX Rat Glut1 mutant 70M coding sequence.
 DE
 XX Rat; yeast; GLUT4; glut transporter; hexose; antidiabetic; anorectic;
 KW vector; mutant; ds.
 KW
 OS Rattus norvegicus.
 OS Synthetic.
 XX
 PN W0200264784-A2.
 XX
 PD 22-AUG-2002.
 XX
 PF 09-FEB-2002; 2002WO-EP001373.
 XX
 PR 14-FEB-2001; 2001DE-01006718.
 XX
 XX (AVET) AVENTIS PHARMA DEUT GMBH.
 PA
 PI Mueller G, Koller K, Boles E, Wiczorke R, Dlugai S;
 XX
 DR WPI; 2002-636632/68.
 XX
 PT New strains of yeast, useful in screening for modulators of hexose
 PT transport, potential antidiabetic and antiobesity agents, lack native
 PT hexose-transport function.
 XX
 PS Claim 24; Page 42-43; 58pp; German.
 XX
 CC The present invention relates to a strain of *Saccharomyces cerevisiae*
 CC that cannot grow on a substrate containing hexose as the only source of
 CC carbon but the ability to grow on such substrates is restored when the
 CC GLUT4 gene is expressed. A strain transformed to express the GLUT1 or
 CC GLUT4 genes can be used to identify compounds that increase/reduce hexose
 CC transport by these proteins. These compounds, optionally after
 CC development, are potential drugs for treating diabetes and obesity. The
 CC present sequence is a mutant version of the rat Glut1 coding sequence as
 CC used in the invention
 XX
 SQ Sequence 2338 BP; 539 A; 609 C; 539 G; 651 T; 0 U; 0 Other;
 Query Match 62.3%; Score 1485.6; DB 6; Length 2338;
 Best Local Similarity 77.7%; Pred No. 0;
 Matches 1854; Conservative 0; Mismatches 484; Indels 48; Gaps 3;
 Qy 1 TCAGCTCTAGAGATCCCTTAAAGCTAATCCTTATGAATCCGAGAAAGCGGGTCTTT 60
 Db 1 TCAGCTCTAGAGATCCCTTAAAGCTAATCCTTATGAATCCGAGAAAGCGGGTCTTT 60
 Qy 61 TAACTCAATAAATTTTCGAAATCCTTTTCTACGGGTTTCTTCGGGAAGCTAGATAG 120
 Db 61 TAACTCAATAAATTTTCGAAATCCTTTTCTACGGGTTTCTTCGGGAAGCTAGATAG 120
 Qy 121 GTGGCTCTTCCACCTGTTTTCATCATTTAGTTTTCGCAAGCCATGCGTGCCTTTTC 180
 Db 121 GTGGCTCTTCCACCTGTTTTCATCATTTAGTTTTCGCAAGCCATGCGTGCCTTTTC 180
 Qy 181 GTTTTTCGATCGGCAACGAGGGCTGGAAAAATTAACGGTACGCGCTCAACGATAGTAA 240

Db 181 GTTTTTCGATGCGCAACGAGGGCTGGAAAAATTAACGGTACGCGCTCAACGATAGTAA 240
 Qy 241 TAGGCCACGCAACTGGCGTGGACGACCAATATAGTCCGCCATTTTATGTTTTCAAAA 300
 Db 241 TAGGCCACGCAACTGGCGTGGACGACCAATATAGTCCGCCATTTTATGTTTTCAAAA 300
 Qy 301 CCTAGCAACCCCAACCAACTTGTATCTGTTCCGGATTACAAATGATATATAAAGCGA 360
 Db 301 CCTAGCAACCCCAACCAACTTGTATCTGTTCCGGATTACAAATGATATATAAAGCGA 360
 Qy 361 TTACAATTTCTACATTTCTAACCCAGATTTGAGATTTCTCTCAATTTCTCTTATATTA 420
 Db 361 TTACAATTTCTACATTTCTAACCCAGATTTGAGATTTCTCTCAATTTCTCTTATATTA 420
 Qy 421 GATTATAGCAACAATAATTAATAAAGACTTATAAAGCAATTAAGCAATGATCTGAAT 480
 Db 421 GATTATAGCAACAATAATTAATAAAGACTTATAAAGCAATTAAGCAATGATCTGAAT 480
 Qy 481 TCCAGCAGATCGGCTCTGAAGATGGGAACCCCTCAGACGAGTGAATGGGACACTGG 540
 Db 481 TCAGCAAGA-----AGTGACGGGCGCCCTTA 507
 Qy 541 TCCTTGCTGTATTTCTAGCTGTGCTTGGCTCCCTTCACTTGGCTATTAACATGGAGTCA 600
 Db 508 TGTGGCGGTGGGAGGGGCGAGTCTCGGATCCCTGCACTTGGCTATTAACACCGGTGTCA 567
 Qy 601 TCACGCGCCCAAGAAAGTGAATGAACAGAGCTCAATGCAACTTGGCTGGGTAGCGCAGG 660
 Db 568 TCAACGCGCCCAAGAAAGTGAATGAGGAGTTCTCAATCAAAACATGGAACCAACCGCTATG 627
 Qy 661 GTCCTGGGGACCGGACTCCATCCCAAGGCAACCTCCTTACCTTGGGCTCTCTCCG 720
 Db 628 G-----AGAGTCCATCCATCCACCACTCTGCTCTCTCTCCG 675
 Qy 721 TGGCCATCTTCTGTGGGTGGCAATGTTCTCTTCTCATTTGGCAATCATTTCTCAAT 780
 Db 676 TGATGATCTTCTGTGGGGGCAATGATTTGGTTCCTTCTGTGGGGCTCTTTGTTAATC 735
 Qy 781 GGTGGGAAGGAAGGGCTATGCTGGCCACAAATGCTTGGCTGTCTGGGGGGCGCC 840
 Db 736 GCITTTGGCAGGGGGAACCTCCATGCTGATGATGAACCTGTTGGCCTTTGTGTCTGGCTGC 795
 Qy 841 TCATGGCCCTAGCAATGCGCGGCTCTCTATGAGATACTCATTTCTCGGAACGGTTCTCTCA 900
 Db 796 TTATGGGTCTTCCAAACTGGCAAGTCTTTGAGATGCTGATCTTGGCGCTTCACTCA 855
 Qy 901 TTGGCGCTTCTACAGGCTAACATCAGGTTGGTGGCTATGATGTGGGAGAAATCGCC 960
 Db 856 TTGGAGTGTACTGTGGCTCGACCAACCGGCTTTGTGCCCATGTATGTGGGGAGGTGTAC 915
 Qy 961 CCATCTCATCTCGGGGTGCTTGGGAACACTCAACCAATTCGCCCATCTCATTTGGCATTC 1020
 Db 916 CCACAGCTCTTGTGGAGGCCCTGGGCACTTGGCACTGGGCACTGCTGTGGATCC 975
 Qy 1021 TGGTTGCCAGGCTTGGGTTTGGAGTCTATGCTGGGCAACAGCTACCTCTGGGCCATTCG 1080
 Db 976 TTATTTGCCAGGCTTGGGCTTAGACTCCATCATGGGCAATGCAAGCTTGTGGCTCTAC 1035
 Qy 1081 TTCTGGCTATCAGATCTCTCTCTCTCTGAGAGTCTCTTGTGGCTCTCTCTCTCTCTG 1140
 Db 1036 TGCTCAGTGTATCTTATCCAGCCCTGCTACAGTGTATCTCTGTGGCTCTCTCTCTCTG 1095
 Qy 1141 AGAGCCCCCATACCTCTACATCATCGGAACCTGGAGGGGCTTCCCGAAGAGTCTAA 1200
 Db 1096 AGAGCCCCCGTCTCTCTCTCATCAATGTAACAGAGGAACCGGGCCAAAGAGTGTCTGA 1155
 Qy 1201 AGCGCTTCACAGGCTGGGCTGATGTGTGTATGCACTGGGCTGAGCTGAAGGATGAGAAAC 1260
 Db 1156 AAAAGCTTCGAGGGACAGCCGATGTGACCCGAGACCTGCAAGAGATGAAAGAGGGTCT 1215
 Qy 1261 GGAAGTTGGAAAGAGAGGCTCCATCTGCTTGTCTGAGCTCTCTGGGAGCGCCACCCACC 1320
 Db 1216 GGCAGATGATGCGGGGGAAGAGGTCCATCTTTGGAGCTGTTCCGCTCAACCCGCTACC 1275

1321	Qy	GGCAGCCTCTGATTTATTTGCGAGTGGTGTCTGACAGCTGAGCCAGCAGCTCTCAGGCATCAATG	1380
1276	Db	GCCAGCCATCCTCATCGCGTGGTGTCTGAGCTGTCCCAGCAGCTCTCGCGGCATCAATG	1335
1381	Qy	CTGTTTTCTACTATTTCAACAGCAGCATCTTTGAGTTAGCTTGGGTTGGACACGCCAGCCTACG	1440
1336	Db	CTGTGTTCTACTCTCAACGAGCACTTTTCGAGAAGGAGAGGTGTGCACAGCCCTGTGTATG	1395
1441	Qy	CCACCATAGGAGCTGGTGTGGTCAATACCGTCTTTACGTTGGTCTCGGTGCTCTTAGTAG	1500
1396	Db	CCACCATCGGCTCGGGTATCGTCAACACGGCCTTCACTGTGGTGTCTGCTGCTGTTCGTGTG	1455
1501	Qy	AGCGAGCTGGGCGAGCGGACACTCATCTCTCTGGGCCCTGGCAGGAGCATGTGTGGCTGTGCCA	1560
1456	Db	AGCGAGCTGGCCGTTCGGACCCCTGATCTCAATTTGGTCTTGGCTGGCATGGCGGGCTGTGCTG	1515
1561	Qy	TCTTGATGACGGTGGCTCTGCTGCTGCTGGAGCGGGTTCCATCCATGAGTTATGTGTCCA	1620
1516	Db	TGCTCATGACCATCGCCCTTGCCCTGCTGTGGAGCAGCTGCCCCTGGAGTCTCTATCTGAGTA	1575
1621	Qy	TCGTGGGCATATTTGGCTTTGTGGCCTCTTTTGAGATTGGTCTCTGGGCCCATCCCCCTGGT	1680
1576	Db	TCGTGGGCATCTTTGGCTTTGTGGCCCTTTCTTTGAAGTAGGCCCTTGGTCTCTATCTCCATGGT	1635
1681	Qy	TCATTTGGGCCGAGCTCTTTCAGCCAGGGCCCCCGCCAGCAGCCATGGCTGTAGCTGGTT	1740
1636	Db	TCATTTGGCCGAGCTGTTCAGCCAGGGCCCCCGACCTGCTGCTGTGTGCTGTGGCTGGCT	1695
1741	Qy	TCTCCAACTGGACCTGTAACTTTCACTGTTTGGCATTGGGTTTCCAGTATGTTGCGGATGCTA	1800
1696	Db	TCTCTAACTGGACCTCAAACCTTCACTCGTGGGCATGTGCTTTCCAATATGTGGAGCAACTGT	1755
1801	Qy	TGGTCCCTCAGCTCTCCCTCTATTTTCGCGTCCTCTGCTTGGCTTCTTCATCTTTCACTT	1860
1756	Db	GTGGCCCTCAGCTCTTCATCATCTTCAGGTGTCTGTGTTGTACTCTTCTTCTCATCTTCACT	1815
1861	Qy	TCCTAAGAGTGCCTGAAACACAGAGCCGGACATTTGACACAGATCTCGGCCACCTTCCGCAC	1920
1816	Db	ACTTCAAAGTTCTTGAGACCAAAGGCCGAGCCTTCGATGAGATCGCTTCGGGCTTCGGC	1875
1921	Qy	GGACACCTTCTCTTAGGACAGAGAGGTGAAACCCAGTACAGAACTTGAATACCTTAGGGC	1980
1876	Db	AGGGGGGTGC---CAGCCAGACAGCGACAAGACACCTGAGGAGCTCTTCCACCCCTCTGGGG	1932
1981	Qy	CAGATGAGATGACTAATCCGATTTGAAGCTGAGACGCTCCCATCATCTCTCTTAATTTTTCA	2040
1933	Db	CTGACTCCCAAGTGTAATCGAATTTGAAGTGAAGCGCTCCCATCATCTCTCTTAATTTTTCA	1992
2041	Qy	TGACTGACGTTTTTTTTCTTCAATTTAAATATCATAGTATTTGTTTGAIAAAAAAAAAAAAAA	2100
1993	Db	TGACTGAGTTTTTTCTTCAITTTAAATATCATAGTATTTGTTTGAIAAAAAAAAAAAAAA	2052
2101	Qy	AAITTCCTTATCAATGATATCCTTACGATTATATAAATTCCTTACCTAAACCTTATTTAT	2160
2053	Db	AAITTCCTTATCAATGATATCCTTACGATTATATAAATTCCTTACCTAAACCTTATTTAT	2112
2161	Qy	TGTGTACATATACAGAGTATTAATACATATATAAACCTTTTTTCTCTAAACACGAAAAAA	2220
2113	Db	TGTGTACATATACAGAGTATTAATACATATATAAACCTTTTTTCTCTAAACACGAAAAAA	2172
2221	Qy	AAAAGAAAACGATAACATGCTCTGCCATCTCTTGTTCACCGAGCAAAATTAATAAACGCAA	2280
2173	Db	AAAAGAAAACGATAACATGCTCTGCCATCTCTTGTTCACCGAGCAAAATTAATAAACGCAA	2232
2281	Qy	AATGAAATTTGCTCCCTATGAAATTTATAAGGACCAACATCACCAGACTTATCTCTGGGGGGT	2340
2233	Db	AATGAAATTTGCTCCCTATGAAATTTATAAGGACCAACATCACCAGACTTATCTCTGGGGGGT	2292
2341	Qy	CCTCTAGAAAAATAAGTCAGGTACTTGGCTGGACHTTCTTCAGTTG	2386
2293	Db	CCTCTAGAAAAATAAGTCAGGTACTTGGCTGGACHTTCTTCAGTTG	2338

RESULT 5	
AAL49310	A ⁺
ID	AAL49310 standard; DNA; 7828 BP.
XX	
AC	AAL49310;
XX	
DT	07-MAN-2002 (first entry)
XX	
DE	Human Glut4 containing vector YEp4H7-HsGLUT4.
XX	
KW	Human; yeast; GLUT4; glut transporter; hexose; antidiabetic; anorectic;
KW	vector; ds.
XX	
OS	Homo sapiens.
XX	
FN	WO200264784-A2.
XX	
PD	22-AUG-2002.
XX	
PF	09-FEB-2002; 2002WO-EP001373.
XX	
PR	14-FEB-2001; 2001DE-01006718.
XX	
PA	(AVET) AVENTIS PHARMA DEUT GMBH.
XX	
PI	Mueller G, Kollier K, Boles E, Wiczorke R, Dlugai S;
XX	
DR	WPI; 2002-636632/68.
XX	
PT	New strains of yeast, useful in screening for modulators of hexose
PT	transport, potential antidiabetic and antiobesity agents, lack native
PT	hexose-transport function.
XX	
PS	Claim 10; Page 34-36; 58pp; German.
XX	
CC	The present invention relates to a strain of <i>Saccharomyces cerevisiae</i>
CC	that cannot grow on a substrate containing hexose as the only source of
CC	carbon but the ability to grow on such substrates is restored when the
CC	GLUT4 gene is expressed. A strain transformed to express the GLUT1 or
CC	GLUT4 genes can be used to identify compounds that increase/reduce hexose
CC	transport by these proteins. These compounds, optionally after
CC	development, are potential drugs for treating diabetes and obesity. The
CC	present sequence is a vector containing the human Glut4 coding sequence
CC	as used in the invention

Sequence 7828 BP; 2009 A; 1928 C; 1771 G; 2120 T; 0 U; 0 Other;

Query Match 51.5% Score 1229; DB 6; Length 7828;

Query Match 51.5%; Score 1225; Pred. No. 2e-290;
Best Local Similarity 85.8%;

Best local similarity 95.0%; Recd. no: 23 230;
Matches 1364; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

0
1
2
3
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QY 468 ATAAATGCTCTGAATTCCAGCAGATCGGCTCTGAAGATGGGGAACCCCTCAGCAGCGAGTG 527

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Db 1 ATGCCGTCGGGCTTCCACAGATAGGCTCCGAAGATGGGAAACCCCTCAGCAGCGAGTG 60

Qy 528 ACTGGACACTGGTCCCTTGCTGTATTCTCAGCTGTGCTTGGCTCCCTTCAGTTGGCTAT 587

Db 61 ACTGGGACCTGGTCTTGCTGTGTTCTCTGCGGTCTGGCTCCCTGCAGTTGGGTAC 120

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Qy
588 AACATTGGAGTTCATCAACGCCCCACAGAAAGTGATTGAAACAGAGCTACAATGCAACTTGG 647
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Db 121 AACATTGGGGTCATCAATGCCCTCAGAGGTGATTGAACAGAGCTACAATGAGACGTGG 180

[illegible]

QY
648 CTGGTAGGCAGGGTCTCTGGGGACCGGACTCCATCCCAAGGCACCCCTCACCTACCCCT 707

181 CTGGGGAGGCAGGGGCGTGGGGACCCAGTCCATCCCTCCAGGCACCCCTGACCACTTC 240

DB 181 CTGGGGAGGCAGGGGCTTGAGGGACCCAGCTCCATCCCTCCAGGCACCCCTCACCCACCCCTC 240

QV 708 TGGGGCTCTCTCCGTGGCCATCTTCTCTGTGGGTGGCATGATTTCTCCCTCTCTCATTTGGC 767

[illegible]

Db 241 TGGGCCCTCTCCGTGGCCATCTTTTCCGTGGGGGGCATGATTTCTCTCTCTCATTTGGT 300

[illegible]

QV 768 ATCATTTCTCAATGGTTGGGAGGAAAGGGCTATGCTGGCCAAACAATGCTTTGGCTGTG 827

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Db 301 ATCATCTCTCAGTGGCTTGGAAGGAAAAGGGCCATGCTGGTCAACAATGTCTGCGGGTG 360
QY 828 CTGGGGGGCGCCCTCATATGGGCGCTAGCCATATCGCGGCGCTCTATAGATATCATATCTC 887
Db 361 CTGGGGGGGAGGCTCATATGGGCGCTAGCCAAAGCGTGTGCTCTCTATGAAATGCTCATCCTT 420
QY 888 GGACGGTCTCTCATATGGGCGCCCTACTCAGGGCTTAAACATCAGGGTGGTGGCTATGATGTG 947
Db 421 GGACGATTTCTCATATGGGCGCCCTACTCAGGGCTGACATCAGGGCTGGTGGCCATGTACGTG 480
QY 948 GGAGAAATCGCCCGCCCATCATCTTCTGGGGGCTTCTGGGAAACATCAACAAATGGGCCATC 1007
Db 481 GGCGAGATTCCTCCCACTCACCTGCGGGCGCGCCCTGGGGAGCGCTCAACCAATGGGCCATT 540
QY 1008 GTCATTTGGCATTTCTGGTGGCCAGGTGTGGGTTGGAGTCTATGCTGGGCGACGCTACC 1067
Db 541 GTTATCGGCAATTTCTGATGCGCCAGGTGTGGGCTTGGAGTCCCTCTGGGCACTGCCAGC 600
QY 1068 CTGTGGCCATTTGCTTCTGGCTATCACAGTACTCCTGCTCTCTGCGAGTCTGTTCTGTTG 1127
Db 601 CTGTGGCCACTGCTCTGGGCTTCAAGTGTACTCTGCTCTCTGCGAGTGGTCTGCTG 660
QY 1128 CCTTCTGTCTGAGAGCCCGCATACCTCTACATCATCCGAAACCTGGAGGGCGCTGCC 1187
Db 661 CCTTCTGTCTGAGAGCCCGCATACCTCTACATCATCCGAAATCTCGAGGGCGCTGCC 720
QY 1188 CGAAGAGTCTAAAGCGCTGACAGGCTGGGCTGATGTCTGATGCACTGGCTGAGCTG 1247
Db 721 AGAAGAGTCTAAAGCGCTGACAGGCTGGGCGGATGTTCTGGAGTGTCTGGCTGAGCTG 780
QY 1248 AAGGATGAGAAACGGAAGTTGGAAGAGAGGCTCCACTGTCTCTGCTGCACTCTCTGGC 1307
Db 781 AAGGATGAGAGCGGAAGCTGGAGCGTGTAGCGGCACTGTCTCTGCTGCACTCTCTGGC 840
QY 1308 AGCGGACCCACCGGAGCTCTCTGATTTATGTCAGTGTGCTGTCAGCTGAGCGAGCTC 1367
Db 841 AGCGGTACCCACCGGAGCGCCCTGATCATTTGGGCTGCTGCTGTCAGCTGAGCGAGCTC 900
QY 1368 TCAGGCTCATGCTGTTTCTACTATTCACAGGCTCTTTCAGTGTAGTGTAGTGGGCTGGA 1427
Db 901 TCTGGCATCAATGCTGTTTCTATTTATTCGACAGCATCTTCGAGACAGAGGGGTAGG 960
QY 1428 CAGCAGCTCAGCCACCATAGAGCTGTGTGTGTCATACGCTCTTCACGTTGCTCTCG 1487
Db 961 CAGCCTGCTTATGCCACCATAGAGCTGTGTGTGTCACACAGTCTTCACCTTGGTCTCG 1020
QY 1488 GTGCTCTTATGAGAGGAGCTGGGCGAGCGGACATCCATCTCTGGGCTGGCAGGCGATG 1547
Db 1021 GTGTTGTGGTGGAGCGGCGGGCGCGGACGCTCCATCTCTGGGCTGGCGGCGATG 1080
QY 1548 TGTGGCTGTGCCATCTTGATGAGGTGGCTGTGCTGCTGGAGCGGGTTCATCCATG 1607
Db 1081 TGTGGCTGTGCCATCTTGATGACTGTGGCTGTGCTGCTGGAGCGAGTTCAGGCCATG 1140
QY 1608 AGTTATGTCTCATCTGTGCCCATATTTGGCTTTGGGCTCTTTGAGATTTGGCTCTGGC 1667
Db 1141 AGCTAGCTCTCATTTGTGGCCATCTTTGGCTTCGTGGCATTTTGTGATTTGGGCTGGC 1200
QY 1668 CCCATCCCTGTTTCAATTTGTGGCCAGCTCTTTTCAGCGAGGGCGCCCGCCAGCGAGCCATG 1727
Db 1201 CCCATTTCTTGTTCATGTGGCCAGCTCTTTTCAGCGAGGGAGCCCGCCCGGAGCCATG 1260
QY 1728 GCTGTAGCTGGTTTCTCCAGTGGACCTGTAACTTCATCTGCTGGCATGGGTTTCCAGTAT 1787
Db 1261 GCTGTGGCTGGTTTCTCCAACTGGACGAGCAATTCATCTGGCATGGGTTTCCAGTAT 1320
QY 1788 GTTGGGATGCTATGGGCTCCCTACGCTCTCTCTTCTATTTGGCTCTCTGCTGGCTTC 1847
Db 1321 GTTGGGAGGCTATGGGCGCCCTACGCTCTCTCTTCTATTTGGGCTCTCTGCTGGCTTC 1380
QY 1848 TTCATCTTCACCTTCTTAAAGTGTGCTGAAACCGAGCGCGGACATTTGACAGATCTCG 1907

Db 1381 TTCTATCTTCCACTTCTTTAAGAGTACCTGAAACTCGAGCGCGAGCGTTTGACAGATCTCA 1440
QY 1508 GCCACCTTTCGAGCGACACCTTCTCTCTTAGAGCAGGAGGTGAAACCCAGTACAGACTT 1967
Db 1441 GCTGCCCTTCCACCGGACACCTCTCTCTTTTAGCAGGAGGTGAAACCCAGCAGCACTT 1500
QY 1568 GAATACTTAGGGCCAGATGAGAAATGACTTAATCGATTTTGAAGTGAGAGCGCTCCATCATCTC 2027
Db 1501 GAGTATTTAGGGCCAGATGAGAACGACTGATAAGCTTATCGATACCGTCCGACCTCGAGTC 1560
QY 2028 TCTTAATTTTCATGACTGACGTTTTTTC 2056
Db 1561 ATGTAATTAGTTATGTCAAGCTTACATTC 1589

RESULT 6

AAF81396

ID AAF81396 standard; cDNA; 2592 BP.

XX AAF81396;

XX AC

XX XX

XX 05-JUN-2001 (first entry)

XX XX

XX Coding sequence for modified GLUT4.

XX GLUT4 glucose transporter; insulin; protein translocation;

XX insulin resistance; adult-onset diabetes; obesity;

XX polycystic ovary syndrome; ss.

XX OS

XX Unidentified.

XX WO200075188-A1.

XX XX

XX 14-DEC-2000.

XX XX

XX 09-JUN-2000; 2000WO-US015904.

XX XX

XX 09-JUN-1999; 99US-0138237P.

XX PR

XX 15-SEP-1999; 99US-0154078P.

XX XX

XX (WHED) WHITEHEAD INST BIOMEDICAL RES.

XX PA

XX (GEHO) GEN HOSPITAL CORP.

XX XX

XX Bogan JS, Lodish H;

XX XX

XX WPI; 2001-050022/06.

XX DR

XX P-PSDB; AAB80940.

XX XX

XX Assessing translocation of proteins such as glucose transporter GLUT4,

XX cystic fibrosis transmembrane conductance regulator by using modified

XX protein of interest comprising the protein and detectable tags.

XX Disclosure; Fig 8; 75pp; English.

XX XX

XX The present sequence is the coding sequence for a modified GLUT4 glucose

XX transporter. Insulin stimulates glucose uptake in muscle and adipose

XX tissue by causing translocation of the GLUT4 glucose transporter from an

XX intracellular compartment to the plasma membrane. This results in an

XX increase in the number of cell-surface GLUT4 transporters and therefore

XX an increased rate of glucose entry into cells. The modified GLUT4

XX transporter was used in a method for assessing the translocation of a

XX protein of interest (e.g. GLUT4) from an intracellular location to the

XX plasma membrane in mammalian cells, when the cells are exposed to a

XX condition or a stimulus. The method is useful for assessing the effect

XX of a drug on translocation of a protein such as GLUT4. Such drugs are

XX useful in treating insulin resistance such as in adult-onset diabetes,

XX obesity and polycystic ovary syndrome. The modified GLUT4 transporter

XX CC encoded by the present sequence has myc epitope tags (see AAB80939) and a

XX GFP fluorescent tag

XX SQ

XX Sequence 2592 BP; 545 A; 767 C; 733 G; 547 T; 0 U; 0 Other;

XX Query Match

XX 44.7%; Score 1066.4; DB 5; Length 2592;

Best Local Similarity 87.5%; Pred. No. 8.7e-251; Matches 1166; Conservative 0; Mismatches 166; Indels 0; Gaps 0;			
QY	663	CTTGGGACCGGACTCATCCCAAGGACCCCTCACTACCTTTTGGGCTCTCTCCGTG	722
DB	511	CTTAAAGGACCCAGCTCCTATCCCTCAGGACCCCTCACACCTCTGGGCCCTCTCCGTG	570
QY	723	GCCATCTTCTGTGGGTGGCATGATTTCTCTCTTTCTCATTTGSCATCATTTCTCAATGG	782
DB	571	GCCATCTTTCCGTGGGCGGCATGATTTCTCTCTCTCTCATTTGGTATCATCTCTCAGTGG	630
QY	783	TTGGGAAGGAAGGGCTATGCTGGCCAACTATGTCCTTGGCTGTGCTGGGGGGGCCCTC	842
DB	631	CTTGGGAAGGAAGGGCCATGCTGGTCAACAATGTCCTGGCGGTCTGGGGGGGAGCCTC	690
QY	843	ATGGGCTTAGCAATATGCGGGCCCTCTATGAGATATCATTTCTCGACAGGTTCTCTCATTT	902
DB	691	ATGGGCTTGCCAAAGCTGTGCTCTCTATGAATATGTCATCTTGGACATTTCTCATTT	750
QY	903	GGGCTTACTCAGGGCTAAATCAGGGTTGGTGCTATGATATGGAGAAATCGCCCCC	962
DB	751	GGGCTTACTCAGGGCTGACATCAGGGCTGGTGCCCATGTACGTGGGGGAGATTGCTCCC	810
QY	963	ACTCATCTTGGGGTGCTTTGGGAACAATCAACAAATGGCCATCGTCAATTTGGCATTCG	1022
DB	811	ACTCACCTGGGGGGCCCTGGGAGACGCTCAACCAACTGGSCATTTGTTATGGCATTCG	870
QY	1023	GTTGCCCAGGTGTTGGGTTTGGAGCTATGCTGGGCACAGTACCCCTGTGGCCATTCGTT	1082
DB	871	ATGCCCCAGGTGTGGGCTTGGAGTCCCTCTCTGGGCATCGCACCTGTGGCCACTGCTC	930
QY	1083	CTGGCTATCACAGTACTCCCTGTCTCTCTGAGCTGTCTTGTGTGCCCTTCTGTCTTGAG	1142
DB	931	CTGGGCTTACAGTGTCTACTCTGCCCTCTCTGAGCTGTCTCTGTGCCCTTCTGTCCCCG	990
QY	1143	AGCCCCGATACCTTACATCATCCGGAACTTGAGGGGGCTGCCCCGAAAGAGTCTAAG	1202
DB	991	AGCCCCGCTACCTTACATCATCCAGAACTCTGAGGGGGCTGCGCAAAAGAGTCTGAAG	1050
QY	1203	CGCTGACAGCTGGGCTGATGTCTGTATGTCACCTGCTGAGCTGAAGGATGAGAAACGG	1262
DB	1051	CGCTGACAGCTGGGCGGATGTTTCTGGAGTGTGGCTGAGCTGAAGGATGAGAGCGG	1110
QY	1263	AAGTTGAAAGAGAGCGTCCACTGTCTGTGTGACGCTCTCTGGGCAGCCGACCCACCGG	1322
DB	1111	AAGCTGAGCGTGAGCGGCCACTGTCTCTGTCTCCAGCTCTCTGGGCAGCCGTAACCCG	1170
QY	1323	CAGCTCTGATTAATGCAAGTGGTCTGCACTGAGCCAGCAGCTCTCAGGGATCAATGCT	1382
DB	1171	CAGCCCCGTGATCATTTGGCGTGTCTGCAGCTGAGCCAGCAGCTCTCTGGCATCAATGCT	1230
QY	1383	GTTTTCTACTATTCAACACAGCATCTTTGAGTTAGCTGGGGTGGAAACAGCCAGCTACGC	1442
DB	1231	GTTTTCTATTATTCGACAGCATCTTTCGACACAGGGGTAGCCAGCTGTGCCATATGCC	1290
QY	1443	ACCATAGAGCTGTGTGGTCAATACCGTCTTTCACGTTGGTCTCGGTGCTCTTAGTAGAG	1502
DB	1291	ACCATAGAGCTGTGTGGTCAACACAGTCTTCACTTGGTCTCGGTGTTGTTGGTGGAG	1350
QY	1503	CGAGCTGGGCGAACGCACTCCATCTCTGGGCCCTGGCAGCATGTGTGGCTGTGCCATC	1562
DB	1351	CGGCGGGGGCGGAGCGCTCATCTCTGGCCCTGGCGGCGATGTGTGGCTGTGCCATC	1410
QY	1563	TTGATGAGCGTGGCTGTCTGCTCTGAGGGGGTTCATCCATGATTTATGTGTCCATC	1622
DB	1411	CTGATGACTGTGGCTGTGCTCTCTCTGGAGCGAGTTCAGCCATGAGCTAGCTCTCCATT	1470
QY	1623	GTGGCCATTTTGGCTTTGTGGCTCTTTTGAGATGCTCTCTGGCCCCATCCCTCGTTC	1682
DB	1471	GTGGCCATCTTTGGCTTCGTGGCATTTTTTGAGATTTGGCCCTGGCCCATCTCTGTGTC	1530
QY	1683	ATTGTGGCCGAGCTCTTTCAGCCAGGGGCCCGCCCGCCAGCAGCCATGGCTGTAGCTGTTTC	1742

Db	1531	ATCGTGCCGAGCTCTTCAGCCAGGGACCCCGCCCGCAGCCATGGCTGTGGCTGGTTC	1590		
Qy	1743	TCCAACTGGACCTGTAACTTTCATCGTTGGCATGGGTTTCCAGTATGTTGGGATGCTATG	1802		
Db	1591	TCCAACTGGACGAGCACTTCATCTGGCATGGGTTTCCAGTATGTTGGGAGGCTATG	1650		
Qy	1803	GGTCCCTACGTCCTTCCTTATTTGGCGTCTCTCTGCTTGGCTTCTTCATCTTCACCTTC	1862		
Db	1651	GGGCGCTTACGTCCTTCCTTATTTGGCGTCTCTCTGCTTGGGCTTCTTCATCTTCACCTTC	1710		
Qy	1863	CTAAGAGTGCCTGAACACGAGCGCGACATTTGACACAGATCTCGGCCACTTCCGACGG	1922		
Db	1711	TTAAGAGTACTGAAACTCCAGGCGCGACGTTTGACACAGATCTCGGCTCGCTTCCACCGG	1770		
Qy	1923	ACACCTTCTCTTTAGACGAGGAGTGAACCCAGTACAGAACTTGAATACTTTAGGCGCA	1982		
Db	1771	ACACCTCTCTTTAGACGAGGAGTGAACCCAGTACAGAACTTGAATACTTTAGGCGCA	1830		
Qy	1983	GATGAGAATGAC	1994		
Db	1831	GATGAGAATGAC	1842		
RESULT 7					
ABL41106					
ID	ABL41106 standard; DNA; 2592 BP.				
XX	XX				
AC	AC ABL41106;				
XX	XX				
DT	12-AUG-2002 (first entry)				
XX	XX				
DE	Modified GLUT4 encoding nucleotide sequence.				
XX	XX				
KW	Protein translocation; plasma membrane; GLUT-4; diabetes mellitus;				
KW	insulin; Gene; GFP; green fluorescent protein; ds.				
XX	XX				
OS	Synthetic.				
XX	XX				
FH	Key	Location/Qualifiers			
FT	CD5	1..2592			
FT		/*tag= a			
FT		/product= "modified GLUT4"			
FT		/note= "contains myc epitope tags and GFP"			
FT	misc_feature	1873..2592			
FT		/*tag= b			
FT		/note= "GFP"			
XX	XX				
FN	US2002052012-A1.				
XX	XX				
PD	02-MAY-2002.				
XX	XX				
PF	28-JUN-2001; 2001US-00894927.				
XX	XX				
PR	22-MAY-1997; 97US-0047433P.				
PR	09-JUN-1999; 99US-0138237P.				
PR	15-SEP-1999; 99US-0154078P.				
PR	09-JUN-2000; 2000US-00591025.				
XX	XX				
PA	(WHED) WHITEHEAD INST BIOMEDICAL RES.				
XX	XX				
PI	Bogan JS, Lodish HF;				
XX	XX				
DR	WPI; 2002-443696/47.				
DR	P-PSDB; ABB07975.				
XX	XX				
PT	Determining protein translocation to the plasma membrane of a mammalian				
PT	cell using a modified protein with an intracellular fluorescent tag and				
PT	an extracellular group tag, useful in finding new drugs, particularly to				
PT	treat diabetes.				
XX	XX				
FS	Example 1; Fig 8a-b; 34pp; English.				
XX	XX				
CC	The invention relates to determining if a protein translocates from an				

CC intracellular location to the plasma membrane of a mammalian cell in the
CC presence of a condition or stimulus. The method involves modifying the
CC protein with a group tag in the extracellular domain and a fluorescent
CC tag in the intracellular domain and determining the proportion of total
CC protein which is at the membrane. The method is used to identify a drug
CC which enhances translocation of a protein from an intracellular location
CC to the plasma membrane of a mammalian cell. The method is particularly
CC used to measure GLUT-4 protein translocation to identify drugs to treat
CC insulin resistance in adult-onset diabetes mellitus. The invention
CC provides a less labour intensive quantitative method for measuring GLUT4
CC translocation than prior art methods. The present sequence represents a
CC modified GLUT4 nucleotide sequence, containing myc epitope tags and green
CC fluorescent protein (GFP) sequences
XX
SQ

Sequence 2592 BP; 545 A; 767 C; 733 G; 547 T; 0 U; 0 Other;

Query Match 44.7%; Score 1066.4; DB 6; Length 2592;

Best Local Similarity 87.5%; Pred. No. 8.7e-251;

Matches 1166; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY	663	CTGCGGACCGGACTCCATCCCAAGGACCCCTCACTACGCTTGGGCTCTCCGCG	722
DB	511	CTTAAAGGACCCAGCTCCATCCCTCCAGGACCCCTCACACCCCTCTCCGCG	570
QY	723	GCCATCTTCTGTGGGTGGCATGATTTCCCTTCTCATTTGGGATCATTTCTCAATGG	782
DB	571	GCCATCTTCTGTGGGTGGCATGATTTCCCTTCTCATTTGGGATCATTTCTCAATGG	630
QY	783	TTGGGAAGGAAAGGGCTATGTGCGCAACAATGTCCTTGGGTGCTGGGGGGCGCCCTC	842
DB	631	CTTGGGAAGGAAAGGGCTATGTGCGCAACAATGTCCTTGGGTGCTGGGGGGCGCCCTC	690
QY	843	ATGGGCTAGCAATGCGCGGCTCTATGATGATCATTTCTCGGACGGTTCCTCATTT	902
DB	691	ATGGGCTAGCAATGCGCGGCTCTATGATGATCATTTCTCGGACGGTTCCTCATTT	750
QY	903	GGCGCTACTCAGGCTTAACATCAGGTTGGTGGCTATGATGAGGAGAAATCGCCCC	962
DB	751	GGCGCTACTCAGGCTTAACATCAGGTTGGTGGCTATGATGAGGAGAAATCGCCCC	810
QY	963	ACTCATTTTGGGGTGGCTTGGGAAACATCAACCAATTTGGGCAATGATGGCAATCTG	1022
DB	811	ACTCATTTTGGGGTGGCTTGGGAAACATCAACCAATTTGGGCAATGATGGCAATCTG	870
QY	1023	GTTCGCCAGGCTGTGGGTTGGAGTCTATGCTGGGACAGCTACCTGTGGCCATTCGTT	1082
DB	871	ATCGGCCAGGCTGTGGGTTGGAGTCTATGCTGGGACAGCTACCTGTGGCCATTCGTT	930
QY	1083	CTGGCTATCACAGTACTCCCTCTCTCTGAGCTGTCTTCTGTGGCCCTTCTGTCTGAG	1142
DB	931	CTGGGCTATCACAGTACTCCCTCTCTCTGAGCTGTCTTCTGTGGCCCTTCTGTCTGAG	990
QY	1143	AGCCCCGATACCTTACATCATCCGAACTTGGAGGGGCTGCCGGAAGAGTCTAAAG	1202
DB	991	AGCCCCGATACCTTACATCATCCGAACTTGGAGGGGCTGCCGGAAGAGTCTAAAG	1050
QY	1203	CGCCTGACAGGCTGGGCTGATGCTGATGATGCTGAGCTGAGCTGAGGATGAGAAAGG	1262
DB	1051	CGCCTGACAGGCTGGGCTGATGCTGATGATGCTGAGCTGAGCTGAGGATGAGAAAGG	1110
QY	1263	AAATTGGAAAGAGCGCTCCATCTTCTGCTGAGCTTCTGGGCGAGCGCCACCCACCGG	1322
DB	1111	AAAGTGGAGCGTGAGGGCCACTGTCTCTGCTGAGCTTCTGGGCGAGCGCCACCCACCGG	1170
QY	1323	CAGCTCTGATATTTGAGTGTGTGCTGAGCTGAGGACGAGCTCTCAGGATCAATGCT	1382
DB	1171	CAGCCCCCTGATCAATTTGCGGTGCTGCTGAGCTGAGGACGAGCTCTCAGGATCAATGCT	1230
QY	1383	GTTCCTTCTACTTCAACAGGATCTTTGAGTGTGCTGGGTTGGAAACAGCCCTACGCC	1442
DB	1231	GTTCCTTCTACTTCAACAGGATCTTTGAGTGTGCTGGGTTGGAAACAGCCCTACGCC	1290
QY	1443	ACCATAGGAGCTGTGTGTGTCAATCCGCTCTTACGTTGGTCTCGGTCTCTAGTAGAG	1502

DB	1291	ACCATAGGAGCTGTGTGTGTCAACACAGTCTTACCTTGGTCTCGGTGTGTGTGGGAG	1350
QY	1503	CGAGCTGGGCGAGCGACACTCCATCTCTTGGGCTTGGCAGGACATGTGTGGCTGTGCCATC	1562
DB	1351	CGGCGGGGCGCGGAGCTCCATCTCTTGGGCTTGGCAGGACATGTGTGGCTGTGCCATC	1410
QY	1563	TTGATGACGGTGGCTCTGTCTCTGAGCGGGTTCCATCCATGAGTTATGTGTCCATC	1622
DB	1411	CTGATGACTGTGGCTCTGTCTCTGAGCGAGTTCCAGGCATGAGCTACGCTCTCCATT	1470
QY	1623	GTGCGCATATTTGGCTTTTGTGGCTTCTTCTGAGATTTGCTTGGCCCATCCCTGGTTTC	1682
DB	1471	GTGCGCATATTTGGCTTTTGTGGCTTCTTCTGAGATTTGCTTGGCCCATCCCTGGTTTC	1530
QY	1683	ATTGTGGCGAGCTCTTTCAGCAGGCGCCCGCCGAGCAGCATGTGTGTGGTGTTC	1742
DB	1531	ATCTGGCGGAGCTCTTTCAGCAGGCGCCCGCCGAGCAGCATGTGTGTGGTGTTC	1590
QY	1743	TCCAACTGGACCTGTAATCTTCACTTGGCATGGTTCAGATGTTTCCAGTATGTTGCGGAGCTATG	1802
DB	1591	TCCAACTGGACGAGCAATCTTCACTTGGCATGGTTCAGATGTTTCCAGTATGTTGCGGAGCTATG	1650
QY	1803	GGTCCCTACGCTCTTCTTCTTATTTTGGCTTCTCTCTGCTTGGCTTCTTCACTTTCACCTTC	1862
DB	1651	GGGCGCTACGCTCTTCTTCTTATTTGGCTTCTCTCTGCTTGGCTTCTTCACTTTCACCTTC	1710
QY	1863	CTAAGAGTCTGAAACAGAGGCGGACATTTGACAGATCTCGGCCACCTTTCGACGG	1922
DB	1711	TTAAGATGACTGAAACTCGAGGCGGACGTTTGACAGATCTCGGCTGCTTCCACCGG	1770
QY	1923	ACACCTTCTCTTAGAGCAGGAGGTGAAACCCAGTACAGAACTTGAATCTTAGGGCCA	1982
DB	1771	ACACCTTCTCTTAGAGCAGGAGGTGAAACCCAGTACAGAACTTGAATCTTAGGGCCA	1830
QY	1983	GATGAGAATGAC 1994	
DB	1831	GATGAGAATGAC 1842	

RESULT 8
AAQ11148
ID AAQ11148 standard; cDNA; 2587 BP.
XX AAQ11148;
AC
XX
DT 04-JUN-1991 (first entry)
XX
DE GTP-gene from Chinese Hamster Ovary cells.
XX
KW Glucose transporter protein; serum-independence; CHO;
KW insulin-independence; ds.
XX
OS Cricetus sp.
FH Key Location/Qualifiers
FT CDS 191..1669
FT /*tag= a
FT /product= "Glucose Transporter Protein"
XX
XX WO9103554-A.
XX
XX 21-MAR-1991.
XX
XX 01-SEP-1989; 89US-00402204.
XX
XX 01-SEP-1989; 89US-00402204.
XX 20-JUN-1990; 90US-00541426.
XX
XX (GETH) GENENTECH INC.
XX Thomas JN, Williams SR;
XX

23-OCT-1995; 95US-00546934.
(TEXA) UNIV TEXAS SYSTEM.
(BETA-) BETAGENE INC.

Newgard CB, Clark SA, Thigpen AE, Normington KD;
WPI; 1997-297737/27.
P-PSDB; AAW17835.

Use of glucose transporter, GLUT-2 or GLUT-2 chimera(s) for cell-killing
- used in negative and double selection protocols and screening methods,
for cancer treatment and treatment of diabetes.

Claim 138; Page 104-106; 169pp; English.

This cDNA sequence codes for human glucose transporter GLUT-1 (AAW17835).
A claimed polynucleotide comprises a contiguous nucleic acid sequence
from human GLUT-1 cDNA and rat GLUT-2 cDNA (see AAW17835). It encodes a
GLUT-1/GLUT-2 chimeric transporter that confers glucose sensing capacity
to a cell but which does not render the cell subject to diabetic immune
destruction, and which does not transport streptozotocin. The claimed
polynucleotide can be administered to a patient to treat diabetes, or
expressed in a cell to prepare a recombinant cell that secretes insulin
in response to glucose and which can be administered to a patient to
treat diabetes

Sequence 1815 BP; 324 A; 572 C; 520 G; 399 T; 0 U; 0 Other;

Query Match 28.5%; Score 679; DB 2; Length 1815;
Best Local Similarity 68.1%; Pred. No. 7.2e-156;
Matches 965; Conservative 0; Mismatches 440; Indels 12; Gaps 1;

506 GGAACCCCTCAGCAGCAGTACTGGACACTGGTCTCTGCTGATTTCTACGCTGTGCT 565
167 GGAGCCCCAGCAGCAAGAAGCTGACGGGTGCGCTCATGCTGGCTGGGAGGACAGTGTCT 226
566 TGGCTCCCTTCAGTTTGGCTATACATTTGGAGTTCATCAACGCCGCCACAGAAAGTGATCA 625
227 TGGCTCCCTTGGCTTGGCTTACACATGGAGTTCATCAATGCCGCCGCCAGAGGTATCGA 286
626 ACAGAGCTACAAATGCAACTTGGCTGGGTAGGACGGGTCTTGGGGGACCGGACTCCATCCC 685
287 GGAGTTCTACACACAGACATGGTCCACCGCTATGG-----GGAGAGCATCTCT 334
686 ACAGGACCCCTCATTACCTTTGGGCTCTCTCGTGGCCATCTTCTCTGTGGGTGGCAT 745
335 GCCCACCACGCTCACCAGGCTCTGGTCCCTCTCAGTGGCCATCTTTCTGTGGGGGCAT 394
746 GATTTCCTCTTCTCATTTGGCATCATTTCTCAATGTTGGGAAGAAAGGCTATGCT 805
395 GATTGGCTCTTCTCTGTGGGCTTTTGGTTAACCGCTTTGGCGGGCGGAAATTCATGCT 454
806 GGCCCAACAATGTTTGGCTGTGCTGGGGGGGGCCCTCATGGGCTTAGCCAAATGCCCGGC 865
455 GATGATGAACCTGCTGGCTTCTGGTGTGGCGCTGCTCATGGCTTCTCGAAATCGGGCAA 514
866 CTCCTTAGAGATCACTCATTTCTGGACGGTTCCTCATTTGGGCGCTTCTCAGGGCTTAACATC 925
515 GTCTTTTGAGATGCTGATCCTGGGCGCTTTCATCATGGTGTGTAAGTGTGAGTGTGAGTGTG 574
926 AGGTTGGTGGCTATGATGTTGGGAGAAATCGCCCCCATCTCATCTCGGGGTGCTTTGGG 985
575 AGGCTTGGTGGCCATGATGTTGGGTAAGTGTGAGTGTGAGTGTGAGTGTGAGTGTGAGTGTG 634
986 AACACTCAACCAATTTGGCCATCGTCAATTTGGCATTTCTGGTTGCCAGGTGTGGGTTTGA 1045
635 CACCCTGACACAGCTGGGATCGTCTGGCATCTCATCGGCCAGGTGTGGGCTTGA 694
1046 GTCTATGTGGGCAAGCTACCTGTGGGCAATGCTTCTGGCTATACAGTATCTCCCTGC 1105
695 CTCCTCATGTGGGCAAGAGGACCTGTGGGCTTCTGGCTATACAGTATCTCCCTGC 754

PN W0200188188-A2.
 XX 22-NOV-2001.
 XX 18-MAY-2001; 2001WO-JP004192.
 XX 18-MAY-2000; 2000JP-00145977.
 XX (UYN1-) UNIV NIHON SCHOOL JURIDICAL PERSON.
 XX Ishikawa K, Asai S, Takahashi Y, Nagata T, Ishii Y;
 XX WPI; 2002-034733/04.
 DR P-PSDB; ABB57244.
 XX
 PT Examining the ischemic condition (e.g. occlusive ischemia) by measuring
 PT expression levels of particular genes defined in the specification or by
 PT determining the expression profile of a gene group comprising these
 PT genes.
 XX
 PS Claim 2; Page 1637-1641; 2690pp; English.
 XX
 CC The present invention describes a method for examining ischemic
 CC conditions, comprising measuring the expression levels of particular
 CC genes (i) in a test sample or determining the expression profile of a
 CC gene group in the sample comprising genes selected from (i). The method
 CC is useful for examining the ischemic condition (e.g. compressive
 CC ischemia, occlusive ischemia or vasospastic ischemia) by measuring the
 CC expression levels of particular genes (ABI99202 to ABI99912, encoding the
 CC protein sequences in ABB57020 to ABB57374) or by determining the
 CC expression profile of a gene group comprising these genes. The expression
 CC levels or expression profiles produced by these genes are used as an
 CC indicator when screening for ischemic condition-improving drugs or
 CC therapeutics for ischemic diseases. ABI99913 and ABI99914 represent PCR
 CC primers for a mouse ischemic condition related sequence, which are used
 CC in the exemplification of the present invention
 XX
 SQ Sequence 2544 BP; 514 A; 719 C; 679 G; 632 T; 0 U; 0 Other;
 Query Match 28.5%; Score 679; DB 6; Length 2544;
 Best Local Similarity 68.1%; Pred. No. 8.5e-156;
 Matches 965; Conservative 0; Mismatches 440; Indels 12; Gaps 1;
 506 GGAACCCCTCAGCAGCGAGTGAATGGGACACTGGTCTCTGTATTTCTCAGCTGTGCT 565
 192 GGATCCCGAGCAGCAAGAGTGAACGGCGCTCATGTGGCTGTGGGAGGAGCAGTGCT 251
 566 TGCTCCCTTCAGTTGGCTATTAACATTGGAGTCATCAAGCCGCCACAGAAAGTATGA 625
 252 CGGATCACTGAGTTCGGCTATTAACACTGGTGTATCAACGCCGCCCGCCAGAGGTTATGA 311
 626 ACAGAGCTACAATGCAACTTGGCTGGGTAGGAGGCTCTGGGGGACCGGACTCCATCCC 685
 312 GGAGTTCTACATCAATCAATGGAACACCGCATCGG-----AGAGCCCATCCC 359
 686 ACAAGGACCCCTCACTACCTTTGGGCTCTCTCGTGGCCATCTCTCTGTGGGTGGCAT 745
 360 ATCCACCACACTACCAAGCTTTGGTCTCTCTCGTGGCCATCTCTCTGTGGGGGCAT 419
 746 GATTTCTCTCTCTCAATGGCATCATTTCTCAATGGTTGGGAAGGAAGGGGTATGCT 805
 420 GATTTGGTCTCTCTCTGCGGCTCTTTGTTAATCGCTTTGGCAGGCGGAACCTCCATGCT 479
 806 GGCCACAATGTCTTGGCTGTGGGGGGCGCCCTCATGGGCTACGCAATGCGCGGC 865
 480 GATGATGAACCTGTGGGCTTTGTGGCTGTGGCTATGGGCTTCTCAAACTGGGCAA 539
 866 CTCCTATGAGATACTCACTTCCTCGGACGGTTCTCAATTTGGGCGCTACTCAGGGCTAAATC 925
 540 GTCTTTTGAGATGCTGATCTCTGGGCGCTTTCATCATCGGTGTGTACTTCGGGCTGACTAC 599
 926 AGGTTGGTCTGATGTGGAGAAATCGCCCCCAGCTCATCTTCGGGGTCTCTGGG 985

600 TGCTTTGTGCCCATGTATGTGGAGAGGTGTCACTACAGCTCTACGTGAGAGCCCTAGG 659
 986 AACACTCAACCAATTTGCCCATCTGTTCATTTGGCATTTCTGGTTCGCCAGGTGTGGGTTTGA 1045
 660 CACACTGCACACAGCTGGGATCTGTGGCATCTTATTTGCCAGGTGTGGTGTGATGA 719
 1046 GTCTATGCTGGGACAGACTACCTGTGGGCCATTTGCTTCTGGCTATCAAGTACTTCTCTGC 1105
 720 CTCATCATGGGCAATGCAGACTTGTGGCTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 779
 1106 TCTCTCTGAGCTGCTTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1165
 780 CTTGCTACAGTGTATCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 839
 1166 CCGGAACCTGAGAGGGCTGTCCCGAAGAGTCTAAAGCGCTTGACAGGCTGGGCTGATGT 1225
 840 TCGTAACGAGAGAACCGGSCCAAGAGTGTCTGTAAGAAGCTTCGAGGGACAGCCGATGT 899
 1226 GTCTGATGCACTGGCTGAGCTGAAGGATGAGAAACGGAAGTTGGAAAGAGAGCGTCCACT 1285
 900 GACCCGAGACTCTGACGAGATGAAGAGAGGGTTCGGCAGATGATGCGGAGAGAAAGGT 959
 1286 GTCTTGTCTGAGCTCTGTGGGAGCGCACCCACCGGAGCGCTCTGTATTTGTCAGTGT 1345
 960 CACCATTTGGAGCTGTTCGCTCACCGCTTACCGGAGCCCATCTCATCGCTGTGT 1019
 1346 GCTGAGCTGAGCAGCAGCTCTCAGGCATCAATGTCTGTCTTCTACTATTTCAACACGAGCAT 1405
 1020 GCTGAGCTGTCCAGCAGCTGTGGGTATCAATGTCTGTCTTCTACTTACTCAACGAGCAT 1079
 1406 CTTTGTAGTTAGCTGGGGTGAACAGCAGCAGCTAGCCACCATAGGAGCTGGTGTGTCAT 1465
 1080 CTTTGAAGAGCAGGCTGTGAGCAGCAGCTGTGTAGCCGACCATCGGCTCCGATATCGTCAA 1139
 1466 TACGCTTTCACCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGTCTGT 1525
 1140 CAGGCTTCTACTGT 1199
 1526 TCTCTGGGCTGGCAGCAGCTGT 1585
 1200 CTTATTTGGCTGTGGCTGGCATGGGCTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1259
 1586 GCTGGAGCGGGTTCATTCATGATGATGTATGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1645
 1260 GCTGGAAACGCTGTCTGT 1319
 1646 CTTCTTTGAGATTGGTCTGTGGCCCATCTCCCTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1705
 1320 CTTCTTTGAAGTAGGCTGT 1379
 1706 GGGCCCCCGCCAGCAGCAGCTGT 1765
 1380 GGGGCCCCGCTGT 1439
 1766 CGTTGGCATGGGTTTCAGTATGTGTGGATGTGTATGGGTCCCTTACGTCTTCTCTCTATT 1825
 1440 TGTGGGCGATGTGTCTCAGTATGTGGAGCAACTGTGGGCGCCCTTACGTCTTCTCTCTATT 1499
 1826 TGGCGTCTCTGT 1885
 1500 CAGGTTGTCTCTGT 1559
 1886 CCGGACATTTGACAGATCTCGGCGCAGCTTTCGAGCGG 1922
 1560 CCGAACCTTCATGAGATCGCTTCCGGCTTCCGGCAG 1596

RESULT 11
 ADB53698
 ID ADB53698 standard; DNA; 2571 BP.
 XX
 AC ADB53698;
 XX

DT 04-DEC-2003 (first entry)
XX Primary rat hepatocyte toxicity modelling related gene SEQ ID NO:4240.
XX toxic effect; gene expression profile; hepatotoxicity; diagnostic marker;
KW toxicity marker; toxicity progression; drug screening;
KW primary rat hepatocyte toxicity modelling; gene; ds.
XX
OS Rattus norvegicus.
XX
XX W02003065993-A2.
XX
XX 14-AUG-2003.
XX
XX 04-FEB-2003; 2003WO-US003482.
XX
XX 04-FEB-2002; 2002US-0353171P.
XX 13-MAR-2002; 2002US-0363534P.
XX 08-APR-2002; 2002US-0370249P.
XX 10-APR-2002; 2002US-0371134P.
XX 10-APR-2002; 2002US-0371135P.
XX 10-APR-2002; 2002US-0371150P.
XX 11-APR-2002; 2002US-0371413P.
XX 19-APR-2002; 2002US-0373601P.
XX 19-APR-2002; 2002US-0373602P.
XX 22-APR-2002; 2002US-0374139P.
XX 08-MAY-2002; 2002US-0378370P.
XX 09-MAY-2002; 2002US-0378652P.
XX 09-MAY-2002; 2002US-0378653P.
XX 09-MAY-2002; 2002US-0378665P.
XX 09-JUL-2002; 2002US-0394230P.
XX 09-JUL-2002; 2002US-0394253P.
XX 04-SEP-2002; 2002US-0407688P.
XX 28-JAN-2003; 2003US-0442900P.
XX
XX (GENE-) GENE LOGIC INC.
XX Mendrick D, Porter M, Johnson K, Higge B, Castle A, Orr M;
PI Elashoff M;
XX WPI; 2003-731472/69.
XX
XX Determining if a compound induces a toxic effect on a tissue or cell, for
PT identifying hepatotoxic compounds, comprises comparing a gene expression
PT profile of a tissue or cell sample to a database of Tox mean and non-Tox
PT mean values.
XX
XX Claim 44; SEQ ID NO 4240; 874pp; English.
XX
XX The present invention describes a method for determining whether a
CC compound induces a toxic effect on a tissue or cell. The method comprises
CC preparing a gene expression profile of a tissue or cell sample exposed to
CC the compound, and comparing the gene expression profile to a database
CC comprising data or information on the Tox mean and non-Tox mean value.
CC The method is useful for predicting or identifying at least one toxic
CC effect, particularly hepatotoxicity, of a test or unknown compound. The
CC genes listed in the specification are useful as diagnostic or toxicity
CC markers for the prediction or identification of the physiological state
CC of tissue or cell sample that has been exposed to a compound, or to
CC identify or predict the toxic effects of a compound or an agent. These
CC may also be used as markers for monitoring toxicity progression or for
CC drug screening. The present sequence represents a primary rat hepatocyte
CC toxicity modelling related gene sequence from the present invention.
XX
XX Sequence 2571 BP; 528 A; 714 C; 686 G; 643 T; 0 U; 0 Other;
SQ
Query Match 28.5%; Score 679; DB 9; Length 2571;
Best Local Similarity 68.1%; Pred. No. 8.5e-156;
Matches 965; Conservative 0; Mismatches 440; Indels 12; Gaps 1;
XX 506 GGAAACCCCTCAGCAGCGAGTACCTGGGACACTGGCTCTGCTGTATTTCTCAGCTGTGCT 565
DB 211 GGAGGCCAGCAGCAAGAGGTACGGGCCGCTTATGTTGGCCGTGGGAGGGGCGAGTGTCT 270

QY 566 TGGCTCCCTTCAGTTTGGCTATACATTTGGAGTCATCAACGCCCCACAGAAAGTGATTCA 625
DB 271 CGGATCCCTCGAGTTGGCTATATAACCGGTGTATCAACGCCCCACAGAAAGTAAATGA 330
QY 626 ACAGAGCTACAAATCAATTTGGCTGGGTGAGCAGGGTCTTGGGGAGCCGGACTCCATCCC 685
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QY 686 ACAAGGCAACCTCACTACCTTTGGGCTCTCTCGTGGCCATCTTCTCTGTGGGTGGCAT 745
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Db 950 CACCATCTTGGAGCTGTTCGGCTCCCGCCCTACCGCAGGCCATCTCATCGTGTGGT 1009
QY 1346 GCTGACGCTGAGCCAGCAGCTCTCAGGCAATCAATCTGTTTCTACTATTCAACAGCAT 1405
~ Db 1010 GCTGACGCTGCCAGCAGCTGTCTGGCATCAACGCTGTCTTACTTACTCCAGAGCAT 1069
QY 1406 CTTTGTAGTTAGCTGGGTGGGAAACAGCCAGCTTACCCACCATAGAGTGTGTGTCAT 1465
Db 1070 CTTTGAAGAGGGGGGTGTCAGCAGCTGTGTATGCCACCATTTGGCTCCGGTATCGTCA 1129
QY 1466 TACCGTCTTACGTTGCTGTGGTCTCTTAGTAGAGCGAGTGGCGACGAGCACTCCA 1525
Db 1130 CAGGCTTTCATGTGCTGTGCTGTGTGTGGAGGAGGAGCGCGGACCTGTGA 1189
QY 1526 TCTCTGGGCTGGCAGGATGTGGCTGTGGCTATCTTATGAGCGGTGCTGTGCTGCT 1585
Db 1190 CTTATAGGCTCGCTGGCATGGCGGGTGTGGCATCTCATGACCATCGCGCTAGCACT 1249
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Db 1250 GCTGAGCAGCTACCTTGGATGTCTATCTGAGCATGTGGCCATCTTTGGCTTTGTGGC 1309
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Db 1310 CTTCTTTGAGTTGGTTCCTGGCCCATCCATGGTTCATCTGTGGTGAACCTTCAGGCA 1369
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Db 1370 GGGTCCAGCTGACCTGCTGATGGCTGTGGCGCTTCTTCCAACTGGACCTCAATTTTCAT 1429
QY 1766 CGTTGGCATGGGTTCCAGTATGTGGGATGCTATGGGTCCCTACGTCCTTCTTATT 1825
Db 1430 TGTGGGCATGTGCTTCCAGATGTGGAGCACTGTGTGGTCCCTACGTCCTTCATCATCTT 1489
QY 1826 TGGCTGCTCTGCTTGGCTTCTTCACTTCACTTCACTTCACTTCACTTCACTTCACTTCA 1885
Db 1490 CACTGTGCTCTTGGTCTTGTCTTCTTCACTTCACTTCACTTCACTTCACTTCACTTCA 1549
QY 1886 CCGGACATTTGACAGATCTCGGCCACCTTCCGACGG 1922
Db 1550 CCGGACCTTCGATGAGATCGCTTCCGGCTTCCGGGAC 1586

RESULT 15
ABV77983

ID XX ABV77983 standard; DNA; 2856 BP.
XX AC ABV77983;
XX
DT 12-NOV-2002 (first entry)
XX
DE Hypoxia-regulated protein coding sequence #3.
XX
KW Cytostatic; vasotropic; tranquiliser; antiatherosclerotic; gene therapy;
KW antiinflammatory; vulnary; gynecological; ophthalmological; vaccine;
KW hypoxia; tumorigenesis; angiogenesis; apoptosis; cancer;
KW ischaemic condition; reperfusion injury; retinopathy; neonatal stress;
KW preclapmsia; atherosclerosis; inflammatory condition; wound healing;
KW inflammation; erythropoiesis; hair loss; human; gene; ds.
XX Homo sapiens.
XX WO200246465-A2.
XX
PD 13-JUN-2002.
XX
PP 10-DEC-2001; 2001WO-GB005458.
XX
PR 08-DEC-2000; 2000GB-00030076.
PR 08-FEB-2001; 2001GB-00003156.
PR 25-OCT-2001; 2001GB-00025666.
XX (OXFO-) OXFORD BIOMEDICA UK LTD.
XX
PA White J, Mundy CR, Ward NR, Krige D, Kingsman SM, Harris RA;
PI Rayner WN;
PI
XX WPI; 2002-627238/67.
XX
PT Identifying a gene involved in disease for treating hypoxia-regulated
PT conditions, comprises comparing the transcriptome/proteome of two cell
PT types under different conditions and identifying a differentially
PT regulated gene.
XX
PS Claim 37; Page 333; 538pp; English.
XX
CC The present invention relates to methods for identifying genes and
CC proteins that are implicated in a specific disease or physiological
CC condition. The method comprises comparing the transcriptome/proteome of a
CC specialised cell type implicated in a disease or condition with that of a
CC second specialised cell type, under two experimental conditions, and
CC identifying a gene that is differentially regulated in the two
CC specialised cell types under experimental conditions. ABV77873-ABV78116
CC and ABP65061-ABP65257 were identified using the methods of the invention.
CC The coding sequences and proteins are useful for treating a disease in a
CC patient, for manufacture of a medicament for treating hypoxia-regulated
CC conditions, and for regulating tumorigenesis, angiogenesis, apoptosis,
CC biological response to hypoxia conditions, or hypoxic-associated
CC pathology in a patient. The coding sequences and proteins are also useful
CC for monitoring the therapeutic treatment of a disease or physiological
CC condition, such as cancer, ischaemic conditions, reperfusion injury,
CC retinopathy, neonatal stress, preclapmsia, atherosclerosis, inflammatory
CC conditions, wound healing, inflammation, erythropoiesis or hair loss
XX
SQ Sequence 2856 BP; 602 A; 804 C; 753 G; 697 T; 0 U; 0 Other;

Query Match 28.5%; Score 679; DB 6; Length 2856;
Best Local Similarity 68.1%; Pred. No. 9e-156;
Matches 965; Conservative 0; Mismatches 440; Indels 12; Gaps 1;

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Qy 566 TGGCTCCCTTCAGTTTGGCTATACATTGAGTCAACGCCCCACAGAAAGTCAATCA 625
Db 242 TGGCTCCCTGCACTTGGCTACAACACTGGAGTCAATGCCCCCAGAGGTGATCGA 301

Qy	626	ACAGAGCTACAAATGCAATCTTGCGTGGATAGCGAGGGCTCTCGGGGGAGCCGAGCATCCATCCC	685
Db	302	GGAGTTTCTCAAAACAGACATGGGTCCAACCGTATGG-----GGAGAGCATCTCT	349
Qy	686	ACAAGGACACCTCACTACTACCTTTTGGGCTCTCCGTGGCCATCTTCTCTGTGTGGTGGCAT	745
Db	350	GCCACACACGGTCAACACGGTCTGGTCCCTCTCAGTGGCCATCTTTTCTGTGTGGGGCAT	409
Qy	746	GATTTCCTCTCTTCTCATATGGCATCATTTCTCAATGGTTGGGAAGAAAAAGGCTATGCT	805
Db	410	GATTGGCTCTCTCTCTGTGGGCCCTTTTCGTTAAACCGCTTTGGCCGGGAATTCATGCT	469
Qy	806	GGCCAAACAATGTCCTGGCTGTGTGGGGGGGGCCCTCATGGGCTTAGCCAAATGCCGGGC	865
Db	470	GATGATGAACCTGTGTGGCCTTCGTGTCCGCGCTCTCATGGGCTTCTCGAAACTGGGCAA	529
Qy	866	CTCCTATGAGATACTCAATCTCGAGACGGTTCCTCATTTGGGCGCTACTCAGGGCTAAATC	925
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Qy	986	AACACTCAACCAATPGGCCATCGTCAATGGGAATCTGGTTGCCAGAGTGTGGTTTGGAA	1045
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Qy	1046	GTCTATGCTGGGCACAGCTACCTGTGGCCATTTGCTTCTGGCTATCACAGTACTCCCTGC	1105
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Qy	1106	TCTCTCTCAGCTGCTTCTGTTGCCCTTCTGTCTCTGAGAGCCCCCGATPACCTCTACATCAT	1165
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Qy	1286	GTCCTTGCTGCAGTCTCTGGGCGCCGACCCACCGGCGAGCTCTGATTAATTCAGTGGT	1345
Db	950	CACCATCTGGAGCTGTTCCGCTCCCCGCTACCGCCAGCCCATCTCTATCGCTGTGGT	1009
Qy	1346	GCTGCACTGAGCCAGCAGCTCTCAGGCATCAATGTGTTTTCTACTATTTCACACAGCAT	1405
Db	1010	GCTGCAGCTGTCCAGCAGCTGTCTGGCATCAACGCTGTCTTCTATTACTCCACGAGCAT	1069
Qy	1406	CTTTTGAGTTAGCTGGGTGGNAAGCAGCAGCTTAGCCACCATAGGAGCTGGTGTGTCAA	1465
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Qy	1466	TACCGTCTTCAACGTTGTCTCGGTGCTTCTAGTAGAGCGAGCTGGGCGACGACACTCCA	1525
Db	1130	CAGGCTTCTACTCTGTGTGTGTGTGTGGTGGAGCGAGCAGCGCGGAGCCCTGCA	1189
Qy	1526	TCTCTGGGCTGGCAGGCATGTGTGGCTGTGCCATCTTGATGACGGTGGCTCTGTGCT	1585
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Qy	1586	GCTGGAGGGGTTCCATCCATGAGTTATGTGTCCATGTTGGCCCATATTTGGCTTTTGGC	1645
Db	1250	GCTGGAGCAGCTACCTCTGGATGTCTATCTGAGCATCGTGGCCATCTTTTGGCTTTTGGC	1309
Qy	1646	CTTCTTTGAGATTGGTCTGGCCCAATCCCTGTGTTCAATGTGGCGAGCTCTTTACGCCA	1705
Db	1310	CTTCTTTGAAGTGGGTCTGGCCCAATCCCATGTTTATGAGCATCGTGGCCATCTTTTGGCT	1369
Qy	1706	GGGCCCCCGGCCAGCAGCCATGGCTGTAGCTGGTTTTCTCAACATGGACCTGTAACTTCAT	1765

Search completed: May 16, 2004, 01:32:07
Job time : 566.671 secs

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GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 16, 2004, 00:27:52 ; Search time 3702.57 Seconds
(without alignments)
19243.679 Million cell updates/sec

Title: US-10-067-449-10
Perfect score: 2386
Sequence: 1 tcgactctgagatccctc.....ctggactttcttcagttg 2386

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

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2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_phg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1203.4	50.4	1497	29	AY421217 Mus muscu
2	1157.8	48.5	3049	11	BC034387
3	1035.4	43.4	1497	29	AY421215 Homo sapi
4	1018.8	42.7	1814	14	CD014068 90134560

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

5	866.4	36.3	1497	29	AY421216
6	669.8	28.1	857	14	CB814984 EST00224
7	667.4	28.0	813	12	BI152694
8	636.6	26.7	688	13	BY740650
9	634.6	26.6	883	13	B0892119
10	581.6	24.4	834	12	BI153345
11	577.4	24.2	1461	29	AY411068
12	575.8	24.1	854	13	BX389357
13	573.2	24.0	1461	29	AY411066
14	571.2	23.9	748	13	BU614385
15	557.6	23.4	1340	11	AK089353
16	549.8	23.0	601	12	BG086161
17	546.8	22.9	3719	11	AK045328
18	546.4	22.9	610	10	AW412024
19	544.2	22.8	801	10	BF540033
20	537.6	22.5	3733	11	BC050095
21	534.8	22.4	936	9	AL521327
22	526.4	22.1	3716	11	AK028041
23	517	21.7	930	9	AL521328
24	479.8	20.1	523	10	BE282589
25	467.4	19.6	892	14	CB193117
26	465	19.5	598	9	AA799760
27	462.8	19.4	662	13	BU612883
28	462.4	19.4	1557	29	AY399002
29	460.8	19.3	2538	11	AK005068
30	460.4	19.3	513	9	AA396478
31	456.2	19.1	1560	29	AY399000
32	455	19.1	1260	29	AY411067
33	452	18.9	967	9	AL547677
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35	422.2	17.7	689	10	BE648013
36	420.4	17.6	964	13	B0846084
37	418.4	17.5	817	12	BG675982
38	417.8	17.5	860	14	CF616390
39	415	17.4	551	10	BF076945
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ALIGNMENTS

RESULT 1	AY421217	AY421217	1497 bp	DNA	linear	GSS 17-DEC-2003
LOCUS	AY421217	Mus musculus SLC2A4 gene, VIRTUAL TRANSCRIPT, partial sequence,				
DEFINITION	AY421217	genomic survey sequence.				
ACCESSION	AY421217	GI:39777174				
VERSION	AY421217.1	GI:39777174				
KEYWORDS	GSS.					
SOURCE	Mus musculus	(house mouse)				
ORGANISM	Mus musculus					
REFERENCE	1	(bases 1 to 1497)				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, P., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sainsky, J.J., Adams, M.D. and Cargill, M.					
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios					
JOURNAL	Science	302 (5652), 1960-1963 (2003)				
PUBMED	14671302					
REFERENCE	2	(bases 1 to 1497)				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, P., Murphy, B., Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sainsky, J.J., Adams, M.D. and Cargill, M.					
TITLE	Direct Submission					

JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence is made by sequencing genomic exons and ordering them
based on alignment.
FEATURES
Source Location/Qualifiers
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/mol_type="genomic DNA"
/db_xref="taxon:10090"
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/gene="SLC2A4"
/locus_tag="HMC7483"
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Query Match 50.4%; Score 1203.4; DB 29; Length 1497;
Best Local Similarity 82.6%; Pred. No. 2e-221;
Matches 1237; Conservative 0; Mismatches 260; Indels 0; Gaps 0;
QY 501 GATGGGAAACCCCTCAGCAGCGAGTGAAGTGGGACACTGGTCTTGTGTTATCTCAGCT 560
DB 1 GATGGGAAACCCCTCGGCAGGAGTGAAGTGGGACACTGGTCTTGTGTTATCTCAGCT 60
QY 561 GTCTTGGCTCCCTTCAGTTTGGCTATAACATTGGAGTCAATCAAGCCGCCACAGAAAGTG 620
DB 61 GTGCTTGGCTCCCTTCAGTTTGGCTATAACATTGGGTTATCAATGCCCCACAGAGGTG 120
QY 621 ATTGAACAGAGTACATGCAACTTGGCTGGGTAGGAGAGGTCTGGGGGACCGGACTCC 680
DB 121 ATTGAACAGAGTACATGCAACTTGGCTGGGTAGGAGAGGTCTGGGGGACCGGATTC 180
QY 681 ATCCCAAGGACCTCACTACCTTGTGGGCTCTCTGGGCACTCTCTCTGTGGGT 740
DB 181 ATCCCAAGGACCTCACTACCTTGTGGGCTCTCTGGGCACTCTCTCTGTGGGT 240
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DB 241 GGCATGATCT 300
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QY 1821 CTATTTCCGCTCTCTGCTGGTCTTCTCATCTTCACTTCTTCAAGAGTGGCTGAAACC 1880
DB 1321 CTATTTCCGCTCTCTGCTGGTCTTCTCATCTTCACTTCTTCAAGAGTGGCTGAAACC 1380
QY 1881 AGAGCCGCGACATTTGACCGAGTCTCGGCCACTTCCGACGACACCTTCTCTCTTAGAG 1940
DB 1381 AGAGCCGCGAGTTTGGACGAGTCTAGTCCCTCCGACGACACCTTCTCTCTTAGAG 1440
QY 1941 CAGGAGTGAACACCCAGTACAGAACTTGAATCTTAGGGCCAGATGAGAACTGACTAA 1997
DB 1441 CAGGAGTGAACACCCAGTACAGAACTTGAATCTTAGGGCCAGATGAGAACTGACTGA 1497
RESULT 2
BC034387
LOCUS
DEFINITION Homo sapiens, Similar to solute carrier family 2 (facilitated
glucose transporter), member 4, clone IMAGE:5187454, mRNA.
ACCESSION BC034387
VERSION BC034387.1 GI:21706716
KEYWORDS HTC.
SOURCE
ORGANISM Homo sapiens (human)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3049)
AUTHORS Strausberg, R.
TITLE Direct Submission
JOURNAL
REMARK NIH-MGC Project URL: <http://mgc.nci.nih.gov>
COMMENT Contact: MGC help desk
Email: cgapb-remail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome
Sequencing Center

Center code: BCM-HGSC
 Web site: <http://www.hgsc.bcm.tmc.edu/cdna/>
 Contact: amg@bcm.tmc.edu
 Gunaratne, P.H., Garcia, A.M., Lu, X., Hulyk, S.W., Hale, S.M.,
 Yoon, V.S., Kowis, C.R., Lawrence, S., Martin, R.G., Muzny, D.M.,
 Richards, S., Gibbs, R.A.

Clone distribution: MGC clone distribution information can be found
 through the I.M.A.G.E. Consortium/LLNL at: <http://image.llnl.gov>
 Series: IRAK Plate: 50 Row: h Column: 18
 This clone was selected for full length sequencing because it
 passed the following selection criteria: matched mRNA gi: 4507010
 This clone has the following problem: frame shifted.

FEATURES

source

Location/Qualifiers
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 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="IMAGE:5187454"
 /tissue_types="Colon, Kidney, Stomach, adult, whole pooled"
 /clone_lib="NIH MGC_116"
 /lab_host="DH10B"
 /note="Vector: pCMV-SPORT6"

ORIGIN

Query Match 48.5%; Score 1157.8; DB 11; Length 3049;
 Best Local Similarity 83.0%; Pred. No. 9.9e-213;
 Matches 1359; Conservative 0; Mismatches 217; Indels 61; Gaps 1;
 455 CTTTAAAGCAATAATGCTGAATCCAGAGAGTGGCTCTGAAGATGGGAACCC 514
 188 CTTTAAAGCAGATGCGCTGGGCTTCCAAACAGATAGGCTCGAAGATGGGAACCC 247
 515 TCAGCAGCAGTCACTGGGACACTGGTCTCTGTGTATCTCAGCTGTGTCTGGCTCCCT 574
 248 TCAGCAGCAGTCACTGGGACACTGGTCTCTGTGTATCTCAGCTGTGTCTGGCTCCCT 307
 575 TCAGTTGGCTATAAATTGGAGTCAATCAAGCCCAAGAAAGTGAATGAACAGAGCTA 634
 308 GCAGTTGGGTACAAATTGGGGTCAATGATGCCCCCTCAGAGAGTGAATGAACAGAGCTA 367
 635 CAATGCACTTGGCTGGTGGTGGGAGGCTCTGGGGGACCGGACTCCATCCCAAGGCAC 694
 368 CAATGAGACGTGGCTGGGAGGAGGAGGCTCTGGGGGACCGGACTCCATCCCTCCAGGCAC 427
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 428 CCTCACACCTCTGGGCTCTCTCCGTGGCCTCTCTCTGTGGGTGGCATGATTTCCCTC 487
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 488 CTTTCTCATTTGGCATCATTTCTCAATGGTTGGAAAGAAAGGGCTATGCTGCCCAACAA 547
 815 TGTCTTGGCTGTCTGGGGGGGCGCTCATGGGCTAGCAATGCCGCGGCTCTCTATGA 874
 548 TGTCTTGGGCTGTCTGGGGGGGCGCTCATGGGCTAGCAATGCCGCGGCTCTCTATGA 607
 875 GATACTCATTTCTCGGACGGTTCTCTCAATGGCGCTACTCAGGGCTAAACATCAGGGTTGGT 934
 608 AATGCTCATCTTGGACGATTTCTCTATTTGGCGCTACTCAGGGCTGACATCAGGGCTGGT 667
 935 GCCTATGATATGTGGGAAATCGCCCCCACTCATTTCTGGGGGTGCTTGGGAACATCTCAA 994
 668 GCCCATGTAGTGGGGAGATTGCTCCCACTCACTTCCGGGGGCGCTGGGGAGCGCTCAA 727
 995 CCAATGGGCACTGTATTTGGCATTTGGTTGGGCTTGGGCTTGGAGTCTATGCT 1054
 728 CCAATGGGCACTGTATTTGGCATTTGGTTGGGCTTGGGCTTGGAGTCTATGCT 787
 1055 GGGCAGCAGCTACCTGTGGGCAATTTGCTTCTGGCTATCAGAGTACTCCCTGCTCTCTGCA 1114
 788 GGGCAGCTGCGAGCTGTGGCACTTGTCTTCTGGGCTTCAAGTCTACCTGCTCTCTGCA 847

QY 1115 GCTGCTTCTGTTGCTCCCTTCTGCTCTGAGAGCCCCCGATACCTCTACATCATTCGGAACT 1174
 DB 848 GCTGCTTCTGTTGCTCCCTTCTGCTCCGAGAGCCCCCGATACCTCTACATCATTCGGAACT 907
 QY 1175 GAGAGGGGCTGCTCCGAAAGAGTCTAAGCGCTGACAGGCTGGGCTGATGCTGATGC 1234
 DB 908 CGAGGGGCTGCTCCGAAAGAGTCTAAGCGCTGACAGGCTGGGCTGATGCTGATGC 967
 QY 1235 ACTGGCTGAGCTGAAAGATGAGAAACGGAAGTTTGGAAAGAGAGCGTCCACTGCTTGGCT 1294
 DB 968 GCTGCTGAGCTGAAAGATGAGAAACGGAAGCTGGAGCGTGGAGCGGCACTGCTCCCTGCT 1027
 QY 1295 GAGCTCTCTGGGAGCGGACCCAGCCAGCTCTGATATTTAGAGTGGTGTGAGCT 1354
 DB 1028 CAGCTCTCTGGGAGCGGCTGACCCAGCGGAGCGCTGATCAATTTGGCTGCTGCTGAGCT 1087
 QY 1355 GAGCCAGAGCTCTCAGGAGCATCAATCTGTTTTTCTACTATTCAACAGAGCATTTTGAAGTT 1414
 DB 1088 GAGCCAGAGCTCTCTGGGATCAATGCTGTTTTCTATTATTCGACAGCATTTTGGAGAC 1147
 QY 1415 AGCTGGGGTGGAAACAGCCAGCTTACGCCACCATAGGAGCTGGTGTGCTCAATACCGTCTT 1474
 DB 1148 AGCAGGGGTAGGCGAGCTGCTATGCCACCATAGGAGCTGGTGTGCTCAACAGCTCTT 1207
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 QY 1487 -----GGTCTCTTAGTAGAGAGCTGGGAGCGGACACATCTCATCTCTCG 1533
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 DB 1328 GCCTGGCAGGCAATGTGGCTGTGCCATCTCTGATGACTGTGGCTGTCTGCTGCTGAGC 1387
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 DB 1388 GAGTTCAGCCATAGCTAGCTTCCATTTGTGGCCATCTTTGGCTTGTGGCTTCTTTG 1447
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 DB 1568 TGGTTCATGATGTTGGGAGGCTATGGGCGCTTACGCTTCTCTTCTATTTGGCTGCT 1627
 QY 1834 TCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1893
 DB 1628 TCTGCTGCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1687
 QY 1894 TTGACAGATCTCGGCGACCTTCCGAGGCACTTCTCTCTTTAGAGCAGGAGTGAAC 1953
 DB 1688 TTGACAGATCTCAGCTGCTTCCACCGGACACCTCTCTTTTAGAGCAGGAGTGAAC 1747
 QY 1954 CAGTACAGACTTGAATTAAGGCGCAGATGAGATGACTAATGATTTGAAGTGA 2013
 DB 1748 CCAGCAGAACTTTAGTATTTAGGCGCAGATGAGAAACGACTGAGGGCGGAGGAGG 1807
 QY 2014 CGCTCCATCATCTCTCT 2030
 DB 1808 GGGAGGCGGAGCTCTCT 1824

RESULT 3

AY421215

LOCUS

DEFINITION

AY421215 1497 bp DNA linear GSS 17-DEC-2003
 Homo sapiens SLC2A4 gene, VIRTUAL TRANSCRIPT, partial sequence,

ACCESSION CD014068
VERSION CD014068.1 GI:37777598
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
AUTHORS Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1814)
Jin, P., Fu, G.K., Wilson, A.D., Yang, J., Chien, D., Hawkins, P.R.,
AUTHORS Au-Young, J. and Stuve, L.L.
TITLE PCR isolation and cloning of novel splice variant mRNAs from known
drug target genes
JOURNAL Unpublished (2003)
COMMENT Contact: Jin, P.
Incyte Corporation
3160 Porter Drive, Palo Alto, CA 94304, USA
Tel: 650 621 8639
Fax: 650 621 8965
Email: pj@incyte.com

FEATURES
source Location/Qualifiers
1..1814
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone_lib="Single gene library"
/notes="Vector: pDrive Cloning Vector; RT-PCR was performed
using gene-specific primers flanking the open-reading
frame. PCR products were subcloned into pDrive Cloning
Vector and sequenced completely using M13 forward and
reverse primers. Sequencing gaps were closed by
re-sequencing using primers flanking the gapped areas."

ORIGIN
Query Match 42.7%; Score 1018.8; DB 14; Length 1814;
Best Local Similarity 80.1%; Pred. No. 6.4e-186;
Matches 1263; Conservative 0; Mismatches 197; Indels 116; Gaps 1;
QY 455 CTTATAAGCAACATATGCTCTGAAATTCACAGAGATCGGCTCTGAAGATGGGAAACCCC 514
DB 115 CTTCTAAGACGAGATCGCTCGGGCTTCCACAGATAGGCTCGAAGATGGGAAACCCC 174
QY 515 TCAGGACGAGTACCTGGGACATGGTCTCTGCTGATCTCAGCTGCTGGCTCCCT 574
DB 175 TCAGGACGAGTACCTGGGACATGGTCTCTGCTGATCTCAGCTGCTGGCTCCCT 234
QY 575 TCAGTTTGGCTATAAATTCGAGTCTCAACGCGCCACAGAAAGTGAATGAACAGAGCTA 634
DB 235 GCAATTTGGGTACAACTTGGGGTCACTCATGCCCCCTCAGAAAGTGAATGAACAGAGCTA 294
QY 635 CAATGCAACTTGGCTGGGTAGGAGGAGTCTTGGGGACCGGACTCCATCCCAAGGCAC 694
DB 295 CAATGAGACGTGGCTGGGAGGAGGAGGCTGAGGGACCCAGCTCCATCCCTCCAGGCAC 354
QY 695 CTTCACTACCTTGGGCTCTCTCGTGGGCATCTCTGCTGGGTGGGATGATTTCTTC 754
DB 355 CTTCACTACCTTGGGCTCTCTCGTGGGCATCTCTGCTGGGTGGGATGATTTCTTC 414
QY 755 CTTTCTCATTTGGCATCATTTCTCAATGTTGGGAAGGAAAGGCTATGCTGGCCAAACA 814
DB 415 CTTTCTCATTTGGTATCATCTCTCAGTGGCTTGAAGAAAGGCAATGCTGGTCAACA 474
QY 815 TGTCTTGGCTGTGCTGGGGGCGCCCTCATGGGCTAGCCAAATGCGCGGCTCTCTATGA 874
DB 475 TGTCTTGGGCTGTGCTGGGGGCGAGCTCATGGGCTGGCCCAACGCTGCTCCCTATGA 534
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DB 535 AATGCTCATCTTGGAGGATTCCTCATTTGGGCTACT----- 572
QY 935 GCCTATGATGTGGAGAAATCGCCCCCACTCATCTTGGGGTGCCTTGGGAACACTCAA 994
DB 573 ----- 572

QY 995 CCAATTTGGCCATCGTCATTTGGGCAATTTCTGGTTCGCCAGGTGTTGGGTTTGGAGTCTATGCT 1054
DB 573 -----CAGGTGCTGGGCTTGGAGTCCCTCT 598
QY 1055 GGGCACAGCTTACCTGTGGCCATTTGCTTCTGGCTATCACAGTACTCCCTGCTCTCCCTGCA 1114
DB 599 GGGCCTGTCAGCTGTGGCCACTGCTTCTGGGCTCACAGTGTACTTCCCTCTCCCTGCA 658
QY 1115 GCTGCTTCTGTTGGCTTCTGCTCTGAGAGCCCCCGATACCTCTTACATCATCCGGAACCT 1174
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QY 1175 GAGGGGCTGCTCCCGAAGAGTCTTAAAGCCCTGACAGGCTGGGCTGATGTCTGATGC 1234
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QY 1235 ACTGGCTGAGCTGAAGGATGAGAAACCGAAGTTGGAAGAGAGCGCTCCACTGCTCTTGTCT 1294
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QY 1295 GCAGCTTCTGGGCGAGCGCACCCACCGGAGCGCTCTGATTTATTTGCACTGCTGCTGAGCT 1354
DB 839 CCAGCTTCTGGGCGAGCGGTACCCACCGGAGCGCTGATCATTTGCGGTCTGCTGAGCT 898
QY 1355 GAGCCAGAGCTCTCAGGCAATCAATGCTGTTTCTACTATTCACAGCATCTTTGAGTT 1414
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QY 1655 GATTGTCTCTGGGCCCATCCCTGTTTCAATTTGGCGGAGCTCTTCAGCCAGGCGCCCGG 1714
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QY 1775 GGGTTTCCAGTATTTGGGATGCTATGGTCCCTAGCTCTTCTCTTATTTGCTCTCT 1834
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DB 1379 CTTGCTTGGCTTCTTCACTTTCACCTTCTTAAGAGTACCTGAAACCTGAGCGCGGAGT 1438
QY 1895 TGAACAGATCTCGGCCACCTTCCGAGGACACCTTCTCTCTTTAGAGCAGAGGTGAAC 1954
DB 1439 TGAACAGATCTCAGCTGCTTCCAGCGGACACCTCTCTCTTTAGAGCAGAGGTGAAC 1498
QY 1955 CAGTACAGACTTGAATCTTAGGCGCAGATGAGATGATCTAATCGATTTGAAGTGAGAC 2014
DB 1499 CAGCAGAACTTGAATTTTAGGGCCAGATGAGAAACGACTGAGGGGCCAGGAGGGGTG 1558
QY 2015 GCTTCCATCATCTCT 2030
DB 1559 GGNAGCCAGCTCTCT 1574

RESULT 5	AY421216	1497 bp	DNA	linear	GSS 17-DEC-2003
LOCUS	Pan troglodytes SLC2A4 gene, VIRTUAL TRANSCRIPT, partial sequence, genomic survey sequence.				
DEFINITION	AY421216				
ACCESSION	AY421216				
VERSION	AY421216.1	GI:39777173			
KEYWORDS	GSS.				
SOURCE	Pan troglodytes (chimpanzee)				
ORGANISM	Pan troglodytes				
REFERENCE	1 (bases 1 to 1497)				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Inferring nonneutral evolution from human-chimp-mouse orthologous gene trios				
JOURNAL	Science 302 (5652), 1960-1963 (2003)				
PUBMED	14671302				
REFERENCE	2 (bases 1 to 1497)				
AUTHORS	Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejarawal, A., Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B., Perriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J., Adams, M.D. and Cargill, M.				
TITLE	Direct Submission				
JOURNAL	Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA				
COMMENT	This sequence is made by sequencing genomic exons and ordering them based on alignment.				
FEATURES	Location/Qualifiers				
source	1..1497				
gene	/organism="Pan troglodytes"				
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	/db_xref="taxon:9598"				
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	/locus_tag="HCM7483"				
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Best Local Similarity	63.1%;	Pred. No.	1.5e-156;		
Matches	945;	Conservative	0;	Mismatches	552;
				Indels	0;
				Gaps	0;
Qy	501	GATGGGGAACCCCTCAGCAGGAGTGA	CTGGGACACTGGTCTCTGTTATTTCTCAGCT	560	
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Qy	561	GTGCTTGGCTCCCTTCAGTTTGGCTATA	CACTTGAAGTCAACGCGCCACAGAAAGTG	620	
Db	61	GTGCTTGGCTCCCTTCAGTTTGGGTACA	CACTTGAAGTCAATGCGCCCTCAGAGGTG	120	
Qy	621	ATTGAACAGAGTACAATGCAATTGGCT	AGGAGGTCCTGGGGGACCGGACTCC	680	
Db	121	ATTGAACAGAGTACAATGCAAGTGGCT	AGGAGGTCCTGGGGGACCGGACTCC	180	
Qy	681	ATCCCAACAGGACCCCTCACTACCTTT	GGGCTCTCTCCGTTGGCCATCTCTCTGGGT	740	
Db	181	ATCCCTCCAGGACCCCTCAACCCCTCT	GGGCCCTCTCCGTTGGCCATCTTTCCGTGGGC	240	
Qy	741	GGCATTGATTTCTCTCTTCTCAATGG	CACTTTCATGTTGGGAAGGAAAGGGCT	800	
Db	241	GGCATTGATTTCTCTCTTCTCAATGG	CACTTTCATGTTGGGAAGGAAAGGGCC	300	
Qy	801	ATGCTGGCCAAACAATGTCTTGGCTGT	GTGGGGGCGCCCTCATGGGCTTAGCCAAATGCC	860	
Db	301	ATGCTGGTCAACAATGTCTGCGGTGT	GTGGGGGCGGCTCATGGGCTTAGCCAAATGCC	360	
Qy	861	GGGGCTCTCATGAGACTCAATTCGGA	CGGTTTCCTCATTTGGGCGCTACTCAGGGCTA	920	
Db	361	GCTGCCCTCTATGAATGCTCATCTCT	TGGACGATTCCTCATTTGGCGCGCTACTCAGGGCTG	420	
Qy	921	ACATCAGGGTTGGTGCCTATGTATGT	TGGGAGAAATCGCCCCCACTCATCTTTCGGGGTGCC	980	
Db	421	ACATCAGGGCTGGTGCCCATGTACGT	TGGGGAGAGTTGCTCCCACTCACCTCGGGGGCGCC	480	
Qy	981	TTGGGAACACTCAACCAATTTGGCCAT	CGTCAATTGGCATTTCTGGTTCGCCAGGTGTGGGT	1040	
Db	481	CTGGGACGCTCAACCAACTGGCCAT	CGTTATTCGGCATNNNTGATCGCCCAAGNNNNNNNN	540	
Qy	1041	TTGGAGTCTATGCTGGGCACAGCTAC	CCCTGTGGCCATTGCTTCTGGCTATCACAGTACTC	1100	
Db	541	NNNNNNNNNNNNNNNNNNNNNNNNNN	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	600	
Qy	1101	CTGCTCTCTCGTGCAGCTGCTTCTGT	TGCCCCCTTCTGCTGAGAGCCCCCGATACCTCTAC	1160	
Db	601	NNNNNNNNNNNNNNNNNNNNNNNNNN	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	660	
Qy	1161	ATCATCCGGAACCTGGAGGGCCCTGCC	CGGAAAGAGTCTAAAGCGCTCAGACGGCTGGGCT	1220	
Db	661	NNNNNNNNNNNNNNNNNNNNNNNNNN	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	720	
Qy	1221	GATGTGCTGATGCACCTGGCTGAGCT	GAAAGATGAGAAACGGAAGTTCGAAAGAGAGCGT	1280	
Db	721	GATGTTCTTGANTCTGGCTGNNNTGA	AGNNNGNNNAAGCGAAGCTGAGCGCTGAGCGG	780	
Qy	1281	CCACTGCTCTGCTGCAGCTCCTGGG	CAGCGCCACCCACCGGAGCTCTGATTATTGCA	1340	
Db	781	CCACTGCTCTGCTGCAGCTCCTGGG	CAGCGCTACCCACCGNNNNNNNNNNNNNNNN	840	
Qy	1341	GTGCTGCTGAGCTGAGCGCAGAGCTCT	CAGGCAATCAATGCTGTTTCTACTATTCAACC	1400	
Db	841	NNNNNNNNNNNNNTGAGCCAGCAGCT	CTCTCGGCATCAATGNNGTTTCTATTATTTCGACC	900	
Qy	1401	AGCATCTTTGAGTTAGCTGGGTGGA	ACAGCAGCCTACGCCACCATAGGAGCTGCTGTG	1460	
Db	901	AGCATCTTCGAGACAGCAGGCGTAG	CGCCAGCTGCTATGCCACCATAGGAGCTGCTGTG	960	
Qy	1461	GTCAATACCGCTTTTCACTGCTCGG	TGCTCTCGGTGTTGTTGGTGGAGCGGCGCGGACG	1520	
Db	961	GTCAACACAGCTTTCACCTTGGTCT	CGGTGTTGTTGGTGGAGCGGCGCGGCGGACG	1020	
Qy	1521	CTCATCTCTTGGGCTGGCAGGCAATG	TGGCTGTGCGCATCTTGCATGACGGTGGCTCTG	1580	
Db	1021	CTCATCTCTTGGGCTGGCAGGCAATG	TGGCTGTGCGCATCTTGCATGACGGTGGCTCTG	1080	
Qy	1581	CTGCTGCTGGAGCGGTTTCCATCAT	GAGTTATGTGTCATCGTGGCCATATTGGCTTT	1640	
Db	1081	CTCTGCTGNNNNNNNNNNNNNNNN	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	1140	
Qy	1641	GTGGCTTCTTTTGAGATTGGTCTCT	GGCCCCCATCCCTCGGTTCAATTGGCCGAGCTCTTC	1700	
Db	1141	NNNNNNNNNNNNNNNNNNNNNNNN	NNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNNN	1200	
Qy	1701	AGCAGGGCCCCCGCCAGCAGCCATG	GCTGCTAGCTGGTTCTCCAACTGGACCTGTAACT	1760	
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Qy	1761	TTTCATCGTTGGCATGGGTTTCCAG	TATGTCAGTGTATGGGTCCTTACCTCTTCTCTT	1820	
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Qy	1821	CTATTTCGCGCTCTCTGCTGGCTTC	TTCACTTTCACCTTCTTAAAGAGTGCCTGAAACC	1880	
Db	1321	CTATTTCGCGCTCTCTGCTGGCTTC	TTCACTTTCACCTTCTTAAAGAGTGCCTGAAACT	1380	
Qy	1881	AGAGCCGCGCATTTTGACAGATCTCG	GCCACCTTCCGACGACCTTCTCTCTTAGAG	1940	
Db	1381	CGAGCCGCGCATTTTGACAGATCTCG	GCCACCTTCTCCACCGGACACCTCTCTTTAGAG	1440	
Qy	1941	CAGGAGGTGAACCCAGGTACAGAACT	TGAAATACCTTAGGGCCAGATGAGAACTGACTAA	1997	
Db	1441	CAGGAGGTGAACCCAGGTACAGAACT	TGAGTATTTAGGGCCAGATGAGAACTGACTGA	1497	

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RESULT 6
CB814984
LOCUS
DEFINITION
  CB814984 rabbit skeleton muscle mRNA to cDNA Oryctolagus cuniculus
  cDNA clone G42 similar to glucose transporter 4 (GLUT4), mRNA
  sequence.
ACCESSION
  CB814984
VERSION
  CB814984.1 GI:29941278
KEYWORDS
  EST.
SOURCE
  Oryctolagus cuniculus (rabbit)
ORGANISM
  Oryctolagus cuniculus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Legomorphia; Leporidae; Oryctolagus.
REFERENCE
  1 (bases 1 to 857)
  Navarrete-Santos, A., Kietz, S., Augustin, R. and Fischer, B.
  Expression of glucose transporters in rabbit preimplantation
  embryos (2003)
  Unpublished (2003)
  Contact: Kietz S
  Department of Anatomy and Cell Biology
  Martin Luther University Halle-Wittenberg, Medical Faculty
  Grosse Steinstrasse 52, D-06097 Halle, GERMANY
  Email: silke.kietz@gmx.de
  Seq primer: T7 Forward
  High quality sequence stop: 857
  POLYA=No.
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ORIGIN
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  Best Local Similarity 86.3%; Pred. No. 1.2e-118;
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Yy 614 GAAAGTATTGAACAGAGCTACATGCACTTGGCTGGGTAGGAGGAGGCTCTGGGGACC 673
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Db 61 CAGTTCCATCCCGCGGACCCCTCACTACCTTGGGCTCTCTCGGTGGCCATCTTCTC 120
Yy 734 TGTGGGTGGCATGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 793
Db 121 CGTGGGCGGATGATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 180
Yy 794 AAGGCTATCTGGCCCAACATGCTTGGCTGTGCTGGGCGGCGGCTCTATGGGCTAGC 853
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Yy 974 GGTGGCTTGGGAGACACTCAACGATTTGGGCTATGTTGGGCTCTCTCTCTCTCTCTCT 1033
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1274 AGAGCTGCACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1333
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1454 TGGTGGTCAATACCG 1470
841 TGGAGTGGTCAACACAG 857

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ACCESSION
  BI152694
VERSION
  BI152694.1 GI:14612695
KEYWORDS
  EST.
SOURCE
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ORGANISM
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  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
  1 (bases 1 to 813)
  NIH-MGC http://mgc.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Robert Strausberg, Ph.D.
  Email: cgabs-r@mail.nih.gov
  Tissue Procurement: Gilbert Smith, Ph.D.
  CDNA Library Preparation: Life Technologies, Inc.
  CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Incyte Genomics, Inc.
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: L14M1185 row: b column: 02
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    providing samples: Gilbert Smith, NIH"
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Matches 654; Conservative 0; Mismatches 33; Indels 0; Gaps 0;

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QY      |||||
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DEFINITION BQ892119 883 bp mRNA linear EST 16-AUG-2002
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BQ892119
VERSION BQ892119.1 GI:22284133
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
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mRNA sequence.
ACCESSION BI153345
VERSION BI153345.1 GI:146113346
KEYWORDS EST.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE NIH-MGC http://mgc.nci.nih.gov/.
JOURNAL National Institutes of Health, Mammalian Gene Collection (MGC)
COMMENT Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs@mail.nih.gov
Tissue Procurement: Gilbert Smith, Ph.D.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LHM11185 row: b column: 05
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Stem cell origin."
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Site 2: NotI; Cloned unidirectionally. Primer: Oligo dt.
Library constructed by Life Technologies. Investigator
providing samples: Gilbert Smith, NIH"

FEATURES
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Best Local Similarity 91.3%; Pred. No. 1.1e-101;
Matches 716; Conservative 0; Mismatches 59; Indels 9; Gaps 9;

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DEFINITION genomic survey sequence.
ACCESSION AY411068
VERSION AY411068.1 GI:39767036
KEYWORDS GSS.
SOURCE Mus musculus (house mouse)
ORGANISM Mus musculus
REFERENCE 1
AUTHORS Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
TITLE 1 (bases 1 to 1461)
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2
AUTHORS 2 (bases 1 to 1461)
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE 2
AUTHORS 2 (bases 1 to 1461)
Clark, A.G., Gnanowski, S., Nielson, R., Thomas, P., Kejarawal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Direct Submission
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JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive, Rockville, MD 20850, USA
COMMENT This sequence was made by sequencing genomic exons and ordering them based on alignment.
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Matches 804; Conservative 0; Mismatches 582; Indels 12; Gaps 1;
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ACCESSION BX389357
VERSION BX389357.1 GI:30462744
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 (bases 1 to 854)
AUTHORS Li, W.B., Gruber, C., Jesse, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Library was constructed by Life Technologies, a division of
Invitrogen. This sequence belongs to sequence cluster 8888.f For
more information about this cluster, see
http://www.genoscope.cns.fr/
cgi-bin/cluster.cgi?seq=CS0BAF002ZG06_AF00144_1&cluster=8888.f.
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/invitrogen Corporation 1600
Paradise Avenue Genoscope sequence ID : CS0BAF002ZG06_AF00144_1.
FEATURES
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ORIGIN  
Query Match      24.1%; Score 575.8; DB 13; Length 854;  
Best Local Similarity 85.8%; Pred. No. 1.4e-100;  
Matches 662; Conservative 0; Mismatches 108; Indels 2; Gaps 2;  
  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1461)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous  
gene trios  
JOURNAL Science 302 (5652), 1960-1963 (2003)  
PUBMED 14671302  
REFERENCE 2 (bases 1 to 1461)  
AUTHORS Clark,A.G., Glanowski,S., Nielson,R., Thomas,P., Kejarival,A.,  
Todd,M.A., Tanenbaum,D.M., Civello,D.R., Lu,F., Murphy,B.,  
Ferriera,S., Wang,G., Zheng,X.H., White,T.J., Shinsky,J.J.,  
Adams,M.D. and Cargill,M.  
TITLE Direct Submission  
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
COMMENT This sequence was made by sequencing genomic exons and ordering  
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 AK089353
 AK089353.1 GI:26354445
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REFERENCE 1
 AUTHORS Carninci, P. and Hayashizaki, Y.
 TITLE High-efficiency full-length cDNA cloning
 JOURNAL Meth. Enzymol. 303, 19-44 (1999)
 MEDLINE 99279253
 PUBMED 10349636

REFERENCE 2
 AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.
 TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes
 JOURNAL Genome Res. 10 (10), 1617-1630 (2000)
 MEDLINE 20499374
 PUBMED 11042159

REFERENCE 3
 AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaka, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.
 TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer
 JOURNAL Genome Res. 10 (11), 1757-1771 (2000)
 MEDLINE 20530913
 PUBMED 11076861

REFERENCE 4
 AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.
 TITLE Functional annotation of a full-length mouse cDNA collection
 JOURNAL Nature 409, 685-690 (2001)
 REFERENCE 5
 AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II team.
 TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

JOURNAL
REFERENCE
AUTHORS

Nature 420, 563-573 (2002)
 6 (bases 1 to 1340)

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, K., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akai, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.

TITLE
JOURNAL

Submitted (16-APR-2002) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.go.jp, URL: http://genome.gsc.riken.go.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Tissues were provided by Dr. John Todd (Dept. of Medical Genetics Wellcome Trust Centre for Molecular Mechanisms in Disease Wellcome Trust/MRC building Addenbrookes Hospital Cambridge) whose assistance we gratefully acknowledge. Please visit our web site for further details. URL: http://genome.gsc.riken.go.jp/ URL: http://fantom.gsc.riken.go.jp/.

FEATURES
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GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

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Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0

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Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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6	679	28.5	2856	4	US-09-606-421B-135
7	679	28.5	2856	4	US-09-221-107-135
8	542.8	22.7	3915	4	US-09-023-655-1104
9	431.4	18.1	5227	4	US-09-919-172-79
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ALIGNMENTS

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; Patent No. 6303373

; GENERAL INFORMATION:

; APPLICANT: Bogan, Jonathan S.

; APPLICANT: Lodish, Harvey F.

; TITLE OF INVENTION: Method of Measuring Plasma Membrane

; FILE REFERENCE: 0399.1210-004

; CURRENT APPLICATION NUMBER: US/09/591,025

; PRIOR FILING DATE: 2000-06-09

; PRIOR APPLICATION NUMBER: 60/154,078

; PRIOR FILING DATE: 1999-09-15

; PRIOR APPLICATION NUMBER: 60/138,237

; PRIOR FILING DATE: 1999-06-09

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; SOFTWARE: FastSeq for Windows Version 4.0

; SEQ ID NO 8

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; FEATURE:

; OTHER INFORMATION: modified GLUT4 containing myc tag sequences

US-09-591-025-8

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Db 1291 ACCATAGGAGTGTGTGTCATACCTCTCTGAGTGTCTCGGTGCTCTTGTGTGGAG 1350
QY 1503 CGAGCTGGGCGACGACACTCTCATCTCTGGGCTGGCAGGATGCTGTGGCTGTGCCATC 1562
Db 1351 CGGGCGGGGCGCGACGCTCTCATCTCTGGGCTGGGCGGATGCTGTGGCTGTGCCATC 1410
QY 1563 TTGATGACGGTGGCTGCTGCTGCTGAGGGGTTCCATCATGAGTTATGTTGCTCATC 1622
Db 1411 CTGATGACTGTGGCTGCTGCTGCTGAGGAGTTCCAGGCATGAGCTAGCTCTCCATT 1470
QY 1623 GTGGCCATATTGGCTTTGTGGCTCTCTTGAGATTGCTCTGGCCCATCCCTGGTTTC 1682
Db 1471 GTGGCCATCTTTGGCTTGTGGCTCTCTTGAGATTGCTCTGGCCCATCTCTTGGTTTC 1530
QY 1683 ATTTGGGCGAGCTCTTCAGCCAGGGGCGCCGCGCCAGAGCATGGCTGTAGCTGGTTTC 1742
Db 1531 ATCTGGGCGAGCTCTTCAGCCAGGGGCGCCGCGCCAGAGCATGGCTGTAGCTGGTTTC 1590
QY 1743 TCCAACTGACCTGTAACCTTCACTTGGCATGGGTTTCCAGTATGTTGGGATGCTATG 1802
Db 1591 TCCAACTGACGAGCAACTTCATCATTTGGCATGGGTTTCCAGTATGTTGGGAGGCTATG 1650
QY 1803 GGTCCCTAGCTCTCTCTTATTTGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1862
Db 1651 GGGCCCTAGCTCTCTCTTATTTGGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1710
QY 1863 CTAAGAGTCCCTGAAACACAGAGCGCGGACATTTGACACAGATCTCGGCCACCTTCGACGG 1922
Db 1711 TTAAGNGTACTGAACTCGAGCGCGGACGTTTGAACAGATCTCGGCTGCTTCCACGG 1770
QY 1923 ACACCTTCTCTTTAGAGCAGAGGTGAAACCCAGTACAGAACTTGAATATCTTAGGGCCA 1982
Db 1771 ACACCTTCTCTTTAGAGCAGAGGTGAAACCCAGTACAGAACTTGAATATTTAGGGCCA 1830
QY 1983 GATGAGATGAC 1994
Db 1831 GATGAGATGAC 1842
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RESULT 2
US-09-894-927B-8
; Sequence 8, Application US/09894927B
; Patent No. 6632924
; GENERAL INFORMATION:
; APPLICANT: Bogan, Jonathan S.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: Method of Measuring Plasma Membrane
; TITLE OF INVENTION: Targeting of GLUT4
; FILE REFERENCE: 0399.1210-005
; CURRENT APPLICATION NUMBER: US/09/894, 927B
; PRIOR FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: US 09/591,025
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: US 60/154,078
; PRIOR FILING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: US 60/138,237
; PRIOR FILING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 2592
; TYPE: DNA
; ORGANISM: Artificial Sequence
; OTHER INFORMATION: modified GLUT4 containing myc tag sequences
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(2592)
US-09-894-927B-8

Query Match 44.6%; Score 1063.2; DB 4; Length 2592;
Best Local Similarity 87.4%; Pred. No. 3.2e-285;
Matches 1164; Conservative 0; Mismatches 168; Indels 0; Gaps 0;

QY 663 CTGGGGGACCGGACTCCATCCCAAGGACCCCTCACTACCTTTGGGCTCTCCCGTG 722
Db 511 CTTAAGGGACCCAGCTCCATCCCTCCAGGACCCCTCACACCCCTCTGGGCCCTCTCCGTG 570
QY 723 GCCATCTTCTGTGGGTGGCATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 782
Db 571 GCCATCTTCTGTGGGTGGCATTTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 630
QY 783 TTGGGAAGGAAAGGGCTATGCTGGCCAAACAATGCTTTGGGCTGTCTGGGGGGCGCCCTC 842
Db 631 CTTGGAAGGAAAGGGCCATGCTGCTCAACAATGCTCTGGCGGTGCTGGGGGGCAGCCTC 690
QY 843 ATGGGCTTAGCAATGCGGGGCTCTCTATGAGATATCTATCTCGGACGGTTCTCATTT 902
Db 691 ATGGGCTTAGCAACGCTGCTGCTCTCTATGAAATGCTCATCTTGGACGATTCCTCATTT 750
QY 903 GGGCCCTACTCAGGGCTAAACATCAGGGTGGTGTATGATGTTGGGAGAAATCGCCCC 962
Db 751 GGGCCCTACTCAGGGCTGACATCAGGGCTGGTGGCCATGTAGTGGGGAGATTTGCTCCC 810
QY 963 ACTCATCTTGGGGTGGCTTGGGAACACTCAACCAATTTGGGCATCTCATTTGGCATTTG 1022
Db 811 ACTCATCTTGGGGGCGCCCTGGGACGCTCAACCACTGGCCATTGTTATCGGCAATCTG 870
QY 1023 GTTGGCCAGGTTGGGTTGGAGTCTATGCTGGGCACAGTACCTCTGTGGCCATTGCTT 1082
Db 871 ATGCCCCAGGTGCTGGGCTTGGAGTCTCTCTCTGGGCACCTGCGCAGCTGTGGCAGCTC 930
QY 1083 CTGGCTATCACAGTACTCCCTGCTCTCTGAGCTGCTTCTGTTGGCCCTCTCTGCTCTGAG 1142
Db 931 CTGGGCTTCAAGTGTACTCTGCTGCTGCTCTCTGAGCTGGTCTGCTGCTCTCTCTGCTCC 990
QY 1143 AGCCCCGATACCTCTACATCATCCGGAACCTGGAGGGGCTGCCCCGAAAGAGTCTAAAG 1202
Db 991 AGCCCCGCTACTCTACATCATCCAGATCTCGAGGGGCTGCGCAGAAAGAGTCTGAG 1050
QY 1203 CGCCTGACGCTGGGCTGATGCTGATGACATCTGGCTGAGCTGAAGATGAGAAACGG 1262
Db 1051 CGCCTGACAGGCTGGGCGGATGTTCTGGAGTGTCTGGCTGAGCTGAAGATGAGAAACGG 1110
QY 1263 AAGTTGGAAGAGAGGCTCCAGTCTCTGCTGCTGAGCTCTGGGCGAGCGCCACCCACGG 1322
Db 1111 AAGCTGGAGCGTGGGCGGCACTGTCCCTCTGCTGCAAGCTCTGGGCGAGCTGACCCACGG 1170
QY 1323 CAGCCTCTGATTTATGCACTGCTGCTGAGCTGAGCCAGAGCTCTCAGGCATCAATGCT 1382
Db 1171 CAGCCCTGATCATTTGGGCTGCTGCTGAGCTGAGCCAGAGCTCTCTGGCATCAATGCT 1230
QY 1383 GTTTTCTACTATTCAACACAGCATCTTTGAGTTAGCTGGGGTGGAAACAGCCAGCTACGCC 1442
Db 1231 GTTTTCTATTATTCGACAGCATCTTCGAGACAGCAGCGGGTAGGCCAGCTGCTATGCC 1290
QY 1443 ACCATAGGAGTGTGTGTCATACCTCTCTGAGTGTCTCGGTGCTCTTGTAGTAGAG 1502
Db 1291 ACCATAGGAGTGTGTGTCATACCTCTCTGAGTGTCTCGGTGCTCTTGTGTGGAG 1350
QY 1503 CGAGCTGGGCGACGACACTCTCATCTCTGGGCTGGCAGGATGCTGTGGCTGTGCCATC 1562
Db 1351 CGGGCGGGGCGCGACGCTCTCATCTCTGGGCTGGGCGGATGCTGTGGCTGTGCCATC 1410
QY 1563 TTGATGACGGTGGCTGCTGCTGCTGAGGGGTTCCATCATGAGTTATGTTGCTCATC 1622
Db 1411 CTGATGACTGTGGCTGCTGCTGCTGAGGAGTTCCAGGCATGAGCTAGCTCTCCATT 1470
QY 1623 GTGGCCATATTGGCTTTGTGGCTCTCTTGAGATTGCTCTGGCCCATCCCTGGTTTC 1682
Db 1471 GTGGCCATCTTTGGCTTGTGGCTCTCTTGAGATTGCTCTGGCCCATCTCTTGGTTTC 1530
QY 1683 ATTTGGGCGAGCTCTTCAGCCAGGGGCGCCGCGCCAGAGCATGGCTGTAGCTGGTTTC 1742
Db 1531 ATCTGGGCGAGCTCTTCAGCCAGGGGCGCCGCGCCAGAGCATGGCTGTAGCTGGTTTC 1590
QY 1743 TCCAACTGACCTGTAACCTTCACTTGGCATGGGTTTCCAGTATGTTGGGATGCTATG 1802
Db 1591 TCCAACTGACGAGCAACTTCATCATTTGGCATGGGTTTCCAGTATGTTGGGAGGCTATG 1650
QY 1803 GGTCCCTAGCTCTCTCTTATTTGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1862
Db 1651 GGGCCCTAGCTCTCTCTTATTTGGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1710
QY 1863 CTAAGAGTCCCTGAAACACAGAGCGCGGACATTTGACACAGATCTCGGCCACCTTCGACGG 1922
Db 1711 TTAAGNGTACTGAACTCGAGCGCGGACGTTTGAACAGATCTCGGCTGCTTCCACGG 1770
QY 1923 ACACCTTCTCTTTAGAGCAGAGGTGAAACCCAGTACAGAACTTGAATATCTTAGGGCCA 1982
Db 1771 ACACCTTCTCTTTAGAGCAGAGGTGAAACCCAGTACAGAACTTGAATATTTAGGGCCA 1830
QY 1983 GATGAGATGAC 1994
Db 1831 GATGAGATGAC 1842
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Db 1010 GCTGACGTGTCCACGACGCTGTGTGGCATCAACGCTGTCTTTACTTACTCCAGGACAT 1069
QY 1406 CTTTGAAGTTAGCTGGGTGGAAACGACCCAGCCTACGCCACCATAGGAGCTGTGTGTCAC 1465
Db 1070 CTTTGAAGAGGGGGGGTGCAGACGCTGTGTATGCCACCATTTGGCTCCGGTATCGTCAA 1129
QY 1466 TACCGTCTTTCAGTTGGTCTCGGTGCTCTTTAGTAGAGCGAGCTGGGCGACGACCTCCA 1525
Db 1130 CACGGCTTTCAGTGTGTGCTGCTTTGTGTGGAGCGAGCGCGCGGACCTGCA 1189
QY 1526 TCTCTGGGCTGGGAGGAGTGTGTGCTGTGTCATCTTGTATGAGGGTGTGCTGTGCT 1585
Db 1190 CTTATAGGCTCGCTGGCATGGCGGGTGTGGCCATCTCATGACCATCGCGCTAGCACT 1249
QY 1586 GCTGAGGCGGGTTCATCATGAGTTATGTGTCCATGTGTCATGTGTCATATTTGGCTTTGTGGC 1645
Db 1250 GCTGAGGAGCTTACCTCGATGTCTATCTGAGCATGTGGCCATCTTTGGCTTTGTGGC 1309
QY 1646 CTTCTTTGAGATTGGTCTCGTGGCCCATCCCTGGTTTCATTGTGGCGGAGCTCTTCAGCCA 1705
Db 1310 CTTCTTTGAGTGGTCTCGTGGCCCATCCCATGGTTTCATCGTGGCTGAACCTTCAGCCA 1369
QY 1706 GGGCCCGCCGACGAGCATGCTGTAGCTGGTTTCTCCAACTGGAGCTGTAACTTCAT 1765
Db 1370 GGGTCCAGCTCAGCTGCCATTGGCGTTGCAAGGCTTCTCCAACCTGGAACCTCAAAATTCAT 1429
QY 1766 CTTTGGCATGGGTTCCAGTATGTGCGGATGCTATGGTCCCTACGTCCTTCTTCTATT 1825
Db 1430 TGTGGGCAATGCTTCCAGTATGTGGAGCAACTGTGTGGTCCCTACGTCCTTCATCATCTT 1489
QY 1826 TGGCGTCTCTGCTTGGCTTCTTCATCTTCCACTTCTCAAGAGTGCCTGAAACGAGG 1885
Db 1490 CACTGTGCTCTGGTCTGTTCTTCTTCTTCTTCACTTCTCAAGTCTCTGAGACTAAAG 1549
QY 1886 CCGGACATTTGACAGATCTCGGCCACCTTCGAGG 1922
Db 1550 CCGGACCTTCGATGAGATCGCTTCGGGCTTCGGGAG 1586

RESULT 4

US-09-480-884A-135
; Sequence 135, Application US/09480884A
; Patent No. 6482597
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Hosken, Nancy A.
; APPLICANT: Kalos, Michael D.
; APPLICANT: Fanger, Gary R.
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C6
; CURRENT APPLICATION NUMBER: US/09/480,884A
; CURRENT FILING DATE: 2001-08-27
; NUMBER OF SEQ ID NOS: 330
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 135
; LENGTH: 2856
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-480-884A-135

Query Match 28.5%; Score 679; DB 4; Length 2856;
Best Local Similarity 68.1%; Pred. No. 2.5e-178;
Matches 965; Conservative 0; Mismatches 440; Indels 12; Gaps 1;
QY 506 GGAACCCCTCAGCAGCGAGTGTGAGGACACTGGTCTGCTGTATTTCTCAGCTGTGCT 565
Db 182 GGAGCCGACGACCAAGAGCTGACCGGTGCGCTCATGTGCTGTGGAGGAGGAGTGTCT 241
QY 566 TGGCTCCCTTTCAGTTGGCTATAACATTTGGAGTGTATCAACGCGCCCAAGAAAGTGTGA 625
Db 242 TGGCTCCCTGCAAGTTGGCTACAACTGGAGTCAATGCTCCCAATGCTGCTGAACTCTCAGCCA 301

QY 626 ACAGAGCTACAATGCAACTTGGCTGGGTAGGACAGGCTCTCTGGGGAACCGGACTCCATCCC 685
Db 302 GGAGTTCTACAAACAGACATGGGTCCACCGCTATGG-----GGAGAGCATCTCT 349
QY 686 ACAAGGCAACCTCTACATACCTTTGGGCTCTCTCGTGCCCATCTTCTCTGTGGGTGGCAT 745
Db 350 GCCCACCACGCTACACACGCTCTGGTCCCTCTCAGTGGCCATCTTTTCTGTGGGGCAT 409
QY 746 GATTTCTCTCTTCTCTCATTTGGCATCATTTCTCAATGTTTGGGAAGAAAGGGCTATGCT 805
Db 410 GATTTGGCTCTCTCTCTGTGGGCTTTTGGTTAAACCGCTTTTGGCGCGGAAATTCATATGCT 469
QY 806 GGCCCAACAATGTCTTGGCTGTCTGGGGGGGGCCCTCATGGGCTTAGCCAAATGCGCGGCG 865
Db 470 GATGATGAACTGTCTGGGCTTCTGTCTGGGCTTCTGTGGGCTTCTGTGAACTGGGCA 529
QY 866 CTCCTATGAGATACATATTCTCGGACGTTTCTCATTTGGGCGCTACTCAGGGCTAACATC 925
Db 530 GTCTTTTGGAGATGCTGATCTGTGGGCGCTTCTCATCTGCTGTACTCTGGGCTTACCCAC 589
QY 926 AGGTTTGGTGGCTATGATGTGGGAGAAATCGCCCCCACTCATCTTTCGGGGTGCCTTGGG 985
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QY 986 AACACTCAAACCAATTTGGCCATCTGTCATTGGCATCTGGTTGCCAGAGTGTGGGTTTGA 1045
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QY 1046 GTCTATGCTGGGCAACGCTACCTGTGGGCAATGCTTCTGTGCTATCACAGTACTCCCTGC 1105
Db 710 CTCCTATCATGGGCAACAGGACCTGTGGGCGCTCTGTCTGAGCATCTATCTTCTTCCCGG 769
QY 1106 TCTCTGAGCTGTCTTGTGTGCTTCTGTCTGTGAGGCGCCCGATACCTCTATCATAT 1165
Db 770 CTTGCTGAGTGCATCTGTGCTGCTTCTGTGCTGAGAGTCCCGCTTCTGCTCTCATCAA 829
QY 1166 CCGGACCTGGAGGGGCTGCGCCGAAAGAGTCTAAAGCGCTGACAGGCTGGGCTGATCT 1225
Db 830 CCGGACAGGAGGAGNACCGGCGCAAGAGTGTCTAAAGAGCTGCGCGGAGCAGCTGACGT 889
QY 1226 GTCTGATGCACTGGCTCAGCTGAGTGAAGATGAGAAACGGAAGTTGGAAAGAGAGCTCCAT 1285
Db 890 GACCATGACCTGACGAGATGAAGAGAGAGTCTGGCAGATGATGCGGAGAGAGAGT 949
QY 1286 GTCTTGTGCTGAGCTCTGGGACGCGCAACCGCGGAGCTCTGATTTATGCAAGTGT 1345
Db 950 CACCATCTGAGGCTGTTCGCTCCCGGCTACCGCGAGCCCATCTCTCATCTGCTGTGT 1009
QY 1346 GCTGAGCTGAGCCAGCAGCTCTCAGGCTCAATGCTGTTTTTCTACTATTCAACAGCAT 1405
Db 1010 GCTGAGCTGTCCAGCAGCTGTCTGGCATCAACGCTGTCTTCTATTATCTCCACGAGCAT 1069
QY 1406 CTTTGAAGTTAGTGGGTGGAACAGCAGCCTTACGCCACATAGAGGCTGTGTGGTCAA 1465
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QY 1526 TCTCTGGGCTGGCAGGCTATGTGCTGTGGCATCTTGTATGAGGCTGGGCTCTGCTGTCT 1585
Db 1190 CTTATAGGCTCGCTGGCATGGGCGGTGTGGCCATCTACTATGACCATCGCGCTAGCACT 1249
QY 1586 GCTGAGCGGGTTCCTCATGAGTATGTGTCCATGTGCGCCATATTTGGCTTTGTGGC 1645
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Qy	1706	GGGCCCCCGCCAGCAGCGATGGCGTGTAGCTGGTTTCTCAACTGGAGACTGTAACTTCAT	1765
Db	1370	GGGTCCACGTCACGCTGCCATTGCGGTGCGAGGCTTCTCAAATGGACCTCAAAATTTTCAT	1429
Qy	1766	CGTTGGCATGGGTTTCCAGTATGTTGGGATGCTATGGTCCCTACGCTCTTCTCTCATTT	1825
Db	1430	TGTGGGCATGTCTTCCAGTATGTGGAGCAACTGTGTGGTCCCTACGCTCTTCATCATCTTT	1489
Qy	1826	TGCCGCTCCTCTGCTTGGCTTCTTCATCTTCACCTTCCTAAGAGTGCTCGAAACACGAGG	1885
Db	1490	CACGTGTGCTCTGTTCTGTCTTCTTCATCTCACCTACTTCAAGTTCTCTGAGACTAAAGG	1549
Qy	1886	CCGGACATTTTGACACAGATCTCGGCCACCTTCCGACGG	1922
Db	1550	CCGGACCTTTCGATGAGATCGCTTCCGGCTTCGGCAG	1586

RESULT 5

US-09-542-615A-135
; Sequence 135, Application US/09542615A

; PATENT NO. 6518236
: GENERAL INFORMATION:

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/ ORGANISM: Homo sapiens
/ APPLICANT: Wang, Tongtong
/ APPLICANT: Fan, Liqun
/ APPLICANT: Kalos, Michael D.
/ APPLICANT: Bangur, Chaitanya S.
/ APPLICANT: Hosken, Nancy A.
/ APPLICANT: Fanger, Gary R.
/ TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY
/ OF LUNG CANCER
/ FILE REFERENCE: 21021.455C8
/ CURRENT APPLICATION NUMBER: US/09/542,615A
/ CURRENT FILING DATE: 2000-04-14
/ NUMBER OF SEQ ID NOS: 350
/ SOFTWARE: FastSeq for Windows Version 3.0
/ SEQ ID NO 135
/ LENGTH: 2856
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-542-615A-135

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Query Match	28.5%	Score 679;	DB 4;	Length 2856;
Best Local Similarity	68.1%	Pred. No. 2.5e-178;		
Matches 965;	Conservative	0;	Mismatches 440;	Indels 12;
				Gaps 1;

Qy	506	GGAAACCCCTCAGCAGCGAGTGA	CTGGGACA	CTGGTCTCTTGGCTGTA	TTCTCAGCTGTGCT	565
Db	182	GGAGCCCGAGCAGCAAGAAGCTG	ACGGGTCG	CCTCATGCTGGCTGTGGAGGAGCAGTGCT		241
Qy	566	TGGCTCCCTTCAGTTTCGCTATAC	ATTGGAGTCA	CAACGCCCCACAGAAAGTGATTGA		625
Db	242	TGGCTCCCTCGAGTTTGGCTACA	CAACTGGAGTCA	TAATGCCCCCCCAGAAAGTGATCGA		301
Qy	626	ACAGAGCTACAATGCACATTTGG	CTGGGTGAGCAGGGTC	CTGGGGGACCGGACTCCATCCC		685
Db	302	GGAGTCTTACAACACAGACATGG	GTCCACCGCTATAG	-----GGAGAGCATCCT		349
Qy	686	ACAGGCAACCTCACTACCTTTGG	GGCTCTCTCGTGGCCGCA	NTCTCTGTGGGTGGCAT		745
Db	350	GCCACACCGCTCACACGCTCTGG	TCCCTCTCAGTGGCCCATCTTT	CTGTGTGGGGCAT		409
Qy	746	GATTTCTCTCTTTCTCATATGSC	ATCTTCTCAATGTTGGAGGAA	AGGGCTATGCT		805
Db	410	GATTGGGTCCCTCTCTGTGGGCC	TTTTCGTTAACCGCTTTTGG	CCGGCGGAATTCATGTCT		469
Qy	806	GGCCAAACAATGTCTTGGCTGTG	CTGGGGGGCGCCCTCATGGCC	TAGCCAAATGCCCGGC		865
Db	470	GATGATGAACCTGTGGCCTCGTG	TCCGCGTGCTCATGGCTTCT	CGAAACTGGGCAA		529
Qy	866	CTCCTATGAGATATCAATTCGAG	ACGGTTCCCTCATTTGGCGCC	TACTCAGGGCTAAATC		925
Db	530	GTCCCTTTGAGATGTGATCTCTGG	CCGCTTCATCATCGTGTGTACT	CTGGGCTTGACAC		589

QY 506 GGAACCCCTCAGCAGGAGTGAACGGACACCTGGTCTGCTGTATTTCTCAGCTGTGCT 565
DB 182 GGAGCCAGCAGCAAGAGTGAACGGTCCCTCATGCTGGCTTGGGAGGACAGTGTCT 241
QY 566 TGCTCCCTTTCAGTTGGCTTAACTTGAATGGAGTCAACAGCCGCCACAGAAAGTGA 625
DB 242 TGCTCCCTTTCAGTTGGCTTAACTTGAATGGAGTCAACAGCCGCCACAGAAAGTGA 301
QY 626 ACAGAGTACAATTCGCTTGGCTGGGTAGGAGGCTTCTGGGGACCGAGCTTCAATCCC 685
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QY 686 AAGAGCACCCTCAGTACCTTGGGCTCTCTCGTGGGCACTTCTCTGTGGGTGGCAT 745
DB 350 GCCCAGCAGCTCAGCAGCTTGGTCCCTCTCAGTGGCCATCTTTCTGTGGGGGCA 409
QY 746 GATTTCTCTCTTCTCATTGGCATCACTTCTCAATGTTGGGAAGAAAGGCTATGCT 805
DB 410 GATGGCTCTCTCTGTGGGCTTTTCTGTTAACCGCTTGGCCGGGGAATTCATGCT 469
QY 806 GGCCAAACAATGTCTGTGCTGTGGGGGGCGCCCTCATGGGCTAGCCAAATCCCGGC 865
DB 470 GATGATGACCTGCTGGCTTCTGTGCGCGTCTCATGGGCTTCTCGAACTGGGCA 529
QY 866 CTCTATGAGATCACTCAATCTCGGACGGTTCCTCATTTGGGCGCTACTCAGGGCTAAATC 925
DB 530 GTCTTTGAGATGCTGATCTGGCGCGCTTTCATCATCGGTGTACTCTGGCGCTGACCAC 589
QY 926 AGGTTGGTCCCTATGATGGGAGAAATCGCCCACTCATCTTCGGGGTCCCTTGG 985
DB 590 AGGCTTCGTGCCATGATGAGGTGAAGTGTACCCACAGCCCTTTCGTGGGGCCCTGG 649
QY 986 AACACTCAACAATGGCCATCGTCAATGGCAATCTGTTGGCCAGGTGTGGGTTTGA 1045
DB 650 CACCTGCACAGCTGGCATCTGTCGCGATCTCATCGCCAGGTGTTCGGCTGGA 709
QY 1046 GTCTATGTGGGACAGCTACCTGTGGGCAATGCTTCTGGCTATCAGAGTATCCCTGC 1105
DB 710 CTCCATCATGGGCAAGAGACCTGTGGCCCTGCTGTGAGCATCATCTTCATCCCGC 769
QY 1106 TCTCTGCACTGCTTCTGTGCTGCTGCTGTGAGCGCCCGGATACCTTACATCAT 1165
DB 770 CTGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 829
QY 1166 CCGGAACCTGGAGGCGCTCCCGAAGAGTCTAAAGCGCTTACAGGCTGGGCTGATGT 1225
DB 830 CCGCAAGAGAGAAACCGGCGCAAGAGTGTCTAAAGAGCTCGCGGAGACAGTACGT 889
QY 1226 GTCTGATGCACTGGCTGAGCTGAAGATGAAGAAACGGAAGTGGAAAGAGAGCTCCACT 1285
DB 890 GACCCATGACCTGAGGAGATGAAGAAAGAGTCCGCGATGATGCGGAGAAAGGT 949
QY 1286 GTCTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1345
DB 950 CACCATCTGAGAGTGTTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1009
QY 1346 GCTGCACTGAGCAGCTCTCAGGCATCAATGCTGTTTCTACTATTAATCAACAGCAT 1405
DB 1010 GCTGCACTGCTCCAGCAGCTGTGCGCATCAAGCTGTCTTATTAATCAACAGCAT 1069
QY 1406 CTTTGAATGAGTGGGTGAACAGCAGCTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1465
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QY 1466 TACGCTTTCAGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1525
DB 1130 CACGGCTTTCAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1189
QY 1526 TCTCTGGGCTGCGCAGGATGTGGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1585
DB 1190 CTTATAGGCTGCTGCGCATGGGGTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1249
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DB 1250 GCTGGAGCAGCTACCTCGATGCTTATCTGAGCATCGTGCCCATCTTTGGCTTGTGGC 1309
QY 1646 CTTCTTTGAGATGCTGCTGGGCCCATCCCTGCTTCAATGTCGCGAGCTCTTTGAGCCA 1705
DB 1310 CTTCTTTGAGTGGTCTTGGGCCCATCCATGCTGCTGCTGCTGCTGCTGCTGCTGCT 1369
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QY 1766 CTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1825
DB 1430 TGTGGCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1489
QY 1826 TGCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1885
DB 1490 CACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1549
QY 1886 CCGGACATTTGACAGATCTCGGCCACCTTCGAGCG 1922
DB 1550 CCGGACCTTCGATGATGCTTCCGCTTCCGCTTCCGCGAG 1586

RESULT 8

US-09-023-655-1104
; Sequence 1104, Application US/09023655
; Patent No. 6607879
; GENERAL INFORMATION:
; APPLICANT: Cocks, Benjamin G.
; APPLICANT: Susan G. Stuart
; APPLICANT: Jeffrey J. Seilhamer
; TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF BLOOD CELL GENE
; TITLE OF INVENTION: EXPRESSION
; NUMBER OF SEQUENCES: 1508
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
; STREET: 3174 PORTER DRIVE
; CITY: PALO ALTO
; STATE: CALIFORNIA
; COUNTRY: USA
; ZIP: 94304
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
; CURRENT APPLICATION DATA:
; FILING DATE: HEREWITH
; CLASSIFICATION:
; APPLICATION NUMBER: US/09/023,655
; PRIOR APPLICATION DATA:
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Zeller, Karen J.
; REGISTRATION NUMBER: 37,071
; REFERENCE/DOCKET NUMBER: PA-0001 US
; TELEPHONE: (650) 855-0555
; TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1104:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 3915 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g183684
; US-09-023-655-1104

Db 496 TTATATTTGCTGGAGAGCATATCAGGACTATATTTGTTGGGCTAAATTTTACGGCTGGTTC 555
QY 937 CTATGTATGTGGGAGAAATCGCCCACTCATCTTTCGGGGTGGCTTGGGAGCACTCAACC 996
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QY 1177 AGGGGCTGCCGGAAGAGTCTAAAGCGCTGTAGAGGCTGGGCTGTGTCTGTATGTCAC 1236
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QY 1655 GATTGTCTCTGGCCCATCCCTGGTTTCAATGTGGCGAGCTCTTCAGCCAGGCGCCCGG 1714
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QY 1835 CTGCTTGGCTTCTTCACTTTCACCTTCTTAAGAGTGTCTGAAACAGAGCGCGGACATT 1894
Db 1456 GCTCTGGCTTTTACCTGTTTACATTTTAAAGTTCCAGAAACCAAGGAAAGTCTTT 1515
QY 1895 TGACCCAGATCTGGGCCACCTTTCGAGCGGACCACTTCTCTTTATAGAGGAGGTGAACC 1954
Db 1516 TGAGGAAATGCTGCAAAATTTCCAAAGA---AGAGTGGCTCAGCCACAGGCGCAAAAGC 1572
QY 1955 CAGTACAGACTTGTACTTTAGGCGCAGATGAGATGACTAA 1997
Db 1573 TGCTGTAGAAATGAAATTCCTAGGAGCTACAGAGACTGTGTAA 1615

RESULT 10 - 392-1
US-09-031-392-1
; Sequence 1, Application US/09031392
; Patent No. 5942398
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Weng, Xun
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES
; TITLE OF INVENTION: ENCODING GLUTEX AND USES THEREOF
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/031,392
; FILING DATE: 26-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/072001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2343 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 73...1761
US-09-031-392-1

Query Match 10.4%; Score 248.4; DB 2; Length 2343;
Best Local Similarity 50.8%; Pred. No. 1.3e-58;
Matches 622; Conservative 0; Mismatches 596; Indels 6; Gaps 1;
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Db 739 GAGCTGCTGGGAAAGAGAGTACCTGGCCATACCTTTTGGAGTATTTGGTCCCTGCC 798
Qy 1107 CTCCTGCACTGCTTCTGTGCTTCTGTCTGAGACCCCGCATACCTCTACATCATC 1166
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RESULT 11

US-09-299-549-1
; Sequence 1, Application US/09299549
; Patent No. 6136547
; GENERAL INFORMATION:
; APPLICANT: Tartaglia, Louis A.
; APPLICANT: Wang, Xun
; TITLE OF INVENTION: NUCLEIC ACID MOLECULES ENCODING
; TITLE OF INVENTION: GLUTEX AND USES THEREOF
; NUMBER OF SEQUENCES: 10

; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson P.C.
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: MA
; COUNTRY: USA
; ZIP: 02110-2804
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: Windows95
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/299,549
; FILING DATE: 26-APR-1999
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 09/031,392
; FILING DATE: 26-FEB-1998
; ATTORNEY/AGENT INFORMATION:
; NAME: Meiklejohn, Ph.D., Anita L.
; REGISTRATION NUMBER: 35,283
; REFERENCE/DOCKET NUMBER: 07334/072002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 617/542-5070
; TELEFAX: 617/542-8906
; TELEX: 200154
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2343 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; FEATURE:
; NAME/KEY: Coding Sequence
; LOCATION: 73...1761
; US-09-299-549-1

Query Match 10.4%; Score 248.4; DB 3; Length 2343;
Best Local Similarity 50.8%; Pred. No. 1.3e-58;
Matches 622; Conservative 0; Mismatches 596; Indels 6; Gaps 1;

Qy 687 CAAGGCACTCTCACTACCTTTGGGCTCTCTCCGTGGCCATCTTCTCTGTGGTGGCATG 746
Db 379 CCAGACACTCTGACTCTGCTGCTGTGACTGTGCTCATATTGCCATCGTGGACTT 438
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Qy 807 GCCAACAAATGTTGGCTGTGCTGGGGGGCGCCCTCATGGGCCCTAGCCAAATGCCCGGGCC 866
Db 499 GCCAAATAGGTTTGCATTTCTGCTGATTTGCTGATTTGCTGCTGCTCGCTCAGGAGGA 558
Qy 867 TCCTATGAGATPACTCATTTCTGGACGGTTCTCATTTGGCGCTACTCAGGGGCTAAACATCA 926
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Qy 927 GGGTTGGTCTATGATGTGGGAGAAATCGCCCCCACTCATCTTCGGGGTCCCTTGGGA 986
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Qy 987 ACCTCAACAAATTTGGCATCTGTTGGCAATTTCTGGTTGCCAGGTGTGGGTTGGAG 1046
Db 679 CAGGTGCTGCACTTTTATCTGATTTGGCGTGTTCATCTGGGCGAGCTTCTGGGCTGCCCC 738
Qy 1047 TCTATGCTGGGCAAGTACCCCTGTGGCAATTTCTTGGGTATCACAGTACTCCCTGTCT 1106
Db 739 GAGCTGCTGGGAAAGAGAGTACCTGGCCATACCTTTGGAGTATTTGTGGTCTCTGCTGCC 798
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Job time : 111.588 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 16, 2004, 08:37:44 ; Search time 635.395 Seconds
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Title: US-10-067-449-10

Perfect score: 2386

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Gapop 10_0 , Gapext 1.0

Searched: 2947324 seqs, 2269024515 residues

Total number of hits satisfying chosen parameters: 5894648

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

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Database : Published Applications NA.*

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- 3: /cgn2_6/ptodata/1/pubpna/US06_NEW_PUB.seq.*
- 4: /cgn2_6/ptodata/1/pubpna/US06_PUBCOMB.seq.*
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- 18: /cgn2_6/ptodata/1/pubpna/US60_NEW_PUB.seq.*
- 19: /cgn2_6/ptodata/1/pubpna/US60_PUBCOMB.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1528.2	64.0	2506	16	US-10-191-803-36
3	1490.4	62.5	2338	15	US-10-067-449-12
4	1488.8	62.4	2338	15	US-10-067-449-13
5	1485.6	62.3	2338	15	US-10-067-449-14
6	1229	51.5	7828	15	US-10-067-449-9
7	1066.4	44.7	2532	9	US-09-894-927A-8
8	679	28.5	2856	9	US-09-735-705-135
9	679	28.5	2856	9	US-09-850-716A-135
10	679	28.5	2856	9	US-09-880-107-2128
11	679	28.5	2856	9	US-09-897-778-135
12	679	28.5	2856	10	US-09-466-396A-135
13	679	28.5	2856	13	US-10-342-887-1294
14	679	28.5	2856	13	US-10-007-700-135

15	679	28.5	2856	13	US-10-172-118-1294	Sequence 1294, Ap
16	679	28.5	2856	13	US-10-170-385-220	Sequence 220, App
17	679	28.5	2856	15	US-10-117-982-135	Sequence 135, App
18	679	28.5	2856	16	US-10-295-027-1031	Sequence 1031, Ap
19	679	28.5	2856	16	US-10-313-986-135	Sequence 135, App
20	679	28.5	2856	16	US-10-159-563-235	Sequence 235, App
21	679	28.5	3366	15	US-10-101-510-473	Sequence 473, App
22	679	28.5	7777	15	US-10-067-449-11	Sequence 11, Appl
23	678.2	28.4	2778	15	US-10-176-847-75	Sequence 75, Appl
24	670.2	28.1	2613	9	US-09-778-927A-7	Sequence 7, Appl
25	667.4	28.0	2683	9	US-09-778-927A-6	Sequence 6, Appl
26	663	27.8	2349	9	US-09-822-849A-381	Sequence 381, App
27	639.2	26.8	2319	9	US-09-778-927A-8	Sequence 8, Appl
28	637.6	26.7	2860	9	US-09-778-927A-9	Sequence 9, Appl
29	589	24.7	3046	9	US-09-778-927A-10	Sequence 10, Appl
30	542.8	22.7	3915	9	US-09-954-456-507	Sequence 507, App
31	542.8	22.7	3915	13	US-10-342-887-1341	Sequence 1341, Ap
32	542.8	22.7	3915	13	US-10-172-118-1341	Sequence 1341, Ap
33	542.8	22.7	3915	13	US-10-170-385-248	Sequence 248, App
34	542.8	22.7	3915	16	US-10-341-434-88	Sequence 88, Appl
35	542.8	22.7	3915	17	US-10-641-643-1104	Sequence 1104, Ap
36	510.8	21.4	1852	13	US-10-257-021-27	Sequence 27, Appl
37	456.2	19.1	3168	9	US-09-880-107-2099	Sequence 2099, Ap
38	456.2	19.1	3168	13	US-10-403-161-33	Sequence 33, Appl
39	456.2	19.1	3168	16	US-10-093-322-33	Sequence 33, Appl
40	456.2	19.1	3168	16	US-10-044-564-33	Sequence 33, Appl
41	454.8	19.1	2573	12	US-10-152-319A-1558	Sequence 1558, Ap
42	454.4	19.0	1587	13	US-10-403-161-37	Sequence 37, Appl
43	453	19.0	1664	13	US-10-403-161-39	Sequence 39, Appl
44	453	19.0	5228	10	US-09-919-039-216	Sequence 216, App
45	452.8	19.0	1587	13	US-10-403-161-35	Sequence 35, Appl

ALIGNMENTS

RESULT 1

US-10-067-449-10
; Sequence 10, Application US/10067449
; Publication No. US20030166258A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Gunter
; APPLICANT: Koller, Klaus-Peter
; APPLICANT: Boles, Eckhard
; APPLICANT: Wiczorke, Roman
; APPLICANT: Dlugai, Silke
; TITLE OF INVENTION: Saccharomyces cerevisiae Yeast Strain With Functional Expression
; TITLE OF INVENTION: GLUT Promoter
; FILE REFERENCE: DEAV2001/00002
; CURRENT APPLICATION NUMBER: US/10/067,449
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: DE 101 06 718.6
; PRIOR FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 10
; LENGTH: 2386
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-067-449-10

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Best Local Similarity	100.0%;	Pred. No. 0;		
Matches 2386;	Conservative 0;	Mismatches 0;	Indels 0;	Gaps 0;
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QY 301 CTTAGCAACCCCAACAACTTGTCATCTGTTCCGGATTCAAAATGATATAAAAGCGA 360
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QY 841 TCATGGGCTAGCCAAATGCGGGCTCTCTATGATATCAATTTCTCGAGCGGTTCTCTCA 900
DB 841 TCATGGGCTAGCCAAATGCGGGCTCTCTATGATATCAATTTCTCGAGCGGTTCTCTCA 900
QY 901 TTGGGCGCTTACTCAGGGCTTAACATCAGGGTGGTGGCTTATGATGTTGGGAGAAATCGCC 960
DB 901 TTGGGCGCTTACTCAGGGCTTAACATCAGGGTGGTGGCTTATGATGTTGGGAGAAATCGCC 960
QY 961 CCACTCATCTTGGGGTGGCTTGGGAACACTCAACCAATTTGGCCATCGTCAATGGCATTC 1020
DB 961 CCACTCATCTTGGGGTGGCTTGGGAACACTCAACCAATTTGGCCATCGTCAATGGCATTC 1020
QY 1021 TGGTTGGCCAGGTGTTGGGTTGGAGTCTATGCTGGGACAGCTACCCCTGGGCAATTCG 1080
DB 1021 TGGTTGGCCAGGTGTTGGGTTGGAGTCTATGCTGGGACAGCTACCCCTGGGCAATTCG 1080
QY 1081 TTTCTGGCTATCAGATCTCCCTGCTCTCTGCTGAGCTGCTTCTGTTGGCCCTTCTGCTG 1140
DB 1081 TTTCTGGCTATCAGATCTCCCTGCTCTCTGCTGAGCTGCTTCTGTTGGCCCTTCTGCTG 1140
QY 1141 AGAGCCCCGATCTTACATCATCCGGAACCTGGAGGGGCTGCGCCGGAAGAGTCTAA 1200
DB 1141 AGAGCCCCGATCTTACATCATCCGGAACCTGGAGGGGCTGCGCCGGAAGAGTCTAA 1200
QY 1201 AGCGCTGACAGGCTGGGCTGATGTCTGATGCACTGGCTGAGGTGAAGGATGAGAAAC 1260

DB 1201 AGCGCTGACAGGCTGGGCTGATGTGTGATGCACTGGCTGAGCTGAAGGATGAGAAAC 1260
QY 1261 GGAAGTTGGAAAAGAGAGCGTCCACTGCTTGTGCTGAGCTCCTGGGCAAGCCGACCCACC 1320
DB 1261 GGAAGTTGGAAAAGAGAGCGTCCACTGCTTGTGCTGAGCTCCTGGGCAAGCCGACCCACC 1320
QY 1321 GGAGCGCTCTGATTTATTTGCAAGTGGTGTGCACTGAGCCAGCAGCTCTCAGGCATCAATG 1380
DB 1321 GGAGCGCTCTGATTTATTTGCAAGTGGTGTGCACTGAGCCAGCAGCTCTCAGGCATCAATG 1380
QY 1381 CTGTTTCTACTATTCAACAGCATCTTTGAGTTAGCTGGGGTGGAAACAGCAGCCTAGC 1440
DB 1381 CTGTTTCTACTATTCAACAGCATCTTTGAGTTAGCTGGGGTGGAAACAGCAGCCTAGC 1440
QY 1441 CCACATAGGAGCTGGTGTGGTCAATACCGTCTTCACTGCTGAGCGGGTTCCATCCATGATGTTAG 1500
DB 1441 CCACATAGGAGCTGGTGTGGTCAATACCGTCTTCACTGCTGAGCGGGTTCCATCCATGATGTTAG 1500
QY 1501 AGCGAGCTGGGCGAGCAGCACTCCATCTCTGGGCTGGCAGGCAATGTTGGCTGGCCA 1560
DB 1501 AGCGAGCTGGGCGAGCAGCACTCCATCTCTGGGCTGGCAGGCAATGTTGGCTGGCCA 1560
QY 1561 TCTTGAAGAGCTGGTGTGGTCAATACCGTCTTCACTGCTGAGCGGGTTCCATCCATGATGTTAG 1620
DB 1561 TCTTGAAGAGCTGGTGTGGTCAATACCGTCTTCACTGCTGAGCGGGTTCCATCCATGATGTTAG 1620
QY 1621 TCGTGGCCATATTTGGGCTTTTGGGCTCTTGTGAGTTGGTCTCGGCCCATCCCTGGT 1680
DB 1621 TCGTGGCCATATTTGGGCTTTTGGGCTCTTGTGAGTTGGTCTCGGCCCATCCCTGGT 1680
QY 1681 TCATTGGCGGAGCTCTTCAAGCAGGCGCCCGCCAGCAGCAGCAGCTGCTGAGCTGGTT 1740
DB 1681 TCATTGGCGGAGCTCTTCAAGCAGGCGCCCGCCAGCAGCAGCAGCTGCTGAGCTGGTT 1740
QY 1741 TCTCCAACTGGACCTGTAACTTCACTGTTGGCATGGGTTTCCAGTATGTTGGGATGCTA 1800
DB 1741 TCTCCAACTGGACCTGTAACTTCACTGTTGGCATGGGTTTCCAGTATGTTGGGATGCTA 1800
QY 1801 TGGTCCCTACGTTCTCTTCAATTTGGCGTCTCTGCTGGGCTTCTTCACTTCACT 1860
DB 1801 TGGTCCCTACGTTCTCTTCAATTTGGCGTCTCTGCTGGGCTTCTTCACTTCACT 1860
QY 1861 TCCTAAGAGTGCCTGAAACAGAGCGGCGGACATTTGACAGATCTCGGCCACCTTCCGAC 1920
DB 1861 TCCTAAGAGTGCCTGAAACAGAGCGGCGGACATTTGACAGATCTCGGCCACCTTCCGAC 1920
QY 1921 GGAACACCTTCTCTTAGAGCAGGAGGTGAACCCAGTACAGAACTTGAATACTTAGGGC 1980
DB 1921 GGAACACCTTCTCTTAGAGCAGGAGGTGAACCCAGTACAGAACTTGAATACTTAGGGC 1980
QY 1981 CAGATGAGATGACTAATCGATTTGAAGTGAAGCTGCTCCATCACTCTCTTAATTTTCA 2040
DB 1981 CAGATGAGATGACTAATCGATTTGAAGTGAAGCTGCTCCATCACTCTCTTAATTTTCA 2040
QY 2041 TGAGTGAAGTGTCTTCTCAATTTTAAATTTATCATGATTTTGTGTTGAAAAAAGAAAAA 2100
DB 2041 TGAGTGAAGTGTCTTCTCAATTTTAAATTTATCATGATTTTGTGTTGAAAAAAGAAAAA 2100
QY 2101 AATTTCCTTATCAATGATATCTTACGATTTATATAATTTCTTACCTTAAACCTTATTT 2160
DB 2101 AATTTCCTTATCAATGATATCTTACGATTTATATAATTTCTTACCTTAAACCTTATTT 2160
QY 2161 TGTGTACATATACAGAGTATTTATACATATATAACCTTTTCTTAAACAGGAAAAA 2220
DB 2161 TGTGTACATATACAGAGTATTTATACATATATAACCTTTTCTTAAACAGGAAAAA 2220
QY 2221 AAAAGAAAAAGATAAATGCTCTGCCATCTTGTTCACCGAGCAAAATTTAAACGCAAA 2280
DB 2221 AAAAGAAAAAGATAAATGCTCTGCCATCTTGTTCACCGAGCAAAATTTAAACGCAAA 2280
QY 2281 AATGAATGTCTTATGAATTTATTAAGGACCAATCAACAGACTTATCTCTGGGGGT 2340
DB 2281 AATGAATGTCTTATGAATTTATTAAGGACCAATCAACAGACTTATCTCTGGGGGT 2340

Db 2281 AATGAATGTCCCTATGAAATTAATAAGACCAACATACACAGACTTATCTCTGGGGGT 2340
QY 2341 CCTCTAGAAAATAAGTCAGGTACTTGGCTGGACTTTCTCCAGTTG 2386
Db 2341 CCTCTAGAAAATAAGTCAGGTACTTGGCTGGACTTTCTCCAGTTG 2386

RESULT 2
US-10-191-803-36
; Sequence 36, Application US/10191803
; Publication No. US20040014040A1
; GENERAL INFORMATION:
; APPLICANT: MENDRICK, Donna
; APPLICANT: PORTER, Mark
; APPLICANT: JOHNSON, Kory
; APPLICANT: HIGGS, Brandon
; APPLICANT: CASTLE, Arthur
; APPLICANT: ELASHOFF, Michael
; TITLE OF INVENTION: Cardiotoxin Molecular Toxicology Modeling
; FILE REFERENCE: 44921-5090US
; CURRENT APPLICATION NUMBER: US/10/191,803
; CURRENT FILING DATE: 2002-07-10
; PRIOR APPLICATION NUMBER: US 60/303,819
; PRIOR FILING DATE: 2001-07-10
; PRIOR APPLICATION NUMBER: US 60/305,623
; PRIOR FILING DATE: 2001-07-17
; PRIOR APPLICATION NUMBER: US 60/369,351
; PRIOR FILING DATE: 2002-04-03
; PRIOR APPLICATION NUMBER: US 60/377,611
; PRIOR FILING DATE: 2002-05-06
; NUMBER OF SEQ ID NOS: 1140
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 36
; LENGTH: 2506
; TYPE: DNA
; ORGANISM: Rattus norvegicus
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20040014040A1 NM_012751
US-10-191-803-36

Query Match 64.0%; Score 1528.2; DB 16; Length 2506;
Best Local Similarity 98.2%; Pred. No. 0;
Matches 1545; Conservative 0; Mismatches 28; Indels 0; Gaps 0;

QY 455 CTTTATAAGCAACATAATGCTCAATTCACAGAGATCGGCTCTGAAGATGGGAAACCCCC 514
Db 128 CTTTATAAACAGATGCCGTGGGTTTCAGAGATCGGCTCTGAAGATGGGAAACCCCC 187
QY 515 TCAGCAGCAGTGAATGGGACACTGGTCTTGTGTTATTCAGCTGTGTGGTCCCT 574
Db 188 TCAGCAGCAGTGAATGGGACACTGGTCTTGTGTTATTCAGCTGTGTGGTCCCT 247
QY 575 TCAGTTTGGCTATTAACATTTGGAGTCAACAGCCGCCACAGAAAGTGAATGAACAGAGCTA 634
Db 248 TCAGTTTGGCTATTAACATTTGGAGTCAACAGCCGCCACAGAAAGTGAATGAACAGAGCTA 307
QY 635 CAATGCAACTTGGCTGGTGGTGGGAGGCTCTGGGGACCGGACTCCATCCCAAGGAC 694
Db 308 CAATGCAACTTGGCTGGTGGTGGGAGGCTCTGGGGACCGGACTCCATCCCAAGGAC 367
QY 695 CCTCACTACCCCTTTGGGCTCTCTCCGTGGCCTATCTCTGTGGGTGGCATGATTTCCCTC 754
Db 368 CCTCACTACCCCTTTGGGCTCTCTCCGTGGCCTATCTCTGTGGGTGGCATGATTTCCCTC 427
QY 755 CTTTCTCATTTGGGATCATTTCTCAATGGTTGGAGAGAAAGGGCTATGCTGGCCAAACAA 814
Db 428 CTTTCTCATTTGGGATCATTTCTCAATGGTTGGAGAGAAAGGGCTATGCTGGCCAAACAA 487
QY 815 TGTCTTGGCTGTGTGGGGGGCGCCCTCATGGGCTAGCCCAATGCGCGGCTCTCTATGA 874
Db 488 TGTCTTGGCTGTGTGGGGGGCGCCCTCATGGGCTAGCCCAATGCGCGGCTCTCTATGA 547
QY 875 GATACTCATTTCCGGACGGTTCTCTCAFTTGGCGCTACTCAGGGCTAACATCAGGGTTGGT 934

Db 548 GATFACCTCAATTTCTGGACGGTTCCTCATTTGGCGCTACTCAGGGCTAACATCAGGGTTGGT 607
QY 935 GCCTATGTATGTGGAGAAATGCCGCCACTCATCTTGGGGTGCCTTGGGAAACACTCAA 994
Db 608 GCCTATGTATGTGGAGAAATGCCGCCACTCATCTTGGGGTGCCTTGGGAAACACTCAA 667
QY 995 CCAATTTGGCCATCGTCAATTTGGCATTTGGTTGCCAGGTTTGGGTTTGGAGTCTATGCT 1054
Db 668 CCAATTTGGCCATCGTCAATTTGGCATTTGGTTGCCAGGTTTGGGTTTGGAGTCTATGCT 727
QY 1055 GGGCAGACACTACCTGTGGCCATTTGCTTCTGGCTATCAGAGTACTCCCTGCTCTCTGCA 1114
Db 728 GGGCAGACACTACCTGTGGCCATTTGCTTCTGGCTATCAGAGTACTCCCTGCTCTCTGCA 787
QY 1115 GCTGCTTCTGTTGGCCCTTCTGCTCTGAGAGCCGCCGATACCTCTACATCATCCGGAACCT 1174
Db 788 GCTGCTTCTGTTGGCCCTTCTGCTCTGAGAGCCGCCGATACCTCTACATCATCCGGAACCT 847
QY 1175 GGAGGGGCTTGGCCGAAAGAGTCTAAAGCGCTTGACAGGCTGGGCTGATGTCTGATGC 1234
Db 848 GGAGGGGCTTGGCCGAAAGAGTCTAAAGCGCTTGACAGGCTGGGCTGATGTCTGATGC 907
QY 1235 ACTGGCTGAGCTGAGAGATGAGAAACGGAAAGTTGAAAGAGAGCGTCCACTGCTTGTCT 1294
Db 908 ACTGGCTGAGCTGAGAGATGAGAAACGGAAAGTTGAAAGAGAGCGTCCACTGCTTGTCT 967
QY 1295 GCAGCTCTTGGGCGAGCGCACCCAGCGGAGCTCTGATTTATTTGAGTGTGCTGCACT 1354
Db 968 GCAGCTCTTGGGCGAGCGCACCCAGCGGAGCTCTGATTTATTTGAGTGTGCTGCACT 1027
QY 1355 GAGCCAGCAGCTCTCAGGAGCATCAATGCTGTGTTTCTACTATTTCAACAGAGCATTTTGA 1414
Db 1028 GAGCCAGCAGCTCTCAGGAGCATCAATGCTGTGTTTCTACTATTTCAACAGAGCATTTTGA 1087
QY 1415 AGCTGGGTTGGAACAGCCAGCTTACGCCACCATAGAGCTGGTGTGTTCAATACCTGCTT 1474
Db 1088 AGCTGGGTTGGAACAGCCAGCTTACGCCACCATAGAGCTGGTGTGTTCAATACCTGCTT 1147
QY 1475 CAGTTTGTGCTCGGTCTCTTAGTAGAGCGAGCTGGGCGAGGACGACACTCCATCTCTCGGG 1534
Db 1148 CAGTTTGTGCTCGGTCTCTTAGTAGAGCGAGCTGGGCGAGGACGACACTCCATCTCTCGGG 1207
QY 1535 CTTGGCAGGAGCATGTGGCTGTGCCATCTTGATGAGCGTGGCTCTGCTGCTGTGGAGCG 1594
Db 1208 CTTGGCAGGAGCATGTGGCTGTGCCATCTTGATGAGCGTGGCTCTGCTGCTGTGGAGCG 1267
QY 1595 GGTTCATCCATGAGTTATGTGTCATCTGTGGCCATATTTGGCTTTGTGGCCTTCTTTGA 1654
Db 1268 GGTTCATCCATGAGTTATGTGTCATCTGTGGCCATATTTGGCTTTGTGGCCTTCTTTGA 1327
QY 1655 GATTTGCTTGGCCCATCCCTGCTTCAATTTGGCGGAGCTCTTCAAGCCAGGCGCCCG 1714
Db 1328 GATTTGCTTGGCCCATCCCTGCTTCAATTTGGCGGAGCTCTTCAAGCCAGGCGCCCG 1387
QY 1715 CCAGCAGGAGCATGGCTGAGCTGGTTTCTCAACTGGACCTGTAACCTTCACTGTTGSCAT 1774
Db 1388 CCAGCAGGAGCATGGCTGAGCTGGTTTCTCAACTGGACCTGTAACCTTCACTGTTGSCAT 1447
QY 1775 GGTTCAGATATGTTGGGATGCTATGGTCCCTAGCTTCTTCTTATTTGGCGCTCT 1834
Db 1448 GGTTCAGATATGTTGGGATGCTATGGTCCCTAGCTTCTTCTTATTTGGCGCTCT 1507
QY 1835 CTTGCTTGGCTTCTTCACTTCACTTCAAGAGTCCCTGAAACAGAGCGCGGACATT 1894
Db 1508 CTTGCTTGGCTTCTTCACTTCACTTCAAGAGTCCCTGAAACAGAGCGCGGACATT 1567
QY 1895 TGAACAGATCTCGGCCACCTTCCAGGAGCACTTCTCTCTAGAGCAGGAGGTGAAC 1954
Db 1568 TGAACAGATCTCGGCCACCTTCCAGGAGCACTTCTCTCTAGAGCAGGAGGTGAAC 1627
QY 1955 CAGTACAGAACTTGAATATCTTAGGGCCAGATGAGATGACTAATTCGATTTGAAGTGAAC 2014

Db 1628 CAGTACAGAACTTGAATACTTAGGGCCAGATGAGAATGACTCAGGGGCAAAATGGTGGGA 1687
Qy 2015 GCTCCATCATCTC 2027
Db 1688 GAGCCACCCCTCCC 1700

RESULT 3
US-10-067-449-12
; Sequence 12, Application US/10067449
; Publication NO. US20030166258A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Gunter
; APPLICANT: Koller, Klaus-Peter
; APPLICANT: Boles, Eckhard
; APPLICANT: Wiczorke, Roman
; APPLICANT: Dlugai, Slike
; TITLE OF INVENTION: Saccharomyces cerevisiae Yeast Strain With Functional Expression
; FILE REFERENCE: DEAV2001/00002
; CURRENT APPLICATION NUMBER: US/10/067,449
; PRIOR FILING DATE: 2002-02-05
; PRIOR FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 12
; LENGTH: 2338
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-067-449-12

Query Match 62.5%; Score 1490.4; DB 15; Length 2338;
Best Local Similarity 77.8%; Fred. No. 0;
Matches 1857; Conservative 0; Mismatches 481; Indels 48; Gaps 3;

Qy 1 TCAGCTCTAGAGATCCCTTAAAGCTAATCCTTATGAATCGGAGAAAGCGGGTCTTT 60
Db 1 TCAGCTCTAGAGATCCCTTAAAGCTAATCCTTATGAATCGGAGAAAGCGGGTCTTT 60

Qy 61 TAACTCAATAAATTTTCGAAATCCTTTTCTACGCGTTTCTTCGGGAACCTAGATAG 120
Db 61 TAACTCAATAAATTTTCGAAATCCTTTTCTACGCGTTTCTTCGGGAACCTAGATAG 120

Qy 121 GTGGCTCTTCCACCTGTTTTCATCAATTTAGTTTTCGAAAGCAATGCTGCTTTC 180
Db 121 GTGGCTCTTCCACCTGTTTTCATCAATTTAGTTTTCGAAAGCAATGCTGCTTTC 180

Qy 181 GTTTTGGGATGGCGAAGCGGCTGGAAATTAACGGTACGCGCCTAACGATAGTAA 240
Db 181 GTTTTGGGATGGCGAAGCGGCTGGAAATTAACGGTACGCGCCTAACGATAGTAA 240

Qy 241 TAGGCACGCAACTGGGTGACGACCAACAATAAGTCCCAATTTTATGTTTTCAAAA 300
Db 241 TAGGCACGCAACTGGGTGACGACCAACAATAAGTCCCAATTTTATGTTTTCAAAA 300

Qy 301 CCTAGCAACCCCAACCAATGTCATCGTTCCGGATTCACAAATGATATAAAGCGGA 360
Db 301 CCTAGCAACCCCAACCAATGTCATCGTTCCGGATTCACAAATGATATAAAGCGGA 360

Qy 361 TTACAATTTCAATTTCAACAGATTTGAGATTTCTCTTCTCAATTTCTTATATTA 420
Db 361 TTACAATTTCAATTTCAACAGATTTGAGATTTCTCTTCTCAATTTCTTATATTA 420

Qy 421 GATTATAGAACCAACAATAAATTAACAAAGACTTATAAGCAACATAATGTCTGAAT 480
Db 421 GATTATAGAACCAACAATAAATTAACAAAGACTTATAAGCAACATAATGTCTGAAT 480

Qy 481 TCCAGCATCGGCTCTGAGATGGGAACCCCTCAGCAGGAGTGACTGGGACACTGG 540
Db 481 TCCAGCAAG-----AGGTGACGGGCGCCCTTA 507

Qy 541 TCCTTGCTGTATTTCTCAGCTGTGCTTGGCTCCCTTCACTTTGGCTATAACATGGAGTCA 600

508 TGTGGCGGTGGAGGGGAGTCTCGATCCCTCGAGTTCCGGCTATAACACCGGTGTCA 567
601 TCAAGCCCCACACAGAAAGTATTGAAACAGAGCTACAATGCAACTTGGCTGGGTAGGCAGG 560
568 TCAAGCCCCCCCCAGAGGTATTGAGGAGTTCTAATCAAAACATCAAAACACCAACCGGTATG 627
661 GTCCCTGGGGACCGGACTCCATCCCAAGGACCCCTCACTACCTTTGGGCTCTCTCCG 720
628 G-----AGAGTCCATCCATCCACCACTACCACTCTGGTCTCTCTCCG 675
721 TGGCCATCTTCTCTGTGGGTGGCAATTTCTCTCTCTCAATGGSCATCATTTCTCAAT 780
676 TGGCCATCTTCTCTGTGGGGCATGATGGTTCTTCTCTGTGGGCTCTTTTGTAAATC 735
781 GGTGGGAAGAAAGGGCTATGTGGCAACAATGTCTTGGCTGTGTGGGGGGGGCC 840
736 GCTTTGGCAGCGGAATCCATGTCTGATGATGAACCTGTGGCCCTTTGTGTGCGGTGC 795
841 TCATGGGCTAGCCCAATGCCGCGCTCTTATGATATCACTCTCGAGCGTTCTCTCA 900
796 TTATGGGTCTTCCAAACTGGGCAAGTCTTTGAGATGCTGATCTGGGCCCTTCAATCA 855
901 TTGGCGCTACTCAGGGCTAACTCAGGGTTGGTGCCTATGTATGTGGGAGAAATCGCCC 960
856 TTGGAGTGTACTGTGGCTGACCAACCGCTTTGTGCCCATGATGTGGGGAGGTGTAC 915
961 CCATCATCTTGGGGTGGTGGGAAACATCAACCAATTTGGCCATGTCTATGGCATTC 1020
916 CCACAGCTCTTGTGGAGCCCTGGGCAACCTGACACAGCTGGGCATCGTGTGGGATCC 975
1021 TGGTTGCCAGGTGTGGGTTTGGAGTCTATGCTGGGCACAGCTACCTGTGGCCATTGC 1080
976 TTATGGCCAGGTCTCGCTTAGCTCCATCATGGGCATATGACACTTGGGCTCTTAC 1035
1081 TTTGGCTATCACAAGTACTCCCTCTCTCTGCGAGCTGCTTCTGTGGCCCTTCTGTCTG 1140
1036 TGCTCAGTGTATCTTCAATCCAGCCCTGCTACAGTGTATCTGTGTGCCCTTCTGCCCC 1095
1141 AGACCCCCCATACCTCTCATCATCGGAACCTTGGAGGGGCTGCCCCGAAAGAGTCTAA 1200
1096 AGACCCCCCGCTTCTCTCATCAATCGTAAACGAGGAAACCGGGCCAAAGATGTGCTGA 1155
1201 AGCCCTTGACAGGTGGGCTGATGTGTGATGCACTGGCTGAGCTGAAGGATGAGAAAC 1260
1156 AAAAGCTTCAGGAGCAGCCGATGTGACCGAGACCTTGACAGAGATGAAAGAGGGTCT 1215
1261 GGAAGTTGGAAGAGAGCGTCCACTGCTTGTGCTGAGCTCCTGGGACGCGCAACCCACC 1320
1216 GGCAGATGATGCGGGAGAGAAGGTCAACATCTTGGAGCTGTTCGGCTCACCCGCTACC 1275
1321 GGCAGCTCTGATTTATTTGCAAGTGTGTGCACTGAGCCAGCAGCTCTCAGGCATCAATG 1380
1276 GCCAGCCATCTCATCCCGTGTGTGCTGAGCTGTCCCAGCAGCTGTCCGCGCATCAATG 1335
1381 CTGTTTCTACTATTCAACAGCATCTTTGAGTTAGCTGGGTGGAACAGCCAGCTACG 1440
1336 CTGTGTTCTACTCTAAAGAGCATCTTCGAAAGGAGGAGGTGTGCAAGAGCTGTGTATG 1395
1441 CCACCATAGGAGTGTGTGTCAATACCGCTTTCAAGTGTGCTGCTGCTCTTCTGTAGTAG 1500
1396 CCACCATCGCTCGGGTATCGTCAACAGCGCTTCACTGTGGTGTGCTGCTGCTGCTGG 1455
1501 AGCAGCTGGGCGACGACACTCCATCTCTGGGCGCTGGCAGGCATGTGTGGCTGGCA 1560
1456 AGCAGCTGGCGCTCGGACCTGATCTCATTTGTGTGGCTGGCATGGCGGCTGTGCTG 1515
1561 TCTTGTAGAGTGGTCTGCTGCTGCTGGAGCGGTTCCATCCATGAGTGTATGTGTCCA 1620
1516 TGCTCATGACCATGCGCCCTGCTGGAGAGCTGCCCTGGATGTCTCTATCTGAGTA 1575
1621 TCGTGGCCATATTGTGGCTTTGTGGCTTCTTTGAGATGTGTCTGGGCCCATTCCTCTGT 1680

Db 1576 TCCTGGGCATCTTTGGCTTTGGCTCTTTGAAAGTAGGCCCTGGTCTCTATTCATGGT 1635
Qy 1681 TCATTGTGGCGAGCTCTTCAGCCAGGGCCCGCCGAGCAGCAGCAGCTGGCTGTAGCTGGT 1740
Db 1636 TCATTGTGGCGAGCTTTTCAGCCAGGGCCCGCCGAGCAGCAGCTGGCTGTAGCTGGT 1695
Qy 1741 TCTCCAACTGGAGCTGTAACTTCATCGTTGGCATGGGTTCCAGTATGTGTGGGATGCTA 1800
Db 1696 TCTCTAACTGGAGCTCAAACTTCATCGTTGGCATGGTCTCCAAATATGTGGAGCAACTGT 1755
Qy 1801 TGGCTCCCTACGCTCTCTCTATTTGGCGCTCTCTCTGCTTGGCTCTCTTCACTTCACCT 1860
Db 1756 GTGGCCCTACGCTCTCTCTATTCATCGTTGGCATGGTCTCCAAATATGTGGAGCAACTGT 1815
Qy 1861 TCCTAAGAGTGGCTGAAACAGAGGGCGGACATTTGACACAGATCTCGGCCACCTCCGAC 1920
Db 1816 ACTTCAAAGTCTGAGACCAAGGGCGGACCTTCGATGAGATCGCTTCGGCTTCGGC 1875
Qy 1921 GGACACCTCTCTCTTAGACGAGGAGGTGAACCCAGTACAGAACTTGAATACCTTAGGGC 1980
Db 1876 AGGGGGGTGC---CAGCCAGAGCGACAAGACCTCGAGGAGCTCTTCCACCCCTCGGGG 1932
Qy 1981 CAGATGAGATGACTAATCCATTTGAAGTGAAGCTCCATCATCTCTCTTAAATTTTCA 2040
Db 1933 CTGACTCCCAAGTGAATCGATTTGAAGTGAAGCTCCATCATCTCTCTTAAATTTTCA 1992
Qy 2041 TGACTGACGTTTTTCTTCAATTTAATTAATGATGATTTGTTGAAAAAAGAAAAA 2100
Db 1993 TGACTGAGTTTTTCTTCAATTTAATTAATGATGATTTGTTGAAAAAAGAAAAA 2052
Qy 2101 AATTTCCTTATCAATGATATCTTACGATTAATTAATTAATTTCTTAAACCTATTAT 2160
Db 2053 AATTTCCTTATCAATGATATCTTACGATTAATTAATTAATTTCTTAAACCTATTAT 2112
Qy 2161 TGTGTACATATACAGAGTATTAATACATATATACCTTTTCCACGAGCAAAATTAAGCA 2220
Db 2113 TGTGTACATATACAGAGTATTAATACATATATACCTTTTCTTAAACAGAAAAA 2172
Qy 2221 AAAAGAAACGATAACATGCTGCCATCTCTGCACTCTTTGTTCCAGGAGCAAAATTAAGCA 2280
Db 2173 AAAAGAAACGATAACATGCTGCCATCTCTGCACTCTTTGTTCCAGGAGCAAAATTAAGCA 2232
Qy 2281 AATGAATTTCCCTATGAATAATTAAGGAGCAGATCAGCAGACTTATCTTGGGGGT 2340
Db 2233 AATGAATTTGCTCTATGAATAATTAAGGAGCAGATCAGCAGACTTATCTTGGGGGT 2292
Qy 2341 CCTCTAGAAATAGTCAGGACTTGGCTGAGCTTTCTTCCAGTTG 2386
Db 2293 CCTCTAGAAATAGTCAGGACTTGGCTGAGCTTTCTTCCAGTTG 2338

RESULT 4
US-10-067-449-13
; Sequence 13, Application US/10067449
; Publication No. US20030166259A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Gunter
; APPLICANT: Koller, Klaus-Peter
; APPLICANT: Boles, Eckhard
; APPLICANT: Wiczorke, Roman
; APPLICANT: Diugai, Silke
; TITLE OF INVENTION: Saccharomyces cerevisiae Yeast Strain With Functional Expression
; FILE REFERENCE: DEAV2001/00002
; CURRENT APPLICATION NUMBER: US/10/067,449
; CURRENT FILING DATE: 2002-02-05
; PRIOR FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 2338
; TYPE: DNA

; ORGANISM: Rattus norvegicus
US-10-067-449-13
Query Match 62.4%; Score 1498.8; DB 15; Length 2338;
Best Local Similarity 77.8%; Pred. No. 0;
Matches 1856; Conservative 0; Mismatches 482; Indels 48; Gaps 3;
Qy 1 TCGACTCTAGAGATCCCTTAAGCTTAATCTCTTATGAATCGGAGAAAGCGGGTCTTT 60
Db 1 TCGACTCTAGAGATCCCTTAAGCTTAATCTCTTATGAATCGGAGAAAGCGGGTCTTT 60
Qy 61 TAACTCAATATAATTTTCGAAATCTTTTCTACGCTTTTCTTCGGAACCTAGATAG 120
Db 61 TAACTCAATATAATTTTCGAAATCTTTTCTACGCTTTTCTTCGGAACCTAGATAG 120
Qy 121 GTGGCTCTTCCACCTGTTTTCATCATTTTAGTCTTTTTCGCAAGCCATGCTGCTCTTTC 180
Db 121 GTGGCTCTTCCACCTGTTTTCATCATTTTAGTCTTTTTCGCAAGCCATGCTGCTCTTTC 180
Qy 181 GTTTTTCGATGGCGAACGAGGCTGGAATAATTAACGGTACGCGCTAAACGATAGTA 240
Db 181 GTTTTTCGATGGCGAACGAGGCTGGAATAATTAACGGTACGCGCTAAACGATAGTA 240
Qy 241 TAGGCCACGCACTGGGCTGGAGCAACAATAAGTCCGCCATTTTATGTTTCAAAA 300
Db 241 TAGGCCACGCACTGGGCTGGAGCAACAATAAGTCCGCCATTTTATGTTTCAAAA 300
Qy 301 CCTAGCAACCCCAACCACTTGTCTCATCTGTTCCCGATTCACAAATGATATAAAGCGA 360
Db 301 CCTAGCAACCCCAACCACTTGTCTCATCTGTTCCCGATTCACAAATGATATAAAGCGA 360
Qy 361 TTAACAATTTACATCTTAACCGATTTGAGATTTCTCTTCTCAATTTCTCTTATATTA 420
Db 361 TTAACAATTTACATCTTAACCGATTTGAGATTTCTCTTCTCAATTTCTCTTATATTA 420
Qy 421 GATTATAAGCAACAATAATTAATTAACAAGACTTTATAAGCAACAATAATGTCGAAT 480
Db 421 GATTATAAGCAACAATAATTAATTAACAAGACTTTATAAGCAACAATAATGTCGAAT 480
Qy 481 TCCAGCAGATCGGCTCTGAAGATGGGGAACCCCTCAGCAGCGAGTACCTGGGACACTGG 540
Db 481 TCCAGCAGATCGGCTCTGAAGATGGGGAACCCCTCAGCAGCGAGTACCTGGGACACTGG 540
Qy 541 TCCTTCTGTATTTCTCAGCTGTGCTTGGCTCCCTTCACTTCTGCTCTCTCTCCG 720
Db 541 TCCTTCTGTATTTCTCAGCTGTGCTTGGCTCCCTTCACTTCTGCTCTCTCTCCG 720
Qy 508 TGTGGCGCTGGGAGGGGAGTGTCTCGATCCCTGCACTTGGCTGATTAACACCGGTGCA 567
Db 508 TGTGGCGCTGGGAGGGGAGTGTCTCGATCCCTGCACTTGGCTGATTAACACCGGTGCA 567
Qy 601 TCACCGCCCAACAGAAAGTGAACAGAGCTACAACTGCAACTTGGCTGGTAGGAGG 660
Db 601 TCACCGCCCAACAGAAAGTGAACAGAGCTACAACTGCAACTTGGCTGGTAGGAGG 660
Qy 661 GTCTGGGGGAGCCGAGCTCCATCCCAAGGCAACCTCCTACCTTCTGCTCTCTCCG 720
Db 661 GTCTGGGGGAGCCGAGCTCCATCCCAAGGCAACCTCCTACCTTCTGCTCTCTCCG 720
Qy 721 TGGCCATCTTCTGTGGGTGGCATGATTTCTCTCTTCTCAATTTGGCATCATTTCTCAAT 780
Db 721 TGGCCATCTTCTGTGGGTGGCATGATTTCTCTCTTCTCAATTTGGCATCATTTCTCAAT 780
Qy 735 TGGCCATCTTCTGTGGGTGGCATGATTTCTCTCTTCTGCTGGGCTCTTTGTTAAATC 735
Db 735 TGGCCATCTTCTGTGGGTGGCATGATTTCTCTCTTCTGCTGGGCTCTTTGTTAAATC 735
Qy 781 GGTGGGAGGAGAAAGGGCTATGCTGGCCAACTATGCTTGGCTGTGCTGGGGGGCCCC 840
Db 781 GGTGGGAGGAGAAAGGGCTATGCTGGCCAACTATGCTTGGCTGTGCTGGGGGGCCCC 840
Qy 736 GCTTTGGCAGGCGGAACTCCATCTGATGATGAACCTGTTGGCTTGTGCTGCCGTGC 795
Db 736 GCTTTGGCAGGCGGAACTCCATCTGATGATGAACCTGTTGGCTTGTGCTGCCGTGC 795
Qy 841 TCATGGGCTTAGCAATGCGCGGCTCCTTATGAGATACCTCATTTCTGGAGCGGTTCTCA 900
Db 841 TCATGGGCTTAGCAATGCGCGGCTCCTTATGAGATACCTCATTTCTGGAGCGGTTCTCA 900
Qy 796 TTAATGGGTTTCTCAAACTGGGCAAGTCTTTGAGATGCTGATCTCTGGCGGCTTCA 855
Db 796 TTAATGGGTTTCTCAAACTGGGCAAGTCTTTGAGATGCTGATCTCTGGCGGCTTCA 855
Qy 901 TTGGCGCCTACTCAGGGCTAAACATCAGGGTGTGGCTATGTATGTGGGAGAAATCGCCC 960
Db 901 TTGGCGCCTACTCAGGGCTAAACATCAGGGTGTGGCTATGTATGTGGGAGAAATCGCCC 960
Qy 856 TTGGAGTGTACTGTGGCTGACCCAGCGCTTGTGGCCCATGTATGTGGGAGGTTGCAC 915
Db 856 TTGGAGTGTACTGTGGCTGACCCAGCGCTTGTGGCCCATGTATGTGGGAGGTTGCAC 915
Qy 961 CCACTCATCTTGGGGTGCCTTGGGAACTCAACCAATTTGGCCATGCTCATTTGGGATTC 1020
Db 961 CCACTCATCTTGGGGTGCCTTGGGAACTCAACCAATTTGGCCATGCTCATTTGGGATTC 1020

Db 916 CCACAGCTCTTCGTGGAGCCCTTGGGACCCCTGCACACAGCTGGGCAATCGTGTGGGATCC 975
Qy 1021 TGGTTGCCAGGTGTTGGGTTGGAGTCTATGCTGGGCACAGCTACCCGTGGCCATTCG 1080
Db 976 TTAATGGCCAGGTGTTGGCTTAGACTCATCATGGGCAATGCAGACTTTGGGCTCTAC 1035
Qy 1081 TTCTGGCTATACAGTACTCCCTGCTCTCTCTGCTGCAGCTGCTTCTGTGTGCCCTTCTGTCCGT 1140
Db 1036 TGCTCAGTGTCTCTTCATCCAGCCCTGTACAGTGTATCTGTGTGCCCTTCTGCCCTG 1095
Qy 1141 AGAGCCCCGATACCTCTACATCATCCGAACTGTGGAGGGGCTGCGCGAAAGAGTCTAA 1200
Db 1096 AGAGCCCCGCTTCTGTCTCATCAATCGTAACGAGGAGAACCGGGCCCAAGAGTGTGCTGA 1155
Qy 1201 AGCGCTGACAGGCTGGGCTGATGTCTGTATGCACTGGCTGAGCTGAAGGATGAGAAAC 1260
Db 1156 AAAGCTTCGAGGGACAGCCGATGTGACCCGAGACCTGCAGAGATGAAAGAGGGTC 1215
Qy 1261 GGAAGTTGAAAGAGAGCGTCCACTGTCTTGTCTGCAGCTCTGTGGCAGCGCCACCCACC 1320
Db 1216 GCAGATGATCGGGAGGAAGGTCAACATCTTGGAGCTGTTCCGCTCACCGCTACC 1275
Qy 1321 GCGAGCTCTGATTAATGAGTGTGTGCTGCTGAGCTGAGCCAGAGCTCTCAGGCATCAATG 1380
Db 1276 GCGAGCCCATCTCATCGCGGTGTGTGCTGCACTGTCCAGAGCTGTGCGGCCATCAATG 1335
Qy 1381 CTGTTTCTACTATTCAACCCAGCATCTTTGATGATGCTGGGTGGAAAGCAGCCCTACG 1440
Db 1336 CTGTGTCTACTACTCAAGAGCATCTTCGAGAAGCAGGTGTGAGAGCTGTGTATG 1395
Qy 1441 CCACCATAGAGCTGTGTGTCATACCGTCTTCACTGTGTCTGCTGCTGCTCTTAGTAG 1500
Db 1396 CCACCATCGCTCGGTATCGTCAACAGCCCTTCACTGTGTGTGCTGTGCTGTG 1455
Qy 1501 AGCAGCTGGGCGAGGACATCTCATCTCTGCGCTGCGAGGAGGTGTGCGCTGTGCCA 1560
Db 1456 AGCAGCTGGGCGTGGACCTGCTCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTG 1515
Qy 1561 TCTTGATGAGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1620
Db 1516 TGCTATGACCATCGCCCTGCGCTGCTGAGAGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1575
Qy 1621 TGTGGCCCATATTGGCTTTGTGGCTTCTTTTGAATGGTCTCTGGGCCCATCCCTGCT 1680
Db 1576 TGTGGCCCATCTTTGGCTTTGTGGCTTCTTTGAAGTAGGCCCTGCTCTATTCCATG 1635
Qy 1681 TCATTGTGCGAGCTCTTACGACAGGCGCCCGCCAGCAGCCATGCTGTAGCTGTG 1740
Db 1636 TCATTGTGCGAGCTGTTTACGACAGGCGCCCGCCAGCTGCTGCTGCTGCTGCTGCTG 1695
Qy 1741 TCTCCAACTGGACCTGTAACCTTCACTGTTGGCATGGGTTTCCAGTATGTTGCGGATGCTA 1800
Db 1696 TCTCTAACTGGACCTCAAACTTCACTGTTGGGATGTGCTTCCAATATGGAGCAACTGT 1755
Qy 1801 TGGGTCCTCTACGCTCTTCTTCTATTGTGGCTCTCTCTGCTTGGCTTCTTCACTTTCACCT 1860
Db 1756 GTGGCCCTTACGCTTCTCATCTTTCAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1815
Qy 1861 TCTTAAGTGTGCTGAAACAGAGGCGCGGACATTTGACCAAGATCTGGGCGACCTTCCGAC 1920
Db 1816 ACTTCAAAGTCTTCTGAGACCAAGGCGCGACCTTCGATGAGATGCTTTCGGGCTTCGGC 1875
Qy 1921 GGACACCTTCTCTTTAGAGCAGGAGGTGAACCCAGTACAGAACTTGAATACTTAGGGC 1980
Db 1876 AGGGGGTGC---CAGCCAGCGGCAAGACACCTTGAGGAGCTCTTCCACCCTCTGGGG 1932
Qy 1981 CAGATGAGAAATGACTAATCGATTGGAAGTGAAGCTCCATCATCTCTCTTTAAATTTTCA 2040
Db 1933 CTGACTCCCAAGTGAATCGATTGGAAGTGAAGCTCCATCATCTCTCTTTAAATTTTCA 1992
Qy 2041 TGACTGAGCTTTTCTTCAATTTAAATATCATAGTATTTGTTGAAAAAAGAAAAA 2100
Db 1993 TGACTGAGCTTTTCTTCAATTTAAATATCATAGTATTTGTTGAAAAAAGAAAAA 2052

Qy 2101 AATTTCCCTTATCAATGATATCCCTTACGATTATATAATTCCTTACCTAAAACTATTAT 2160
Db 2053 AATTTCCCTTATCAATGATATCCCTTACGATTATATAATTCCTTACCTAAACCTATTAT 2112
Qy 2161 TGTGTACATATATCAGAGTATTATTACATATATAACCTTTTCTCTAAAAACAGGAAAAA 2220
Db 2113 TGTGTACATATATCAGAGTATTATTACATATATAACCTTTTCTCTAAAAACAGGAAAAA 2172
Qy 2221 AAAAGAAAACGATACATGCTCTGCCATCCTTTGTTACCCGAGCAAAATTTAAAAAGCAA 2280
Db 2173 AAAAGAAAACGATACATGCTCTGCCATCCTTTGTTACCCGAGCAAAATTTAAAAAGCAA 2232
Qy 2281 AATGAATTTGCTCCCTATGAAATTTTAAAGGACCAATCACCAGACTTATCTCTGGGGGT 2340
Db 2233 AATGAATTTGCTCCCTATGAAATTTTAAAGGACCAATCACCAGACTTATCTCTGGGGGT 2292
Qy 2341 CCTTAGAAAAATAGTCAGGTACTTGGCTGGACTTTCTTCCAGTTG 2386
Db 2293 CCTTAGAAAAATAGTCAGGTACTTGGCTGGACTTTCTTCCAGTTG 2338

RESULT 5
US-10-067-449-14
; Sequence 14, Application US/10067449
; Publication No. US20030166258A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Gunter
; APPLICANT: Koller, Klaus-Peter
; APPLICANT: Boles, Eckhard
; APPLICANT: Wieszorke, Roman
; APPLICANT: Diugai, Silke
; TITLE OF INVENTION: Saccharomyces cerevisiae Yeast Strain With Functional Expression
; FILE REFERENCE: DEAV2001/00002
; CURRENT APPLICATION NUMBER: US/10/067,449
; PRIOR FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: DE 101 06 718.6
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 2338
; TYPE: DNA
; ORGANISM: Rattus norvegicus
US-10-067-449-14

Query Match 62.3%; Score 1485.6; DB 15; Length 2338;
Best Local Similarity 77.7%; Pred. No. 0;
Matches 1854; Conservative 0; Mismatches 484; Indels 48; Gaps 3;

Qy 1 TCGACTCTAGAGGATCCCTTAAGCTAATCCTTATGAATCCGGAGAAAAGCGGGGTCTTT 60
Db 1 TCGACTCTAGAGGATCCCTTAAGCTAATCCTTATGAATCCGGAGAAAAGCGGGGTCTTT 60
Qy 61 TAACCTCAATAAAATTTTCCGAAATCCTTTTCTACGCTTTTCTTCGGGAACCTAGATAG 120
Db 61 TAACCTCAATAAAATTTTCCGAAATCCTTTTCTACGCTTTTCTTCGGGAACCTAGATAG 120
Qy 121 GTGGCTCTTCCACTGTTTTCATCATTTTATGTTTTTTCGAAAGCAGTGGCTTTTC 180
Db 121 GTGGCTCTTCCACTGTTTTCATCATTTTATGTTTTTTCGAAAGCAGTGGCTTTTC 180
Qy 181 GTTTTTTCCGATGGCAAGGCTGGAAATTAACGGTACGCGCTTACGATAGTAA 240
Db 181 GTTTTTTCCGATGGCAAGGCTGGAAATTAACGGTACGCGCTTACGATAGTAA 240
Qy 241 TAGGCCACGCAACTGGGCTGGACCAACAATAAGTCGCCCAATTTTATGTTTTCAAAA 300
Db 241 TAGGCCACGCAACTGGGCTGGACCAACAATAAGTCGCCCAATTTTATGTTTTCAAAA 300
Qy 301 CTTAGAACCCCAACCAAACTTGTCTCCGGATTCAAAATGATATATAAAGCGA 360

301 CCTAGCAACCCCAACCACTTGTCTCATCGTTCCGGATTACAAATGATATATAAAGCGA 360
361 TTAACAATTTACATTTCAACAGATTGAGATTTCCTTTCTCAATTCCTCTTAATTA 420
361 TTAACAATTTCAATTTCAACAGATTGAGATTTCCTTTCTCAATTCCTCTTAATTA 420
421 GATTATAGAAACAACAATTTAAATTTACAAAGAACTTTATAAGCAACAATATCTGAAAT 480
421 GATTATAGAAACAACAATTTAAATTTACAAAGAACTTTATAAGCAACAATATCTGAAAT 480
481 TCAGACAGATCGGCTCTGAAGATGGGGAACCCCTCAGCAGCAGAGTGACTGGGACACTGG 540
481 TCAGCAGA-----AGGTGACGGGGCGGCTTA 507
541 TCCTTGTCTGATTTCTCAGCTGTGCTTGGCTCCCTTCAGTTTGGCTATAAATTTGAGATCA 600
508 TGTGGCCGTGGGAGGGGAGTGTCTGGATCCCTGCGAGTTTCGGCTATAACACCGGTGTCA 567
601 TCAACGGCCCAAGAAAGTGAATTAACAGAGCTACAAATGCAACTTGGCTGGGTAGGAGG 660
568 TCAACGGCCCAAGAAAGTGAATTTAGAGAGTTCTACAATCAACAATGGAACACCGCTATG 627
661 GTCTTGGGGACCGGACTCCATCCCAAGGCAACCCCTCAGTACCCCTTTGGGCTCTCTCGG 720
628 G-----AGAGTCCATCCCATCCACCACTCACCACACTCTGGTCTCTCTCCG 675
721 TGGCCATCTTCTCTGTGGGTGGCATGATTTCTCTCTCTTCTCAATTGGGCATCAATTTCTCAAT 780
676 TGATGATCTTCTGTCTGGGGGATGATTTGGTTCTCTCTGTGGGCTCTTTGTTAATC 735
781 GGTGGGAAGAAAGGGCTATGCTGGCCCAACAATGTCTTGGCTGTCTGGGGGGGCGCC 840
736 GCTTTGGCAGCGGAACTCCATGCTGATGATGAACCTGTGTGGGCTTTGTCTGCGCGTGC 795
841 TCATGGCCCTAGCAATGCGCGGCTCCTATGAGATCACTTCTCGGACGCTTCTCTCA 900
796 TTATGGGTTTCTCAAACTGGGCAAGTCTTTGAGATGCTGATCTCTGGGCGGCTTCAATCA 855
901 TTGGCGCTACTCAGGCTAACATCAGGGTTGGTGGCCTATGATGTGGGAGAAATCGCCC 960
856 TTGGAGTGTACTGTGGCTGACCAACCGGCTTTGTGCCCATGATGTGGGGGAGGTGTAC 915
961 CCACTCATCTTGGGGTGTCTGGGAACAACAACAATTTGGCCATGCTCAATTTGGGATTC 1020
916 CCAAGCTCTTCTGTGGAGCCCTGGGCAACCCCTGCAACAGCTGGGCACTCGTGTGGATCC 975
1021 TGGTTCGCCAGGTGTGGGTTTGGAGTCTATGCTGGGCAAGCTACCTCTGGCCCATTCG 1080
976 TTATTTGCCAGGTGTTCGGCTTAGACTCCATCATGGGCAATGAGACTTGTGGCCCTTAC 1035
1081 TTCTGGCTATCACAGTACTCCCTGCTCTCTGAGCTGTCTTCTTGGCCCTTCTGTCTCTG 1140
1036 TGCTCAGTGTCACTTTCATCCAGCCCTGTCTACAGTGTATCTTGTGGCCCTTCTGCCCCTG 1095
1141 AGAGCCCCCGATACCTCTCATCATATCCGGAACCTGGAGGGGCTGCCCCGAAGAGTCTAA 1200
1096 AGAGCCCCCGCTTCTCTCTCATCAATCGTAACGAGGAGAACCCGGGCCCAAGAGTGTCTGA 1155
1201 AGCGCTGACAGGCTGGGCTGATGTCTGATGCACTGGCTGAGCTGAAGGATGAGAAC 1260
1156 AAAAGCTTCGAGGAGACGCGATGTGACCCCGAGACCTTCAGGAGATGAAAGAGAGGGTC 1215
1261 GGAAGTTGGAAGAGAGCGTCCACTGTCCTTGTGTCAGCTCCTGGGCGAGCGCACCCACC 1320
1216 GGAGATGATGGGGAGAGAGGTCAACCATCTTGGAGCTGTTCGGCTCACCCGCTACC 1275
1321 GGAGCCCTCTGATTTATTTGAGTGGTGTCTGAGCTGAGCCAGAGCTCTCAGGCATCAATG 1380
1276 GGCAGCCCATCTCATCGCGTGTGTCTGAGCTGTCCAGCAGCTGTCTGGGCATCAATG 1335
1381 CTGTTTCTACTATTGAACAGCATCTTTGAGTTAGCTGGGTGGAAACAGCCAGCTACG 1440
1336 CTGTGTTCTACTACTCAACAGCATCTTTCAGAGAGGCGAGGTGTGACAGCAGCCTGTGATG 1395

QY 1441 CACACCATAGAGCTGTGTGGTCAATACCGTCTTCAAGTTGGTCTCGGTGCTCTTAGTAG 1500
DB 1396 CCACCATCGGCTCGGGTATCGTCAACACAGCCCTTCACTGTGGTGTGCTGCTTCTGCTGG 1455
QY 1501 AGCGAGCTGGGCGAGCGACATCCATCTCTGGGCTTGGCAGCAGTGTGGCTGTGGCCA 1560
DB 1456 AGCGAGCTGGGCTGGGACCCCTGCATCTCANTGGTCTGGCTGGCAGTGGCGGGCTGTCTG 1515
QY 1561 TCTTGATGAGCGGTGGCTGTCTGTCTGTGGAGGGGTTCATCATCATGAGTTATGTGTCCA 1620
DB 1516 TGCTCATGACCATCGCCCTGGCCCTGCTGGAGCAGCTGCCCTGGATGTCTCTATCTGAGTA 1575
QY 1621 TGTGGCCATATTTTGGCTTTTGGCCCTTCTTTGAGATTTGGTCTGTGGCCCATCCCTGGT 1680
DB 1576 TGTGGCCATCTTTTGGCTTTTGGCCCTTCTTTGAGATTTAGGCCCTGTCTTATTTCCATGGT 1635
QY 1681 TCATTTGGCCGAGCTCTTTCAGCCAGGCGCCCGCCAGCAGCATGTTGCGGATGCTA 1740
DB 1636 TCATTTGGCCGAGCTGTTCAGCCAGGCGCCCGCCAGCTGCTGTCTGTGTGGCTGGCT 1695
QY 1741 TCTCCAACTGGACCTCTAACTTTCATCGTTGGCATGGGTTTCCAGTATGTTGCGGATGCTA 1800
DB 1696 TCTCTAACTGGACCTCAAACTTTCATCGTTGGCATGTTGCTTCCAAATATGTGAGCNACTGT 1755
QY 1801 TGGGTCTCTACGTTCTTCTTCTTATTTGGCCCTCTCTGTCTGTGGCTTCTTCACTTCACT 1860
DB 1756 GTGGCCCTACGTTCTTCTCATCTTTCACGCTGTCTGTGGTACTTCTTCTTCACTTCACT 1815
QY 1861 TCTTAGAGTGTCTGAAACAGGAGCGCGGACATTTGACAGATCTCGGCCACCTTCCGAC 1920
DB 1816 ACTTCAAGTGTCTGAGACCAAAAGCGCGACCTTCGATGAGATCGCTTCCGGCTCCGGC 1875
QY 1921 GGAACCTTCTCTCTTTAGAGCAGGAGTGAACCCAGTACAGAACTTGAATCTTAGGGC 1980
DB 1876 AGGGGGGTG---CAGCCAGAGCGACAGACACTGAGGAGCTTCTCCACCTCTGGGGG 1932
QY 1981 CAGATGAGAAATGACTAATCGATTTGAAGTGAGAGCTCCATCACTCTCTTAAATTTTCA 2040
DB 1933 CTGACTCCCAAGTGTAAATCGATTTGAAGTGAGAGCTCCATCATCTCTTAAATTTTCA 1992
QY 2041 TGACTACGTTTTTCTTCAATTTAATTTATCATAGTATTTGTTGAAAAAATAAAAAA 2100
DB 1993 TGACTACGTTTTTCTTCAATTTAATTTATCATAGTATTTGTTGAAAAAATAAAAAA 2052
QY 2101 AATTTCCCTTATCAATGATATCTTACGATTTATATAAATTCCTTACCTAAACCTTATTT 2160
DB 2053 AATTTCCCTTATCAATGATATCTTACGATTTATATAAATTCCTTACCTAAACCTTATTT 2112
QY 2161 TGTGTACATATATCAGAGTATTTATACATATATAAATTTCTTAAATAACAGAAAAA 2220
DB 2113 TGTGTACATATATCAGAGTATTTATACATATATAAATTTCTTAAATAACAGAAAAA 2172
QY 2221 AAAAGAAACGATAACATGCTCTGCCATCTTTGTTGACGAGCAAAATTTAAACGCAA 2280
DB 2173 AAAAGAAACGATAACATGCTCTGCCATCTTTGTTGACGAGCAAAATTTAAACGCAA 2232
QY 2281 AATGAATTTGCTTATGAAATTTAAAGGACCACTACAGAGCTTATCTCTGGGGGGT 2340
DB 2233 AATGAATTTGCTTATGAAATTTAAAGGACCACTACAGAGCTTATCTCTGGGGGGT 2292
QY 2341 CCTCTAGAAAAATAGTCAGTACTTCCCTGGAGCTTTCTTCCAGTTG 2386
DB 2293 CCTCTAGAAAAATAGTCAGTACTTCCCTGGAGCTTTCTTCCAGTTG 2338

RESULT 6

US-10-067-449-9

; Sequence 9, Application US/10067449

; Publication No. US20030166258A1

; GENERAL INFORMATION:

; APPLICANT: Muller, Gunter

; APPLICANT: Koller, Klaus-Peter

APPLICANT: Boles, Eckhard
APPLICANT: Wiczorke, Roman
APPLICANT: Dlugai, Silke
TITLE OF INVENTION: Saccharomyces cerevisiae Yeast Strain With Functional Expression
TITLE OF INVENTION: GLUT Promoter
FILE REFERENCE: DEAV2001/00002
CURRENT APPLICATION NUMBER: US/10/067,449
PRIOR APPLICATION DATE: 2002-02-05
PRIOR APPLICATION NUMBER: DE 101 06 718.6
PRIOR FILING DATE: 2001-02-14
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 7828
TYPE: DNA
ORGANISM: Homo sapiens
US-10-067-449-9

Query Match 51.5%; Score 1229; DB 15; Length 7828;
Best Local Similarity 85.8%; Pred. No. 7,3e-301;
Matches 1364; Conservative 0; Mismatches 225; Indels 0; Gaps 0;

QY 468 ATAAATGCTGGAATTCAGCAGATCGGCTCTGAAGATGGGAAACCCCTCAGCAGCGAGTG 527
DB 1 ATGCGGTCGGGCTCCAAACAGATAGGCTCCGAAGATGGGAAACCCCTCAGCAGCGAGTG 60

QY 528 ACTGGGACACTGCTTCTGCTGATTTCTCAGCTGTGCTTGGCTCCCTTCACTTTGGCTAT 587
DB 61 ACTGGGACCTGGTCTGCTGTGTTCTCTCGGCTGTGCTCCCTCAGTCTTGGGTAC 120

QY 588 AACATTGAGTGCATCAACGCCCCACAGAAAGTGAATGAACAGAGCTACAACTTGG 647
DB 121 AACATTGGGCTCATCAATGCCCTCAGAAAGTGAATGAACAGAGCTACAACTTGG 180

QY 648 CTGGGAGCAGGGCTCTGGGAGCCGAGCTCCATCCCAAGGACCCCTCACTACCCCT 707
DB 181 CTGGGAGCAGGGCTCTGGGAGCCGAGCTCCATCCCTCAGGACCCCTCACTACCCCT 240

QY 708 TGGGCTCTCTCGTGGCCATCTTCTCTGCTGGGTGCATGATTTCTCTCTCTCTCTCTCT 767
DB 241 TGGGCTCTCTCGTGGCCATCTTCTCTGCTGGGTGCATGATTTCTCTCTCTCTCTCTCT 300

QY 768 ATCAATTTCTCAATGTTGGGAGGAAAGGGCTAGCTGGGCAACAATGCTCTGGCTGTG 827
DB 301 ATCAATTTCTCAATGTTGGGAGGAAAGGGCTAGCTGGGCAACAATGCTCTGGCTGTG 360

QY 828 CTGGGAGGCGCCCTCATGAGGCTCTAGCAATGCGGCGCTCTCTATGAGATCACTATCTC 887
DB 361 CTGGGAGGCGCCCTCATGAGGCTCTAGCAATGCGGCGCTCTCTATGAGATCACTATCTC 420

QY 888 GGAGGCTTCTCATTTGGGCGCTTCTCAGGCTTAACATCAGGGTGGTGGCTATGATGTG 947
DB 421 GGAGGCTTCTCATTTGGGCGCTTCTCAGGCTTAACATCAGGGTGGTGGCTATGATGTG 480

QY 948 GGAGAAATCGCCCACTCATCTCGGGGTGCTTGGGAAACACTCAACAAATGGCCATC 1007
DB 481 GGAGAAATCGCCCACTCATCTCGGGGTGCTTGGGAAACACTCAACAAATGGCCATC 540

QY 1008 GTCAATGGCAATCTGGTGGCCAGGTGTGGGTTTGGAGTCTATGCTGGGACAGCTACC 1067
DB 541 GTTATCGGCAATCTGATCGCCAGGTGTGGGTTTGGAGTCTATGCTGGGACAGCTACC 600

QY 1068 CTGTGGCAATCTGCTTGGCTATCAGTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1127
DB 601 CTGTGGCAATCTGCTTGGCTATCAGTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 660

QY 1128 CCTTCTGTCTGAGAGCCCGGATACCTCTACATCATCCGAACTCTGAGGGGCTGCC 1187
DB 661 CCTTCTGTCTGAGAGCCCGGATACCTCTACATCATCCGAACTCTGAGGGGCTGCC 720

QY 1188 CGAAAGAGTCTAAAGCGCTGACAGGCTGGGCTGATGTCTGATGCACTGGCTGAGCTG 1247
DB 721 AGAAAGAGTCTAAAGCGCTGACAGGCTGGGCTGATGTCTGATGCACTGGCTGAGCTG 780

QY 1248 AAGGATGAGAAACGGAAGTTGGAAGAGAGCGTCCACTGTCTTGTCTGCTCAGCTCCTGGGC 1307
DB 781 AAGGATGAGAAACGGAAGTTGGAAGAGAGCGTCCACTGTCTTGTCTGCTCAGCTCCTGGGC 840

QY 1308 AGCGCACCCACCGGACGCTCTGATTTATGCACTGTGCTGCACTGAGCAGGAGCTC 1367
DB 841 AGCGGTACCCACCGGACGCTCTGATTTATGCACTGTGCTGCACTGAGCAGGAGCTC 900

QY 1368 TCAGGCAATCAATGCTGTTTCTACTATTTCAACACGAGCATTTTGAATGAGTGGGCTGGA 1427
DB 901 TCTGGCATCAATGCTGTTTCTATTTATTCGACAGCATTTTCGAGACAGGAGGTAGGC 960

QY 1428 CAGCCAGCTACGCCACCATAGGAGCTGGTGTGTGCTCAATACCGCTTCACTGCTGTCTGC 1487
DB 961 CAGCTGCTATGCCACCATAGGAGCTGGTGTGTGCTCAACAGATCTTCACTTGTGTCTGC 1020

QY 1488 GTGCTCTTAGTAGCAGGCTGGGCGAGCGGACATCTCCATCTCTCTGGGCTGTCAGAGCATG 1547
DB 1021 GTGTTGTGTGAGCGGCGGCGCGGACGCTCCATCTCTCTGGGCTGTCGCGGCGCATG 1080

QY 1548 TGTGGCTGTGCCATCTTGAATGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1607
DB 1081 TGTGGCTGTGCCATCTTGAATGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1140

QY 1608 AGTTATGTGTCCATCTGTTGGCCATATTTGGCTTTTGTGGCTTTCTTTGAGATTTGGTCT 1667
DB 1141 AGTTATGTGTCCATCTGTTGGCCATATTTGGCTTTTGTGGCTTTCTTTGAGATTTGGTCT 1200

QY 1668 CCCATCCCTGTTTCTTGTGGCGAGCTTTCAGCCAGGCGGCGGCGGCGGCGGCGGCGGCGG 1727
DB 1201 CCCATCCCTGTTTCTTGTGGCGAGCTTTCAGCCAGGCGGCGGCGGCGGCGGCGGCGGCGG 1260

QY 1728 GCTGTAGCTGTTTCTTCAACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 1787
DB 1261 GCTGTAGCTGTTTCTTCAACTGCACTGCACTGCACTGCACTGCACTGCACTGCACTGCACT 1320

QY 1788 GTTGGGATGCTATGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1847
DB 1321 GTTGGGATGCTATGGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1380

QY 1848 TTCACTTCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1907
DB 1381 TTCACTTCACTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1440

QY 1908 GCCACCTTCCGACGACGACCTTCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1967
DB 1441 GCTGCTTCCACCGGACACCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1500

QY 1968 GAATACTTAGGGCCAGATGAGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAA 2027
DB 1501 GAGTATTTAGGGCCAGATGAGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAACTGAA 1560

QY 2028 TCTTAAATTTTCTGAGTACGCTTTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 2056
DB 1561 ATGTAATTTAGTATGTCAGGCTTACATTC 1589

RESULT 7
US-09-894-327A-8
; Sequence 8, Application US/09894927A
; Patent No. US20020052012A1
; GENERAL INFORMATION:
; APPLICANT: Bogan, Jonathan S.
; APPLICANT: Lodish, Harvey F.
; TITLE OF INVENTION: Method of Measuring Plasma Membrane
; FILE OF INVENTION: Targeting of GLUT4
; FILE REFERENCE: 0399.1210-004
; CURRENT APPLICATION NUMBER: US/09/894, 927A
; CURRENT FILING DATE: 2001-06-28
; PRIOR APPLICATION NUMBER: 09/591, 025
; PRIOR FILING DATE: 2000-06-09
; PRIOR APPLICATION NUMBER: 60/154, 078


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; PRIOR FILLING DATE: 1999-09-15
; PRIOR APPLICATION NUMBER: 60/138,237
; PRIOR FILLING DATE: 1999-06-09
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 2592
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: modified GLUT4 containing myc tag sequences
US-09-894-927A-8

Query Match      44.7%; Score 1066.4; DB 9; Length 2592;
Best Local Similarity 87.5%; Pred. No. 7.4e-260;
Matches 1166; Conservative 0; Mismatches 166; Indels 0; Gaps 0;

QY 663 CCTGGGGGACCGGACTCCATCCACAGGACCCCTCACTACCCCTTTGGGGCTCTCCGTC 722
DB 511 CTTAAGGGACCAAGCTCCATCCCTCAGAGCACCCTCACACCCTCTGGGGCCCTCTCGTG 570
QY 723 GCATCTCTCTCTGGGTGGCATGATTTCTCTCTCTCTCAATGGCATCAATTTCTCAATGG 782
DB 571 GCCATCTTTTCCGTGGGGGCGCATGATTTCTCTCTCTCTCAATGGCATCAATTTCTCAATGG 630
QY 783 TTGGGAAGAAAGGGGTATGCTGGGCAACAATGCTTGGCTGTCTGGGGGGGGCCCTC 842
DB 631 CTTTGAAGAAAGGGGCGCATGCTGGTCAACAATGCTTGGGGGGGGGGGGGGGGGGGG 690
QY 843 ATGGGCTAGCCATGCGGGGCTCTATGATGATGATGATGATGATGATGATGATGATGATG 902
DB 691 ATGGGGCTGGCCCAACGCTGCTGCTCTCTATGAAATGCTATGATGATGATGATGATGAT 750
QY 903 GCGGCTTACTCAGGGCTAAATCAGGGTGGTGGCTATGATGATGATGATGATGATGATGATG 962
DB 751 GCGGCTTACTCAGGGCTGATCAGGGCTGGTGGCTATGATGATGATGATGATGATGATGATG 810
QY 963 ACTCATCTTCGGGGTGGTGGGAAACACTCAACAAATGGGCAATGTCATTTGGCATTTG 1022
DB 811 ACTCATCTGGGGGCGGCTGGGAGCGCTCAACCAATGGGCAATGTCATTTGGCATTTG 870
QY 1023 GTTGGCCAGGTGTTGGGTGGGAGTCTATGCTGGGACAGCTACCTGTGGCCATTTGCT 1082
DB 871 ATGCCCCAGGTGTTGGGTGGGAGTCCCTCTGGGACAGCTACCTGTGGCCATTTGCT 930
QY 1083 CTGGCTATCAGTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1142
DB 931 CTGGGCTTCAAGTGTACTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 990
QY 1143 AGCCCCCGATACCTTACATCATCCGGAACCTGGAGGGGCTCTCCCGAAAGAGTCTAAAG 1202
DB 991 AGCCCCCGCTTACCTTACATCATCCGGAATCTCGAGGGGCTCTCCCGAAAGAGTCTGAAG 1050
QY 1203 CGCTGACAGGCTGGGCTGATGTCGTGATGATGATGATGATGATGATGATGATGATGATG 1262
DB 1051 CGCTGACAGGCTGGGCGGATGTTCTGGAGTCTCTGGGAGTGAAGATGAGAGCGG 1110
QY 1263 AAGTTGGAAGAGAGCGCTCCACTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1322
DB 1111 AAGCTGAGGCTGAGCGGCGCATGTCCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1170
QY 1323 CAGCCTCTGATTTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1382
DB 1171 CAGCCCCGTATCTTGGGTCGTGTCAGCTGAGCCAGCAGCTCTCTGGCATCAATGCT 1230
QY 1383 GTTTTCTACTATTCAACAGCATCTTTAGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1442
DB 1231 GTTTTCTATTATTGACAGCATCTTCGACAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1290
QY 1443 ACCATAGGAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1502
DB 1291 ACCATAGGAGCTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGGTGG 1350
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QY 1503 CGAGCTGGGGGACGGACACATCTCTCTGGGCTGGCAGGCAATGCTGGCTGTGCCATC 1562
DB 1351 CGGGCGGGGCGCGCGGACGCTTCCATCTCTCTGGGCTGGCAGGCAATGCTGGCTGTGCCATC 1410
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DB 1411 CTGATGACTGTGGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1470
QY 1623 GTGGCCATATTGGCTTTTGGGCTTTTGGGCTTTTGGGCTTTTGGGCTTTTGGGCTTTT 1682
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QY 1683 ATTGTGGCGAGCTCTTCCAGCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1742
DB 1531 ATCGTGGCGAGCTCTTCCAGCCAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 1590
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DB 1591 TCCAACTGGACCGAGCAACTTCACTGCTGGCATGGGTTTCCAGTATGTTGGGAGGCTATG 1650
QY 1803 GGTCCCTAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1862
DB 1651 GGGCCCTAGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 1710
QY 1863 CTAAGAGTGGCTGAACCAAGAGCGCGGACATTTGACAGATCTCGGCGACCTTCCGACGG 1922
DB 1711 TTAAGAGTACTGAAACTCGAGCGCGGACGTTTGAACAGATCTCGGCTGCTCCACCGG 1770
QY 1923 ACACCTTCTCTCTAGAGCAGGAGGTGAACCCAGTACAGACTTGAATACTTATGGGCCA 1982
DB 1771 ACACCTTCTCTCTAGAGCAGGAGGTGAACCCAGTACAGACTTGAATACTTATGGGCCA 1830
QY 1983 GATGAGATGAC 1994
DB 1831 GATGAGATGAC 1842

RESULT 8
US-09-735-705-135
; Sequence 135, Application US/09735705
; Patent No. US20020052329A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Fan, Liqun
; APPLICANT: Kalos, Michael D.
; APPLICANT: Bangur, Chaitanya S.
; APPLICANT: Hosken, Nancy
; APPLICANT: Fanger, Gary R.
; APPLICANT: Li, Samuel X.
; APPLICANT: Wang, Aijun
; APPLICANT: Skeiky, Yasir A.W.
; APPLICANT: Henderson, Robert A.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C14
; CURRENT APPLICATION NUMBER: US/09/735,705
; CURRENT FILING DATE: 2000-12-12
; NUMBER OF SEQ ID NOS: 419
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 135
; LENGTH: 2856
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-735-705-135

Query Match      28.5%; Score 679; DB 9; Length 2856;
Best Local Similarity 68.1%; Pred. No. 2.4e-161;
Matches 965; Conservative 0; Mismatches 440; Indels 12; Gaps 1;

QY 506 GGAACCCCTCAGCAGGAGTGAATGCTGGACACTGCTTGTGTTATCTCAGCTGTGCT 565
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182 GGAGCCAGCAGCAAGAAGCTGACGGGTGCGCTCATCTGCTGGGTGGAGGAGCAGTGTCT 241
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242 TGGCTCCCTTGCAGTTTGGCTACAACTGGAGTCAATGCCCCCAGAAAGGTGATCGA 301
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Db
302 GGAGTTCTACACAGACATGGTCCACCGCTATGG-----GGAGAGCATCTCT 349
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686 ACAGAGCCCTTCACTACCTTTGGGCTCTCTCGTGGCCATCTTCTCTGTGGGTGGCAT 745
Db
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746 GATTTCTCTCTTCTCATTTGGCATCATTTCTCAATGGTTGGAGAGAAAGGGCTATGCT 805
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470 GATGATGAACCTGCTGGCTTGGTCTCGCGCTGCTCATGGCTTCTGAAACTGGGCA 529
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866 CTCCTATGAGTACTCATTTCTGGAAGCTTCTCATTTGGCGCTTACTCAGGGCTAAATC 925
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770 CTGCTGAGTGCATGCTGTGCTGCTTCTGTGCGGAGAGTCCCCGCTTCTGCTCATCAA 829
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1226 GTCTGATGACTGGCTGAGCTGAAGGATGAGAAACGGAAGTTGAAAGAGAGCTTCACT 1285
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1010 GCTGAGCTGTCCAGCAGCTGTCTGGCATCAACGCTGTCTTCTATTAATCAAGCAT 1069
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1070 CTTTGAAGAGGGGGGTGACAGAGCTGTGTATGCCACCATTTGCTCCGGTATCGTCAA 1129
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1586 GCTGAGCGGGTTCCATCCATGAGTTATGTGTCCATGCGGCCATATTTGGCTTTTGGC 1645
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1430 TGTGGGATGTTGTTCCAGTATGTTGGAGCAACTGTGTGGTCCCTACGTTCTTCTCATCTCT 1489
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1826 TGGCGTCTCTGCTTGGCTTCTTCACTTCACTTCCCTTAAGAGTGCCTGAACACAGAGG 1885
Db
1490 CACTGTGCTCTGTTCTTCTTCTTCTTCACTTCACTTCAAGTTCTTGAGACTAAAGG 1549
QY
1886 CCGGACATTTGACAGATCTCGGCCACTTCCGACGG 1922
Db
1550 CCGGACCTTCGATGAGATGCTTCCGGCTTCCGGCAG 1586

RESULT 9

US-09-850-716A-135
; Sequence 135, Application US/09850716A
; Patent No. US20020115139A1
; GENERAL INFORMATION:
; APPLICANT: Kalos, Michael D.
; APPLICANT: McNeill, Patricia D.
; APPLICANT: Retter, Marc W.
; TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C15
; CURRENT APPLICATION NUMBER: US/09/850,716A
; CURRENT FILING DATE: 2001-05-07
; NUMBER OF SEQ ID NOS: 440
; SOFTWARE: Fast-Seq for Windows Version 3.0
; SEQ ID NO 135
; LENGTH: 2856
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-850-716A-135

Query Match 28.5%; Score 679; DB 9; Length 2856;
Best Local Similarity 68.1%; Pred. No. 2.4e-161;
Matches 965; Conservative 0; Mismatches 440; Indels 12; Gaps 1;

QY
506 GGAACCCCTCAGCAGCAGTGTGCTGGGACACTGGTCTTCTGTATTTCTCAGCTGTGCT 565
Db
182 GGAGCCAGCAGCAAGAAGCTGACGGGTGCGCTCATGCTGTGGGAGGAGCAGTGTCT 241
QY
566 TGGTCCCTTTCAGTTTGGCTATACATTTGAGTCAATCAACGCCCCACAGAAAGTGA 625
Db
242 TGGTCCCTTTCAGTTTGGCTATACATTTGAGTCAATCAACGCCCCAGAAAGTGA 301
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302 GGAGTTCTACACAGACATGGTCCACCGCTATGG-----GGAGAGCATCTCT 349
QY
686 ACAAGGACCCCTCATACTACCTTTGGGCTCTCTCGTGGCCATCTTCTCTGTGGGTGGCAT 745
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350 GCCCACCAGCTTCAACAGCTCTGGTCCCTCTCAGTGGCCATCTTTCTGTGGGGGAT 409
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746 GATTTCTCTCTTCTCATTTGGCATCATTTCTCAATGGTTGGAGAGAAAGGGCTATGCT 805
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410 GATTTGGCTCTCTCTCTGTGGGCTTTTCTGTTAACCGCTTTGGCGGGGGAATTCATGCT 469
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Db
470 GATGATGAACCTGCTGGGCTTGTGTGGGCTTCTGAGCGCTTCTGAAACTGGGCA 529
QY
866 CTCCTATGAGTACTCATTTCTGGAAGCTTCTCATTTGGCGCTTACTCAGGGCTAAATC 925

Db 530 GTCTTTGAGATGCTGATCTCTGGCCGCTTCATCATCGGTGTGTACTGCTGGCCCTGACCAC 589
Qy 926 AGGTTGGTCCCTATGATGTTGGAGAAATCGCCCCACATCATCTTGGGGTGCCTTGGG 985
Db 590 AGGCTTGGTCCCTATGATGTTGGTGAAGTGTACCCACACAGCTTTCGTGGGGCCCTGGG 649
Qy 986 AACACTCAACCAATGGCCATGCTCATTTGCATTTCTGGTTGCCACAGGTGTGGGTTTGA 1045
Db 650 CACCTTGCACCACTGGGCATGCTGCTGCGCATCTCATCGCCACAGGTGTTCGGCCCTGGA 709
Qy 1046 GTCTATGCTGGGCACAGCTACCTGTGGCCATGCTTCTGGCTATCACAGTACTCCCTGC 1105
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Qy 1106 TCTCTGACGCTCTTCTGTGTGCTTCTGCTGAGAGCCCGCATACCTCTACATCAT 1165
Db 770 CTTGCTGACGTGATGCTGCTGCTGCTTCTGCGGAGAGTCCCGCTTCTGCTCATCA 829
Qy 1166 CCGGAACCTGGAGGGGCTCCCGAAGAGCTTAAGCGCTGACAGGCTGGGCTGATGT 1225
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Qy 1226 GTCTGATGCACTGCTGAGCTGAAGATGAGAAACGAACTTGAAGAGAGCGTCCACT 1285
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Qy 1286 GTCTTGTGCTGAGCTCTCTGGGAGCGCACCCACCGGACGCTCTGATTTAGAGTGT 1345
Db 950 CACCATCTGGAGCTGTTCGCTCCCGGCTTACCGGACGCCCATCTCATGCTGTGT 1009
Qy 1346 GCTGAGCTGAGGACGAGCTCTCAGGCATCAATGCTGTTTCTATTTCAATTTCAACAGCAT 1405
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Qy 1406 CTTTGAAGTGTAGCTGGGTGAACAGCAGCTACGCCACCATAGGAGCTGTGTGTCAA 1465
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Db 1310 CTTCTTTGAGTTGCTGCTGGCCCATCCCATGCTTCACTGCTGCTGCTGCTGCTGCTGCT 1369
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Db 1430 TGTGGGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1489
Qy 1826 TGGCGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1885
Db 1490 CACTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1549
Qy 1886 CCGGACATTTGACAGATCTGGGACCTTTCCAGCG 1922
Db 1550 CCGGACCTTCATGAGATGCTTCCGGCTTCCGGCAG 1586

RESULT 10

US-09-880-107-2128

; Sequence 2128, Application US/09880107
; Patent No. US20020142981A1
; GENERAL INFORMATION:
; APPLICANT: Horne, Darci T.
; APPLICANT: Vockley, Joseph G.
; APPLICANT: Scherf, Uwe
; APPLICANT: Gene Logic, Inc.
; TITLE OF INVENTION: Gene Expression Profiles in Liver Cancer
; FILE REFERENCE: 44921-5028-WO
; CURRENT APPLICATION NUMBER: US/09/880,107
; CURRENT FILING DATE: 2001-06-14
; PRIOR APPLICATION NUMBER: US 60/211,379
; PRIOR FILING DATE: 2000-06-14
; PRIOR APPLICATION NUMBER: US 60/237,054
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 3950
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2128
; LENGTH: 2856
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURES:
; OTHER INFORMATION: Genbank Accession No. US20020142981A1 K03195
US-09-880-107-2128

Query Match 28.5%; Score 679; DB 9; Length 2856;
Best Local Similarity 68.1%; Pred. No. 2,4e-161;
Matches 965; Conservative 0; Mismatches 440; Indels 12; Gaps 1;

Qy 506 GGNACCCCTCAGCAGCGAGTGAATGGGACATGGTCTTGTCTGCTGCTGCTGCTGCTGCT 565
Db 182 GGAGCCCGCAGCAGCAAGCTGACGGTGCCTCATGCTGGCTGTGGAGGAGCGTGT 241
Qy 566 TGCTCTCCCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 625
Db 242 TGCTCTCCCTTCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 301
Qy 626 ACAGAGCTCAATGCAACTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 685
Db 302 GGAGTTCTCAACACAGACATGGGTCCACGCTATGG-----GGAGAGCATCT 349
Qy 686 ACAGAGCAGCTCACTACCTTGGGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 745
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Qy 1106 TCTCTGCGAGCTGCTTCTGTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1165
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QY 1166 CCGGAACTGAGGGGCTGCCGAAAGAGTCTAAAGCGCCTGACAGGCTGGGTGATGT 1225
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830 CCGCAACGAGGAGAACCGGGCCCAAGAGTGTCTTAAAGAGCTGCGCGGACAGCTGACGT 889
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DB 1287 GTCTGATGACATGCTGAGCTGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 1346
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DB 1347 GCTGAGCTGAGCCAGCAGCTCTCAGGAGTCAATGCTGTTTCTACTATTCAACACAGCAT 1406
1010 GCTGAGCTGAGCCAGCAGCTCTCAGGAGTCAATGCTGTTTCTACTATTCAACACAGCAT 1069
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QY 1466 TACCGTCTTACGTTGGTCTCGGTGCTCTTGTAGAGCGAGCTGGGCGACGACCTCA 1525
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DB 1887 CCGGACATTTGACAGATCTCGGCCACCTTCCGACGG 1586
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RESULT 11

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US-09-897-778-135
; Sequence 135, Application US/0989778
; Patent No. US20020147143A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; APPLICANT: Marnerakis, Margarita
; APPLICANT: Fanger, Gary R.
; APPLICANT: Vedvick, Thomas S.
; APPLICANT: Carter, Darrick
; APPLICANT: Watanabe, Yoshihiro
; APPLICANT: Henderson, Robert A.
; APPLICANT: Peckham, David W.
; APPLICANT: Fanger, Neil
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
; FILE REFERENCE: 210121.455C16
; CURRENT FILING DATE: 2001-06-28
; NUMBER OF SEQ ID NOS: 467
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; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 135
; LENGTH: 2856
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-897-778-135
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Query Match 28.5%; Score 679; DB 9; Length 2856;

Best Local Similarity 68.1%; Pred. No. 2.4e-161;

Matches 965; Conservative 0; Mismatches 440; Indels 12; Gaps 1;

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QY 506 GGAACCCCTCAGCAGCAGTGAAGTGGGACACTGGTCTCTGCTGTATTTCTCAGCTGTGCT 565
DB 507 GGAACCCCTCAGCAGCAGTGAAGTGGGACACTGGTCTCTGCTGTATTTCTCAGCTGTGCT 566
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QY 566 TGGTCTCTCTCAGTGTGGCTATAAATGAGTGAAGTGAAGTGAAGTGAAGTGAAGTGAAG 625
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DB 687 ACAAGGACCTCACTACCTTTGGGCTCTCTCGGTGGCCATTTCTCTGTGGGTGGCAT 746
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530 GTCCTTTGAGATGCTGATCTGCGGCTTCTCATCGGTGTACTGCGGCTGACCCAC 589
QY 926 AGGTTGGTGGCTATGATGAGGAGAAATGCGGCTTCTCATCTTGGGGTGGCTTGGG 985
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QY 1226 GTCTGATGACATGCTGAGCTGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 1285
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890 GACCCATGACCTGACGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 949
QY 1286 GTCTGATGACATGCTGAGCTGAGAGTGAAGAGTGAAGAGTGAAGAGTGAAGAGTGAAG 1345
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1010 GCTGAGCTGAGCCAGCAGCTCTCAGGAGTCAATGCTGTTTCTACTATTCAACACAGCAT 1069
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Qy 1706 GGGCCCCCGCCAGCAGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 1765
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RESULT 12
US-09-466-396A-135
; Sequence 135, Application US/09466396A
; Publication No. US20030119763A1
; GENERAL INFORMATION:
; APPLICANT: Wang, Tongtong
; TITLE OF INVENTION: COMPOUNDS AND METHODS FOR THERAPY AND
; TITLE OF INVENTION: DIAGNOSIS OF LUNG CANCER
; FILE REFERENCE: 210121.455C4
; CURRENT APPLICATION NUMBER: US/09/466,396A
; CURRENT FILING DATE: 1999-12-17
; NUMBER OF SEQ ID NOS: 224
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 135
; LENGTH: 2856
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-466-396A-135

Query Match 28.5%; Score 679; DB 10; Length 2856;
Best Local Similarity 68.1%; Pred. No. 2.4e-161;
Matches 965; Conservative 0; Mismatches 440; Indels 12; Gaps 1;

Qy 506 GGAAACCCCTCAGCAGCAGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGTGT 565
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Qy 566 TGGCTCCCTCAGTTGGCTTATACATTTGGAGTCAACAGCCGCCACAGAAAGTGTATGA 625
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Qy 806 GGGCAACAATGTCTGGCTGTGTGGGGGGCGCCCTCATGGGCTAGCCAAATGCGCGGC 865
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Qy 1046 GTCTATGTGGGCGACAGCTACCTGTGGGCAATTTGTCTTGGCTATCACAGTACTCCCTGC 1105
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```


APPLICANT: Wang, Aijun
APPLICANT: Skeiky, Yasir A.W.
APPLICANT: Li, Samuel X.
APPLICANT: Kalos, Michael D.
APPLICANT: Henderson, Robert A.
APPLICANT: McNeill, Patricia D.
APPLICANT: Fanger, Neil
APPLICANT: Retter, Marc W.
APPLICANT: Durham, Margarita
APPLICANT: Fanger, Gary R.
APPLICANT: Vedvick, Thomas S.
APPLICANT: Carter, Darick
APPLICANT: Watanabe, Yoshihiro
APPLICANT: Peckman, David W.
APPLICANT: Cai, Feng
APPLICANT: Foy, Teresa M.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE THERAPY
TITLE OF INVENTION: AND DIAGNOSIS OF LUNG CANCER
FILE REFERENCE: 210121.455C17
CURRENT APPLICATION NUMBER: US/10/007,700
CURRENT FILING DATE: 2001-11-30
NUMBER OF SEQ ID NOS: 469
SOFTWARE: FastSeq for Windows Version 4.0
SEQ ID NO 135
LENGTH: 2856
TYPE: DNA
ORGANISM: Homo sapiens
US-10-007-700-135

Query Match 28.5%; Score 679; DB 13; Length 2856;
Best Local Similarity 68.1%; Pred. No. 2.4e-161;
Matches 965; Conservative 0; Mismatches 440; Indels 12; Gaps 1;

QY 506 GGAAACCCCTCAGCAGCGAGTGGACACTGGTCTTGGTGATTTCTCAGCTGTGCT 565
DB 182 GGAGCCAGCAGCAAGAGCTGAGGGTGCCTCATGCTGGCTGTGGAGGACAGTGTCT 241
QY 566 TGCGTCCCTTTCAGTTTGGCTATACATTTGGAGTCATCAACGCCGCCACAGAAAGTGA 625
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QY 626 ACAGAGTACAAAGCAACTTGGCTGGGTAGGAGGGTCTGGGGGACCGACTCCATCC 685
DB 302 GGAGTTCTACAAACAGACATGGGTCCACCGCTATGG-----GGAGAGCATCT 349
QY 686 ACAAGGACCCCTCACTACCTTTGGGCTCTCCGTGGCCATCTTCTGTGGGTGGCAT 745
DB 350 GCCACACGCTCACACGCTTGGTCCCTCTCAGTGGCCATCTTTCTGTGGGGCAT 409
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DB 1550 CCGGACCTTCGATGAGATGCTTCCGCTTCCGCGCAG 1586

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; Sequence 1294, Application US/10172118
; Publication No. US20030224374A1
; GENERAL INFORMATION:
; APPLICANT: Dai, Hongyue
; APPLICANT: He, Yudong
; APPLICANT: Linsley, Peter
; APPLICANT: Mao, Mao
; APPLICANT: Roberts, Chris
; APPLICANT: Van 't Veer, Laura
; APPLICANT: Van de Vijver, Marc
; APPLICANT: Bernards, Rene
; TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
; FILE REFERENCE: 9301-175-999
; CURRENT APPLICATION NUMBER: US/10/172,118

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/ CURRENT FILING DATE: 2002-06-14
/ PRIOR APPLICATION NUMBER: 60/380,770
/ PRIOR FILING DATE: 2002-05-14
/ NUMBER OF SEQ ID NOS: 2699
/ SEQ ID NO 1294
/ LENGTH: 2856
/ TYPE: DNA
/ ORGANISM: Homo sapiens
/ PUBLICATION INFORMATION:
/ DATABASE ACCESSION NUMBER: NM 006516
/ DATABASE ENTRY DATE: 2001-06-18
us-10-172-118-1294

Query Match      28.5%; Score 679; DB 13; Length 2856;
Best Local Similarity 68.1%; Pred. No. 2,4e-161;
Matches 965; Conservative 0; Mismatches 440; Indels 12; Gaps 1;

Qy 506 GGAACCCCTCAGCAGCAGTGAAGTGGACACTGGTCTCTGTATTTCTCAGCTGTGCT 565
Db 182 GGAGCCAGCAGCAAGAGCTGACGGTGCCTCATGCTGTGGAGGAGCAGTGTCT 241
Qy 566 TGGCTCCCTTCACTTGGCTATTAACATTGGAGTCAATCAAGCCCAACAGAAAGTATGA 625
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Db 302 GGAGTTCTAACACAGACATGGGTCCACGGTATGG-----GGAGACATCCT 349
Qy 686 ACAAGGCAACCTCACTACCTTTGGGCTCTCCGGTGGCCATCTTCTGTGGGTGGCAT 745
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Qy 866 CTCCTATGAGATPACTCATTTCTCGACGGTTCCTCATTTGGCCCTACTCAGGGCTAAATC 925
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Db 1490 CACTGTCTCTGCTTGTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1549
Qy 1886 CCGGACATTTGACCAAGATCTCGGCGCACCTTCCGACGG 1922
Db 1550 CCGGACCTTCGATGAGATCGCTTCGGGCTTCGGGCGAG 1586
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Job time : 644.395 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: May 15, 2004, 22:29:22 ; Search time 19566.2 Seconds
(without alignments)
17340.609 Million cell updates/sec

Title: US-10-067-449-9

Perfect score: 7828

Sequence: 1 atgcgcgtcggttcaca.....tttttaatttcaatacaaaa 7828

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3470272 segs, 21671516995 residues

Total number of hits satisfying chosen parameters: 6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

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- 3: gb_in:*
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- 38: em_sy:*
- 39: em_htgo_hum:*
- 40: em_htgo_mus:*
- 41: em_htgo_other:*

Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB	ID	Description
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2	6975.2	89.1	7777	6	AX573333	Sequence
3	5908	75.5	6360	6	AX573337	Sequence
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VERSION	AX573331.1	GI:26005217				
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SOURCE	Homo sapiens					
ORGANISM	Homo sapiens					
REFERENCE	1					
AUTHORS	Mueller, G., Koller, K.P., Boles, E., Wiczorke, R. and Dlugai, S.					
TITLE	Yeast strain of saccharomyces cerevisiae with functional expression of a glut transporter					

JOURNAL Patent: WO 02064784-A 9 22-AUG-2002;
Aventis Pharma Deutschland GmbH (DE)
FEATURES Location/Qualifiers
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ORIGIN

Query Match 100.0%; Score 7828; DB 6; Length 7828;
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Matches 7828; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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AX573333
LOCUS AX573333
DEFINITION Sequence 11 from Patent WO02064784.
ACCESSION AX573333
VERSION AX573333.1 GI:26005219
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1
AUTHORS Mueller,G., Koller,K.P., Boles,E., Wiczorke,R. and Dlugai,S.
TITLE Yeast strain of saccharomyces cerevisiae with functional expression
of a glut transporter
JOURNAL Patent: WO 02064784-A 11 22-AUG-2002;
Aventis Pharma Deutschland GmbH (DE)
FEATURES
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ORIGIN
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Matches 7297; Conservative 0; Mismatches 478; Indels 15; Gaps 2;

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QY	7239	CTGGAAGCGGCGAGTGAGCGCAACCGCAATTAATGTGAGTTACTCATATTAGGACCC	7298
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RESULT 3
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LOCUS
DEFINITION
Sequence 15 from Patent WO02064784.
AX573337
ACCESSION
VERSION
AX573337.1 GI:26005223
KEYWORDS
synthetic construct

ORGANISM	synthetic construct		
REFERENCE	1. artificial sequences.		
AUTHORS	Mueller,G., Koller,K.P., Boles,E., Wiczorke,R. and Dlugai,S.		
TITLE	Yeast strain of sacccharomyces cerevisiae with functional expression of a glut transporter		
JOURNAL	Patent: WO 02064784-A 15 22-AUG-2002;		
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	/mol_type="unassigned DNA"		
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ORIGIN			
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	Best Local Similarity	100.0%;	Pred. No. 0;
	Matches 5908; Conservative	0; Mismatches	0; Indels 0; Gaps 0;
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Db	453	AAGCTTATCGATACCGTCGACCTCGAGTCATGTAATAGTTATGTACCGCTTACATTAC	512
Qy	1592	GCGCTCCCGCCACATCCGCTCTAACCGAAAAGAGAGGTAGACAACTGGAAGCTAGG	1651
Db	513	GCGCTCCCGCCACATCCGCTCTAACCGAAAAGAGAGGTAGACAACTGGAAGCTAGG	572
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Qy	1772	AGAAGGTTTTGGACGCTCGAAGGCTTTAATTTGCGGCGCGGTACCCAAATTCGCCCTATAG	1831
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QY	6752	CCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAAAGCGCCACGCTTCCCGAAG	6811
Db	5673	CCTACACCGAACTGAGATACCTACAGCGTGAGCTATGAAAGCGCCACGCTTCCCGAAG	5732
QY	6812	GGAGAAAGCGGACGAGGTATCCGGTAAGCGGAGCGGTCGGAAACAGGAGCGCACGAGGG	6871
Db	5733	GGAGAAAGCGGACGAGGTATCCGGTAAGCGGAGCGGTCGGAAACAGGAGCGCACGAGGG	5792
QY	6872	AGCTTCAGGGGAAACCGCTCGGTATCTTTATAGTCTTGTGCGGGTTTCGCCACCTCTGAC	6931
Db	5793	AGCTTCAGGGGAAACCGCTCGGTATCTTTATAGTCTTGTGCGGGTTTCGCCACCTCTGAC	5852
QY	6932	TTGAGCGTCGATTTTGTGATGCTCGTCAGGGGGCGGAGCTATGGAACACCGCAGCA	6991
Db	5853	TTGAGCGTCGATTTTGTGATGCTCGTCAGGGGGCGGAGCTATGGAACACCGCAGCA	5912
QY	6992	ACGGGCTTTTACGGTTCTCGGCTTTTGTGCGGCTTTTGTCTCACATGTTCTTTCCTG	7051
Db	5913	ACGGGCTTTTACGGTTCTCGGCTTTTGTGCGGCTTTTGTCTCACATGTTCTTTCCTG	5972
QY	7052	CGTATPCCCTCACTTGTGGATAACCGTATPACCGCTTTTGAAGTGAAGTGAACCGCTC	7111
Db	5973	CGTATPCCCTCACTTGTGGATAACCGTATPACCGCTTTTGAAGTGAAGTGAACCGCTC	6032
QY	7112	CGCGACCGAAGACCGGACCGGACGAGTCACTGAGCGAGGAGCGAAGCGGCCAA	7171
Db	6033	CGCGACCGAAGACCGGACCGGACGAGTCACTGAGCGAGGAGCGAAGCGGCCAA	6092
QY	7172	TACGCAACCGCTCTCCCGCGCTTGGCGGATTCATTAATGACGCTGGCAGCAGCAGGT	7231
Db	6093	TACGCAACCGCTCTCCCGCGCTTGGCGGATTCATTAATGACGCTGGCAGCAGCAGGT	6152
QY	7232	TTCCGACCTGGAAGCGGCGAGTGAAGCGCAACGCAATTAATGTGAGTTACCTCACTCAT	7291
Db	6153	TTCCGACCTGGAAGCGGCGAGTGAAGCGCAACGCAATTAATGTGAGTTACCTCACTCAT	6212
QY	7292	AGGACCCCGAGCTTACATTTATGCTTCCGGCTTCTATGTTGTGGAAATGTGAGCG	7351
Db	6213	AGGACCCCGAGCTTACATTTATGCTTCCGGCTTCTATGTTGTGGAAATGTGAGCG	6272
QY	7352	GATACAAATTTACACAGGAAACAGCTATGACATGATTAAGCCAGCGCAATTAACC	7411
Db	6273	GATACAAATTTACACAGGAAACAGCTATGACATGATTAAGCCAGCGCAATTAACC	6332
QY	7412	CTCACTAAAGGAAACAAAGCTGGAGCT	7439
Db	6333	CTCACTAAAGGAAACAAAGCTGGAGCT	6360

RESULT 4
AX006823/c
LOCUS Sequence 8 from Patent WO0001846. 7209 bp DNA linear PAT 06-SEP-2000
DEFINITION AX006823
ACCESSION AX006823
VERSION AX006823.1 GI:9994839
KEYWORDS synthetic construct
SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS Mortier,K., Bogaert,T., Plaetinck,G. and Platteeuw,C.
TITLE Characterisation of gene function using double stranded rna inhibition
JOURNAL Patent: WO 0001846-A 8 13-JAN-2000;
MORTIER KATHERINE (BE); BOGAERT THIERRY (BE); DEVGEN N V (BE);
PLAETINCK GEERT (BE); PLATTEEUW CHRIST (BE)
FEATURES
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1. .7209
Location/Qualifiers
/organism="synthetic construct"
/mol_type="synthetic DNA"

		/db xref="taxon:32630" /note="plasmid DNA"	
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		Best Local Similarity	87.3%; Pred. No. 0;
		Matches 5104; Conservative	0; Mismatches 629; Indels 114; Gaps 12;
QY	1559	TCATGTAATAGTTATGTCACGCTTACATTCACGCCCTCCGCCACATCCGCTCTAAACCG	1618
Db	5982	TCATGTAATAGTTATGTCACGCTTACATTCACGCCCTCCGCCACATCCGCTCTAAACCG	5923
QY	1619	AAAAGGAAGAGTTAGACCAACCTGAAGTCTAGGTCCTATTTATTTTATAGTTATGT	1678
Db	5922	AAAAGGAAGAGTTAGACCAACCTGAAGTCTAGGTCCTATTTATTTTATAGTTATGT	5863
QY	1679	TAGTATTAAGAACGTTATTTATATTTTCAAAATTTTCTTTTCTGTACAGACGGTGT	1738
Db	5862	TAGTATTAAGAACGTTATTTATATTTTCAAAATTTTCTTTTCTGTACAGACGGTGT	5803
QY	1739	ACGCATCTAACATTAATCTGAACACCTTGTCTGAGAGGTTTGGGACGCTCGAAGGCTT	1798
Db	5802	ACGCATCTAACATTAATCTGAACACCTTGTCTGAGAGGTTTGGGACGCTCGAAGGCTT	5743
QY	1799	TAATTTCCGGCGGTACCAATTCGCCCTATAGTGAAGTCGTATTTACGGCGCTCACTGCG	1858
Db	5742	TAATTTG-----CAAAGCTCGGATCTCGAGCTCGGAAAGCTTGGAGCTGCG	5693
QY	1859	CGTCGTTTTCACAGTCTGTGCTGGGAAACCTCTGGGTTTACCCAACTTAATTCGGCTTCG	1918
Db	5692	CGTCGTTTTCACAGTCTGTGCTGGGAAACCTCTGGGTTTACCCAACTTAATTCGGCTTCG	5633
QY	1919	AGCACATCCCTTTTCGCCAGCTGGCTTAATAGCGAGAGCGCCGACGATCGGCCCTTC	1978
Db	5632	AGCACATCCCTTTTCGCCAGCTGGCTTAATAGCGAGAGCGCCGACGATCGGCCCTTC	5573
QY	1979	CCAAAGTTCGGCAGCTGAATGCGCGGACGCGCCCTGTAGCGGCGCATTAAG	2038
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QY	2039	CGCGCGGGTGTGTGTTACGCGCAGCGTGAACCGCTACATTTGCGACGCGCCTAGCGCC	2098
Db	5512	CGCGCGGGTGTGTGTTACGCGCAGCGTGAACCGCTACATTTGCGACGCGCCTAGCGCC	5453
QY	2099	CGCTCTTTTCGCTTTCTTCTCGCCAGCTTCCGCGCTTTCGCCGCTTTCGCCGCTTTC	2158
Db	5452	CGCTCTTTTCGCTTTCTTCTCGCCAGCTTTCGCCGCTTTCGCCGCTTTCGCCGCTTTC	5393
QY	2159	TCTAAATCGGGGCTCCCTTTAGGGTTCCGATTTAGTCTTTTACGGCACCTCGACCCCAA	2218
Db	5392	TCTAAATCGGGGCTCCCTTTAGGGTTCCGATTTAGTCTTTACGGCACCTCGACCCCAA	5333
QY	2219	AAAACCTTGAATGAGGTGATGTTCAAGTATGAGGATTTTTCGGGATTTTCGGGCTTA	2278
Db	5332	AAAACCTTGAATGAGGTGATGTTCAAGTATGAGGATTTTTCGGGATTTTCGGGCTTA	5273
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Db	5272	CCCTTTGACGTTGGAGTCCAGCTTCTTTATAGTGGACTCTTGTTCCTAACTGGGACAC	5213
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Db	5212	ACTCAACCTTATCTCGGCTTATCTTTTATTAAGGATTTTTCGGGATTTTCGGGCTTA	5153
QY	2399	TTGTTTAAAAATGAGCTGATTTTAAACAAAAATTTTAAACGCGAATTTTAAACAAATTAAC	2458
Db	5152	TTGTTTAAAAATGAGCTGATTTTAAACAAAAATTTTAAACGCGAATTTTAAACAAATTAAC	5093
QY	2459	GTTTTACAAATTTCTGATGCGGTTATTTCTCTTACGATCTGTGGGATTTTTCACACCG	2518
Db	5092	GTTTTACAAATTTCTGATGCGGTTATTTCTCTTACGATCTGTGGGATTTTTCACACCG	5033
QY	2519	ATAGGGTAATAACTGATATAATTAATTAAGAGCTCTAATTTTGTGAGTTTGTATATATGC	2578

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Db ||||| 4972 TTAGCATTTTGGAGAAATTTGCTATTTTGTAGTCTTTTACACCATTTGTCTCCACA 4913
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Db ||||| 4824 GTAAGCTTTGCGGCTCTCTTGCTT-----CCNACCACTGAAATCGNGTTCNAATC 4770
QY ||||| 2819 GTAACTTCAATCTCTCCACCCATGCTCTTTGAGCAATAAAGCCGATAAACAAATCTTT 2878
Db ||||| 4769 CAAAAGTTCACTGTCCAC-----CTGCTTCTGAATCAAAACAAGGGAATAAACGAATG 4716
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Db ||||| 4715 AGGTTCTGTGAAGCTGCATGAGTAGTATGTTGCAAGTCTTTTGGAAATACGAGTCTTTT 4656
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QY ||||| 2999 CTGCTTCAACCGCTAAACAATCCTGGGCCACACACCGGTGTGCAATTCGTAATGTCTGC 3058
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Db ||||| 4550 CTTAGGTTGATACGAACACGCGCAACCAAGTATTTTGGAGTGCCTGAACTATTTTATA 4491
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QY ||||| 3179 CTTAACTGTGCCCTCCATGGAATAATCAGTCAAGATATCCACATGTGTTTTTATAGTAAACA 3238
Db ||||| 4442 TCTCTTCTATTTGGGCACATATAATACCCAGCAAGTCAGCATCGAATCTAG--AGCA 4385
QY ||||| 3239 AATTTTGGGACCTAAATGCTTCAACTAACTCCAGTAATTCCTTGGTGTAC--GAACATCCA 3297
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Db ||||| 4264 GTGCTCAATAGTCACCAATGCCCTCCCTCTTGGCCCTCTCC-----TTTCTTTT 4216
QY ||||| 3418 TCTGCGAGTTTTTGTCTGTGAGTTGGGTGAAGATATCTGGGCAATTTTCATGTTCTTT 3477
Db ||||| 4215 TTTTCCGACCGAATTAATTTCTTAATCGGCAAAAAAAGAAAGCTCCGGA-----T 4168
QY ||||| 3478 CAACACTACATATGCGTATATATACCAATCTAAGTCTGTGCTCTCTCTTCTTCTTCT 3537
Db ||||| 4167 CAAGATTGTAGTAAGTGACAGACTATTTTTCATTAAGAATATCTTCCACTACTGCCA 4108
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Db ||||| 4107 TCTGGCTCATACCTGCAAGTACACATATTA-----CGATGCTGCTCTATTAAAT 4056
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Db ||||| 3995 GCTCTGATCGCGCATAGTTTAAAGCCAGCCCGCACACCCGCGCAACACCCGCTGACGCGCCT 3936
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Db ||||| 3935 GACGGCTTGTCTGCTCCCGGCATCCGCTTACAGACAAAGCTGTGACCGTCTCCGGAGCT 3876
QY ||||| 3778 GCATGTGTACAGAGTTTTCACCGTCATCACCGAAGCGCGGAGACGAAAGGCTCGTGA 3837
Db ||||| 3875 GCATGTGTACAGAGTTTTCACCGTCATCACCGAAGCGCGGAGACGAAAGGCTCGTGA 3816
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Db ||||| 3815 TAGCCCTATTTTATAGGTTTAAATGTATGATATATGTTTCTTAATATGATCCAATAT 3756
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Db ||||| 3755 CAAAGAAATGATAGCAATTGAAGGATGAGACTAATCCAATTGAGGAGTGGCAGCATATAG 3696
QY ||||| 3958 AACAGCTAAAGGCTAGTGTGAAGGAGCATACGATACCCCGCATCGAATGGCATATAT 4017
Db ||||| 3695 AACAGCTAAAGGCTAGTGTGAAGGAGCATACGATACCCCGCATCGAATGGCATATAT 3636
QY ||||| 4018 CACAGAGGTACTAGACTACTCTTTCATCTCATATAAATAGACATATAGTACGCAATTT 4077
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QY ||||| 4078 AAGCATAAACACGCACTATGCGCTTCTCTCATGTATATATATATATACAGCAACACGCAAG 4137
Db ||||| 3575 AAGCATAAACACGCACTATGCGCTTCTCTCATGTATATATATATATACAGCAACACGCAAG 3516
QY ||||| 4138 ATATAGTGGCGAGCTGAAACAGTGAGCTGTATGTGCGCAGCTCGCTTGCATTTTCGGAAG 4197
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QY ||||| 4258 TAGGAATCTTACAGCGCTTTTGAACCCAAAGCGCTCTGAAAGACGCACTTTCAAANAAC 4317
Db ||||| 3395 TAGGAATCTTACAGCGCTTTTGAACCCAAAGCGCTCTGAAAGACGCACTTTCAAANAAC 3336
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Db ||||| 3215 TCACCTTTTGGCTCTTGAACCTTGAACCTTGAACCTTGAACCTTGAACCTTGAACCTTGAACCT 3156
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QY ||||| 4618 CGTTCAATATTTTCTGACCAATGAAGATCATCAACGCTATCACTTTCTGTTTCAAAAGT 4677
Db ||||| 3035 CGTTCAATATTTTCTGACCAATGAAGATCATCAACGCTATCACTTTCTGTTTCAAAAGT 2976
QY ||||| 4678 ATGCGCAATCCACATCGGTATAGAAATTAATCGGGATGCTTTATCTTGAANAATGCA 4737
Db ||||| 2975 ATGCGCAATCCACATCGGTATAGAAATTAATCGGGATGCTTTATCTTGAANAATGCA 2916

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Db	2915	CCCGCAGCTTCCTAGTAAATCAAGTAAACCGCGGAAGTGAAGTCAAGCTTTTTTATGGAA	2856	1835	ATGGGGGATCATGTAACTCGCTTGATCGTTGGGAAACGGAGCTGAATGAAGCCATACCA	1776
QY	4798	GAGAAATAGACACCAAGTAGCTCTTCTAAACCTTAACCGACCTACAGTGCAAAAAGT	4857	5878	AACGACAGCGTGACACACGATGCCCTGTAGCAATGCAACAAAGTTGCGCAAACTATTA	5937
Db	2855	GAGAAATAGACACCAAGTAGCTCTTCTAAACCTTAACCGACCTACAGTGCAAAAAGT	2796	1775	AACGACAGCGTGACACACGATGCCCTGTAGCAATGCAACAAAGTTGCGCAAACTATTA	1716
QY	4858	TATCAAGAGACTGCATTATAGAGCCACAAAGGAGAAAAGTAATCTAAGATGCTTTG	4917	5938	ACTGGCGAACTACTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGATGAGCGCGAT	5997
Db	2795	TATCAAGAGACTGCATTATAGAGCCACAAAGGAGAAAAGTAATCTAAGATGCTTTG	2736	1715	ACTGGCGAACTACTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGATGAGCGCGAT	1656
QY	4918	TTAGAAAATAGCGCTCTCGGATGCATTTTGTAGAAACAAAAGAGATAGATTCTT	4977	5998	AAAGTTCAGAGACCACTTCTCGCTCGGCCCTTCGGCTGCTGGTTTATGCTGATAAA	6057
Db	2735	TTAGAAAATAGCGCTCTCGGATGCATTTTGTAGAAACAAAAGAGATAGATTCTT	2676	1655	AAAGTTCAGAGACCACTTCTCGCTCGGCCCTTCGGCTGCTGGTTTATGCTGATAAA	1596
QY	4978	TGTTGGTAAATAGCGCTCTCGGTTGCAATTTCTGTTCTGTAAATGCAAGTTC	5037	6058	TCTGGAGCCGCTGAGCGTGGGTCTCGCGGTATCAATTCGACACTGGGGCCAGATGGTAAG	6117
Db	2675	TGTTGGTAAATAGCGCTCTCGGTTGCAATTTCTGTTCTGTAAATGCAAGTTC	2616	1595	TCTGGAGCCGCTGAGCGTGGGTCTCGCGGTATCAATTCGACACTGGGGCCAGATGGTAAG	1536
QY	5038	TTTGTGTTGAAAATAGCGCTCTCGGTTGCAATTTTGTGTTTACAAAATGCAAGCAGA	5097	6118	CCCTCCCGTATCGTAGTTATCTACACGACGGGAGTCAAGGCAACTATTCGATGAAACGAAT	6177
Db	2615	TTTGTGTTGAAAATAGCGCTCTCGGTTGCAATTTTGTGTTTACAAAATGCAAGCAGA	2556	1535	CCCTCCCGTATCGTAGTTATCTACACGACGGGAGTCAAGGCAACTATTCGATGAAACGAAT	1476
QY	5098	TTCTTCGTTGTAATAAGCGCTTCGCGTTGCAATTTCTGTTCTGTAAATAAGCGCTCA	5157	6178	AGACAGATCGCTGAGTAGGTGCTCTACTGATTAAGCAATTCGTTAACTCTCTCAGACCAAGTT	6237
Db	2555	TTCTTCGTTGTAATAAGCGCTTCGCGTTGCAATTTCTGTTCTGTAAATAAGCGCTCA	2496	1475	AGACAGATCGCTGAGTAGGTGCTCTACTGATTAAGCAATTCGTTAACTCTCTCAGACCAAGTT	1416
QY	5158	GATCTCTGTTGAAAATAGCGCTCTCGGTTGCAATTTTGTGTTTACAAAATGCAAGCA	5217	6238	TACTCATATATACCTTTAGATTGATTTAAACTTCATTTTAAATTTAAAGGATCTAGGTG	6297
Db	2495	GATCTCTGTTGAAAATAGCGCTCTCGGTTGCAATTTTGTGTTTACAAAATGCAAGCA	2436	1415	TACTCATATATACCTTTAGATTGATTTAAACTTCATTTTAAATTTAAAGGATCTAGGTG	1356
QY	5218	CAGATGCTTCGTTAGGTGCACTTTTCGGGGAATGTCGGGAAACCCCTATTTGTTTA	5277	6298	AAGATCCTTTTGTATAATCTCATGACCAAAATCCCTTAAACGTAGTTTTCGTTCCACTGA	6357
Db	2435	CAGATGCTTCGTTAGGTGCACTTTTCGGGGAATGTCGGGAAACCCCTATTTGTTTA	2376	1355	AAGATCCTTTTGTATAATCTCATGACCAAAATCCCTTAAACGTAGTTTTCGTTCCACTGA	1296
QY	5278	TTTTTCTAAATACATTTCAATATGATCCGCTCATGAGACAATAACCCCTGATAAATGCTT	5337	6358	GGGTACAGCCCGTGAAGAAAGATCAAGGATCTTCTTGAGATCTCTTTTCTGCGCGTA	6417
Db	2375	TTTTTCTAAATACATTTCAATATGATCCGCTCATGAGACAATAACCCCTGATAAATGCTT	2316	1295	GGGTACAGCCCGTGAAGAAAGATCAAGGATCTTCTTGAGATCTCTTTTCTGCGCGTA	1236
QY	5338	CAATAATATGAAAAGGAAGTAGATATCAACATTTCCGTTGCTCCCTTATTTCCC	5397	6418	ATCTGCTGCTTGCAAAACAAAACCCAGCGCTACAGCGGTGGTTTGTTCGGGATCAA	6477
Db	2315	CAATAATATGAAAAGGAAGTAGATATCAACATTTCCGTTGCTCCCTTATTTCCC	2256	1176	ATCTGCTGCTTGCAAAACAAAACCCAGCGCTACAGCGGTGGTTTGTTCGGGATCAA	1176
QY	5398	TTTTTGGCGCAATTTGCTTCTCTTTTGTCTACCCAGAAACGCTGGTGAAGTAAAA	5457	6478	GAGCTACCAACTCTTTTTCGGAAGTAACTGGCTTACGAGAGCGCAGATACCAATACT	6537
Db	2255	TTTTTGGCGCAATTTGCTTCTCTTTTGTCTACCCAGAAACGCTGGTGAAGTAAAA	2196	1175	GAGCTACCAACTCTTTTTCGGAAGTAACTGGCTTACGAGAGCGCAGATACCAATACT	1116
QY	5458	GATGCTGAAGATCAGTTGGGTGACAGTGGGTACATCGAATCGAATCTCAACAGCGGT	5517	6538	GTCTTCTAGTGTAGCGGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCTACA	6597
Db	2195	GATGCTGAAGATCAGTTGGGTGACAGTGGGTACATCGAATCGAATCTCAACAGCGGT	2136	1115	GTCTTCTAGTGTAGCGGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCTACA	1056
QY	5518	AAGATCCTTTAGAGTTTTCGCCCCGAAGACGTTTCCAAATGATGAGCACTTTTAAAGTT	5577	6598	TACTCTGCTCTGCTAAATCTGTTTACAGTGGCTGCTGCCAGTGGCGATAAGTCTGTCTT	6657
Db	2135	AAGATCCTTTAGAGTTTTCGCCCCGAAGACGTTTCCAAATGATGAGCACTTTTAAAGTT	2076	1055	TACTCTGCTCTGCTAAATCTGTTTACAGTGGCTGCTGCCAGTGGCGATAAGTCTGTCTT	996
QY	5578	CTGCTATGTCGCGGTATTTCCGTTATTTGACGCGGGGCAAGACACTCGGTGCGCG	5637	6658	ACCGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCCGGCTGAACGGGG	6717
Db	2075	CTGCTATGTCGCGGTATTTCCGTTATTTGACGCGGGGCAAGACACTCGGTGCGCG	2016	995	ACCGGTTGGACTCAAGACGATAGTTACCGGATAAGGCGCAGCGGTCCGGCTGAACGGGG	936
QY	5638	ATACACTATTTCTCAGAACTGCTTGGTTGAGTACTCACCGAGTCAAGAAAAGCATCTTACG	5697	6718	GGTTCTGTCACACAGCCAGCTTCGAGCGAAACGCTTACACCGAACTGAGATACCTACAG	6777
Db	2015	ATACACTATTTCTCAGAACTGCTTGGTTGAGTACTCACCGAGTCAAGAAAAGCATCTTACG	1956	935	GGTTCTGTCACACAGCCAGCTTCGAGCGAAACGCTTACACCGAACTGAGATACCTACAG	876
QY	5698	GATGCACTACAGTAAAGAAATATGCAAGTGTGCTGCCATAACATGAGTGATAACCTGCG	5757	6778	CGTGAGCTATGAGAAAGGCGCACCGCTTCCGAAAGGGAAGGCGGACAGGTATCCGGTA	6837
Db	1955	GATGCACTACAGTAAAGAAATATGCAAGTGTGCTGCCATAACATGAGTGATAACCTGCG	1896	875	CGTGAGCTATGAGAAAGGCGCACCGCTTCCGAAAGGGAAGGCGGACAGGTATCCGGTA	816
QY	5758	GCCAACTTCTCTGCAACGATCGGAGCGAAGAGAGCTTAAACGCTTTTTTTCACAAAC	5817	6838	AGCGCAGGGTTCGGAACAGGAGAGCGCACAGGAGGAGCTTCCAGGGGGGAAAACCCCTGGTAT	6897
Db	1895	GCCAACTTCTCTGCAACGATCGGAGCGAAGAGAGCTTAAACGCTTTTTTTCACAAAC	1836	815	AGCGCAGGGTTCGGAACAGGAGAGCGCACAGGAGGAGCTTCCAGGGGGGAAAACCCCTGGTAT	756
				6898	CTTTATAGTCTGTGCGGTTTTCGCCACCTCTGACTTGAGCGCTCGATTTTGTGTGCTCG	6957

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Db 755 CTTTATAGTCCTGTGGGTTTGCACCTCTGACTTGAGCGTGGATTTTGTGATCG 696
Qy 6958 TCAGGGGGGGGAGCCTATGGAAGAAACCGCAGCAAGCGCGCTTTTATCGGTTCTTGCGC 7017
Db 695 TCAGGGGGGGGAGCCTATGGAAGAAACCGCAGCAAGCGCGCTTTTATCGGTTCTTGCGC 636
Qy 7018 TTTTGTGCGCCTTTTGTCTCATGTTCTTCTTCTGCGTTATCCCTGATTTCTGGAATAAC 7077
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Qy 7078 CGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCGCAGCGAGCGACCGCGCAGC 7137
Db 575 CGTATTACCGCCTTTGAGTGAGCTGATACCGCTCGCGCAGCGAGCGAGCGAGCGCAGC 516
Qy 7138 GAGTCAGTGAGCGAGGAGCGAGCGCGCAATACGCAAAACCGCTCTCCCGCGCGT 7197
Db 515 GAGTCAGTGAGCGAGGAGCGAGCGCGCAATACGCAAAACCGCTCTCCCGCGCGT 456
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LOCUS
DEFINITION
Sequence 8 from Patent EP1197567.
ACCESSION
AX417671
VERSION
AX417671.1 GI:21522831
KEYWORDS
synthetic construct
synthetic construct
artificial sequences.
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Plaatnick, G., Platteau, C., Mortier, K. and Bogaert, T.
AUTHORS
Characterisation of gene function using double stranded rna
TITLE
inhibition
JOURNAL
Patent: EP 1197567-A 8 17-APR-2002;
Devgen NV (BE)
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Matches 5104; Conservative 0; Mismatches 629; Indels 114; Gaps 12;
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6778	CGTAGCTATGAGAAACGCCACGCTTCCGAAAGGAGAAAGCGGACAGGTATCCGGTA	6837
875	CGTAGCTATGAGAAAGCGCACGCTTCCGAAAGGAGAAAGCGGACAGGTATCCGGTA	816
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RESULT 6
BD223877/c
LOCUS BD223877 7209 bp DNA linear PAT 17-JUL-2003
DEFINITION Evaluation of gene function by using double-stranded RNA
inhibition.
ACCESSION BD223877
VERSION BD223877.1 GI:33033647
KEYWORDS JP 2002519072-A/8.
SOURCE synthetic construct
ORGANISM
artificial sequences.
REFERENCE 1 (bases 1 to 7209)
AUTHORS Platinck, G., Platinck, C., Mortier, K. and Bogaert, T.
TITLE Evaluation of gene function by using double-stranded RNA inhibition
JOURNAL Patent: JP 2002519072-A 8 02-JUL-2002;
DEVGEN NV
COMMENT OS Artificial Sequence
PN JP 2002519072-A/8
PD 02-JUL-2002
PE 02-JUL-1999 JP 2000558236
PR 03-JUL-1998 GB 9814536.0, 09-DEC-1998 GB 9827152.1 PI
BOGAERT PLAETINCK, CHRIST PLATTEUW, KATHERINE MORTIER, THIERRY PI
PC C12Q1/68, C12N1/15, C12N1/19, C12N1/21, C12N5/10, C12N5/09, C12N5/
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FEATURES
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Query Match 57.4%; Score 4492.6; DB 6; Length 7209;
Best Local Similarity 87.3%; Pred. No. 0;
Matches 5104; Conservative 0; Mismatches 629; Indels 114; Gaps 12;
Qy 1559 TCATGTAATAGTATGTCACGCTTACATTCACGCGCTCCCGCCACATCCGCTCAACCG 1618
Db 5982 TCATGTAATAGTATGTCACGCTTACATTCACGCGCTCCCGCCACATCCGCTCAACCG 5923
Qy 1619 AAAGGAGGAGTATGACAACTGAGTCTAGTCCCTATTTATTTTATAGTTATGT 1678
Db 5922 AAAGGAGGAGTATGACAACTGAGTCTAGTCCCTATTTATTTTATAGTTATGT 5863
Qy 1679 TAGTATTAAGACGTTATTTATTTATTTATTTATTTTCTCTCTGACAGCGCGT 1738
Db 5862 TAGTATTAAGACGTTATTTATTTATTTATTTATTTTCTCTCTGACAGCGCGT 5803
Qy 1739 AGCATGTAACTATTAATCTGAAACCTGCTTGAAGAGTTTGGGACGCTCGAAGGCTT 1798
```


Db 2615 |||||TTTGTGAAAATTTAGCGCTCTCGGTTGCAATTTTGTGTTTACAAAATGAAACACAGA 2556
QY 5098 TTTCTTGGTTGTAATAAGCGTTTCGGGTTGCAATTTCTGTTGTAATAAATGACGTCA 5157
Db 2555 TTTCTTGGTTGTAATAAGCGTTTCGGGTTGCAATTTCTGTTGTAATAAATGACGTCA 2496
QY 5158 GATTCCTTTGTAATAAATAGCGCTCTCGGTTGCAATTTTGTGTTACAAAATGAAAGCA 5217
Db 2495 GATTCCTTTGTAATAAATAGCGCTCTCGGTTGCAATTTTGTGTTACAAAATGAAAGCA 2436
QY 5218 CAGATGCTTTGTTAGGTGCGACTTTTCGGGGAATGTGCGGAACCCCTATTGTTTA 5277
Db 2435 CAGATGCTTTGTTAGGTGCGACTTTTCGGGGAATGTGCGGAACCCCTATTGTTTA 2376
QY 5278 TTTTCTTAATACATTCAAATATGTATCGGCTCATGAGACAATTAACCTGTATAATGCTT 5337
Db 2375 TTTTCTTAATACATTCAAATATGTATCGGCTCATGAGACAATTAACCTGTATAATGCTT 2316
QY 5338 CAATAATATTGAAAAGGAAGTATGATTTCAACATTTCCGTTGTCGCCCTTATTCCC 5397
Db 2315 CAATAATATTGAAAAGGAAGTATGATTTCAACATTTCCGTTGTCGCCCTTATTCCC 2256
QY 5398 TTTTGTGGCGCAATTTGCTTCTCTGTTTGTCTCACCAGAAACGCTGGTGAAAGTAAAA 5457
Db 2255 TTTTGTGGCGCAATTTGCTTCTCTGTTTGTCTCACCAGAAACGCTGGTGAAAGTAAAA 2196
QY 5458 GATGCTGAAGATCAGTTGGGTGACAGTGGGTTACATCGAACTGGATCTCAACAGCGGT 5517
Db 2195 GATGCTGAAGATCAGTTGGGTGACAGTGGGTTACATCGAACTGGATCTCAACAGCGGT 2136
QY 5518 AAGATCCTTTGAGATTTTCGCCCGGAAGACGTTTCCAAATGATGAGCACATTTTAAAGTT 5577
Db 2135 AAGATCCTTTGAGATTTTCGCCCGGAAGACGTTTCCAAATGATGAGCACATTTTAAAGTT 2076
QY 5578 CTGCTATGTGGCGCGGTATTATCCGTTATGACGCGGGGAAGAGCAACTCGGTCGCCGC 5637
Db 2075 CTGCTATGTGGCGCGGTATTATCCGTTATGACGCGGGGAAGAGCAACTCGGTCGCCGC 2016
QY 5638 ATACACTATTCTCAGATGAATGTTGGTTGAGTACTACACAGTCAACAGAAAGCATCTTACG 5697
Db 2015 ATACACTATTCTCAGATGAATGTTGGTTGAGTACTACACAGTCAACAGAAAGCATCTTACG 1956
QY 5698 GATGCGATGACAGTAAAGAAATATGACGTGCTGCTCAATACCATGAGTAAACACTGCG 5757
Db 1955 GATGCGATGACAGTAAAGAAATATGACGTGCTGCTCAATACCATGAGTAAACACTGCG 1896
QY 5758 GCCAACTTACTTCTGACAAACGATCGGAGGACCGAAGGAGCTTAACCGCTTTTTCACAAC 5817
Db 1895 GCCAACTTACTTCTGACAAACGATCGGAGGACCGAAGGAGCTTAACCGCTTTTTCACAAC 1836
QY 5818 ATGGGGATCATGTAATCTGCGCTTATGATCGTTGGGACCGGAGCTGAATGAAGCATACCA 5877
Db 1835 ATGGGGATCATGTAATCTGCGCTTATGATCGTTGGGACCGGAGCTGAATGAAGCATACCA 1776
QY 5878 AACGACGAGCGTGACACACAGATGCTGTAGCAATGGCAACAACTGTCGCAAACTATTA 5937
Db 1775 AACGACGAGCGTGACACACAGATGCTGTAGCAATGGCAACAACTGTCGCAAACTATTA 1716
QY 5938 ACTGCGAACTACTTACTTCTAGCTTTCCGCGCAACAAATTAATAGACTGGATGAGGCGGAT 5997
Db 1715 ACTGCGAACTACTTACTTCTAGCTTTCCGCGCAACAAATTAATAGACTGGATGAGGCGGAT 1656
QY 5998 AAAGTTGACGAGCACTTCTGCGCTCGGCCCTTCGGCTGCTGGTTTATGCTGATAAA 6057
Db 1655 AAAGTTGACGAGCACTTCTGCGCTCGGCCCTTCGGCTGCTGGTTTATGCTGATAAA 1596
QY 6058 TCTGAGCGCGTGACGCTGGGTCTCGCGGTATCATTTGACGACACTGGGCGCAGATGGTAAG 6117
Db 1595 TCTGAGCGCGTGACGCTGGGTCTCGCGGTATCATTTGACGACACTGGGCGCAGATGGTAAG 1536
QY 6118 CCTCCCGCTATCGTATGTTATCTTACACGACGCGGAGTCAAGCAACTATGATGAACGAAAT 6177

Db 1535 CCTCCCGTATCGTAGTTATCTTACACGACGGGAGTCAAGCAACTATGATGATGAACGAAAT 1476
QY 6178 AGACAGATCCTGATAGTAGGTGCTCACTGATTAAGCATTTGGTAACCTCTCAACCAAGTT 6237
Db 1475 AGACAGATCCTGATAGTAGGTGCTCACTGATTAAGCATTTGGTAACCTCTCAACCAAGTT 1416
QY 6238 TACTCATATATACCTTTAGATTGATTTAAACCTTCAATTTTAAATTTAAAGGATCTAGGTG 6297
Db 1415 TACTCATATATACCTTTAGATTGATTTAAACCTTCAATTTTAAATTTAAAGGATCTAGGTG 1356
QY 6298 AAGATCCTTTTGTATATCTCATGACCAAAATCCCTTAAACCTGAGTTTTGTCCTACATGA 6357
Db 1355 AAGATCCTTTTGTATATCTCATGACCAAAATCCCTTAAACCTGAGTTTTGTCCTACATGA 1296
QY 6358 GCGTCAGACCCCGTAGAAAAGATCAAGAGTCTCTTCTGAGATCCTTTTCTGCGCGTA 6417
Db 1295 GCGTCAGACCCCGTAGAAAAGATCAAGAGTCTCTTCTGAGATCCTTTTCTGCGCGTA 1236
QY 6418 ATCTGCTGCTTGCAAAACAAAAACCAACCGCTACACGCGTGGTGGTTTGTTCGCGGATCAA 6477
Db 1235 ATCTGCTGCTTGCAAAACAAAAACCAACCGCTACACGCGTGGTGGTTTGTTCGCGGATCAA 1176
QY 6478 GAGCTACAACTCTTTTTCGAAAGGTAACTGGCTTTCAGCAGAGCGCAGATACCAATACT 6537
Db 1175 GAGCTACAACTCTTTTTCGAAAGGTAACTGGCTTTCAGCAGAGCGCAGATACCAATACT 1116
QY 6538 GTCCCTTCTAGTGTAGCCGTAGTAGGCGCACCACTTCAAGAACTCTGTAGCACCGCTACA 6597
Db 1115 GTCCCTTCTAGTGTAGCCGTAGTAGGCGCACCACTTCAAGAACTCTGTAGCACCGCTACA 1056
QY 6598 TACCTCCTCTGCTTAATCTCTTACCAAGTGGCTGCTGCAAGTGGCGATAAGTCTGTCTT 6657
Db 1055 TACCTCCTCTGCTTAATCTCTTACCAAGTGGCTGCTGCAAGTGGCGATAAGTCTGTCTT 996
QY 6658 ACCGGTGTGATCAACAGCATAGTTACCGGATTAAGCGCAGCGGTGCGGTGAACGGGG 6717
Db 995 ACCGGTGTGATCAACAGCATAGTTACCGGATTAAGCGCAGCGGTGCGGTGAACGGGG 936
QY 6718 GGTTCGTGACACAGCCAGCTTGAGGCGACGACTACACCGAATCAGATACCTACAG 6777
Db 935 GGTTCGTGACACAGCCAGCTTGAGGCGAAGACGACTACACCGAATCAGATACCTACAG 876
QY 6778 CGTGAGCTATGAGAAAGCGCCACCTTCCGAAAGGAGAAAGGCGGACAGGTATCCGGTA 6837
Db 875 CGTGAGCTATGAGAAAGCGCCACCTTCCGAAAGGAGAAAGGCGGACAGGTATCCGGTA 816
QY 6838 AGCGGAGGTGCGAAACAGGAGCGCAGAGGAGCTTCCAGGGGGGAAAACGCTTGGTAT 6897
Db 815 AGCGGAGGTGCGAAACAGGAGCGCAGAGGAGCTTCCAGGGGGGAAAACGCTTGGTAT 756
QY 6898 CTTTATAGTCTGTCGGGTTTCGCCACTCTGACTTGAGCGCTCGAATTTTGTGATGCTCG 6957
Db 755 CTTTATAGTCTGTCGGGTTTCGCCACTCTGACTTGAGCGCTCGAATTTTGTGATGCTCG 696
QY 6958 TCAGGGGGGCGGAGCCTATGGAATAACCGCAAGAACCGGCTTTTTCAGGTTCTCGGCC 7017
Db 695 TCAGGGGGGCGGAGCCTATGGAATAACCGCAAGAACCGGCTTTTTCAGGTTCTCGGCC 636
QY 7018 TTTTGTGCGGCTTTTGTCTACATGTTCTTCTCGGTTATCCCTGATTTCTGTGATTAAC 7077
Db 635 TTTTGTGCGGCTTTTGTCTACATGTTCTTCTCGGTTATCCCTGATTTCTGTGATTAAC 576
QY 7078 CGTATTAACCGCTTTTGTGATGAGTACCGCTCGCGCAGCGCAACGACAGCGGCGACG 7137
Db 575 CGTATTAACCGCTTTTGTGATGAGTACCGCTCGCGCAGCGCAACGACAGCGGCGACG 516
QY 7138 GAGTCACTGAGCGAGGAAAGCGGAGAGCGCCCAATAGCAAAACCGCTCTCCCGCGGT 7197
Db 515 GAGTCACTGAGCGAGGAAAGCGGAGAGCGCCCAATAGCAAAACCGCTCTCCCGCGGT 456
QY 7198 TGCGCGATTTATTAATCGAGTGGCAGACGAGTTTCCGATCTGGAAGCGGCGATGAG 7257
Db 455 TGCGCGATTTATTAATCGAGTGGCAGACGAGTTTCCGATCTGGAAGCGGCGATGAG 396

QY 3119 AGCAAAATTTCTGCTCTCGAAGAGTAAAAAATGTGCTTGGCGATATGCTTTAGCGG 3178
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 3179 CTTAACTGTGCCCTCCATGGAATAATCAAGTCAAGATATCCATGCTGTTTTAGTAAACA 3238
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 3239 AATTTTGGGACCTAATGCTTCAACTAACTCCAGTAAATTTCTTGGTGGTAC--GAACATCCA 3297
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 3298 ATGAAGACACACAAGTTTGTGCTTTTCTGTCATGATATAAATAGCTTGGCAGCAACAG 3357
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 3358 GACTAGGATGAGTACAGCAGCTTCTTATATGATAGCTTTTCGACATGATTTTATCTTGCT 3417
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 3418 TCGTCAAGGTTTTGTTCTGTCAGTGTGGTTAAGAACTACTGGGCAATTTTCACTGTTCTT 3477
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 4183 TTTTCGACCGAATTAATTTCTTAATCGGCAAAAAAAGAAAGCTCCGGA-----T 4136
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 3478 CAACACTACATATGCTATATATACCAATCTAAGTCTGTGCTCTCTTCTGTTCTTCTCT 3537
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 4135 CAAGATTTGTAAGTGAAGTGAAGTCTATTTTCAATAAAGAAATATCTTCCACTACTGCCA 4076
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 3538 TCTGTTCGGAGATTAACCGAATCAAAAAATTTTCAAGAAACCGAAATCAAAAAAAGAAAT 3597
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 4075 TCTGGCGTCATAACTGCAAGTACACATATATTA-----CGATGCTGTCTTAAAT 4024
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 3598 AAAAAAATGATGATTAAGTGAATGAAAGCTGTGGTATGTCATCTCTCAGTACATCT 3657
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 4023 GCTTCTATTTATATATATAGTAATGTGCTGTTGATCTATGTGTCATCTCTCAGTACATCT 3964
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 3658 GCTCTGATGCCCATAGTTAAGCCAGCCGACACCCGCCCAACACCCGCTCAGCGGCCCT 3717
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 3963 GCTCTGATGCCCATAGTTAAGCCAGCCGACACCCGCCCAACACCCGCTCAGCGGCCCT 3904
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 3718 GACGGGCTGTCTGCTCCGGCATCCGCTTACAGAAAGCTGTGACCGTCTCCGGGAGCT 3777
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 3903 GACGGGCTGTCTGCTCCGGCATCCGCTTACAGAAAGCTGTGACCGTCTCCGGGAGCT 3844
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 3778 GCATGTGTCAGAGGTTTTACCGCTCATCCGNAAGCCGCGAGACGAAAGGCTCTCGTGA 3837
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 3843 GCATGTGTCAGAGGTTTTACCGCTCATCCGNAAGCCGCGAGACGAAAGGCTCTCGTGA 3784
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 3838 TACGCTATTTTATAGGTTAATGTTCATGATAATATGTTTCTTAGTATGATCCAAATAT 3897
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 3783 TACGCTATTTTATAGGTTAATGTTCATGATAATATGTTTCTTAATATGATCCAAATAT 3724
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 3898 CAAAGGAATGATAGCATTTGAAGTATGATCTAATCCAAATGAGGAGTGGCAGCATATAG 3957
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 3723 CAAAGGAATGATAGCATTTGAAGTATGATCTAATCCAAATGAGGAGTGGCAGCATATAG 3664
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 3958 AACAGCTAAAGGTTAGTCTGAAGGAGCATACGATACCCCGCATGGAAATGGATATATAT 4017
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 3663 AACAGCTAAAGGTTAGTCTGAAGGAGCATACGATACCCCGCATGGAAATGGATATATAT 3604
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 4018 CACAGGAGTACTAGACTTACCTTTTCTCATATAATAGACGATATATAGTACGATTT 4077
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 3603 CACAGGAGTACTAGACTTACCTTTTCTCATATAATAGACGATATATAGTACGATTT 3544
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 4078 AAGCATAAACACGCACTAGTCCGTTCTTCTCATGATATATATATACAGGCAACACGAG 4137
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 3543 AAGCATAAACACGCACTAGTCCGTTCTTCTCATGATATATATATACAGGCAACACGAG 3484
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 4138 ATATAGTGCAGGCTGACAGTGTATGTGCGGAGCTCGGTTGCAATTTTCGGAAG 4197
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 3483 ATATAGTGCAGGCTGACAGTGTATGTGCGGAGCTCGGTTGCAATTTTCGGAAG 3424
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411

QY 4198 CGCTCGTTTTCGGAAACGCTTTGAAGTTCTTATTCGAAAGTTCTTATCTCTAGAAAGTA 4257
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 3423 CGCTCGTTTTCGGAAACGCTTTGAAGTTCTTATTCGAAAGTTCTTATCTCTAGAAAGTA 3364
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 4258 TAGGAACCTTCAGAGCGCTTTTGAAGAACCAAAAGCGCTCTGAAGAGCGACTTTCAAAAAC 4317
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 3363 TAGGAACCTTCAGAGCGCTTTTGAAGAACCAAAAGCGCTCTGAAGAGCGACTTTCAAAAAC 3304
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 4318 CAAAAACGCGACCGGACCTGTAAACGAGCTACTAAAAATATTGCGAAATACCGCTTCCACAAACA 4377
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 3303 CAAAAACGCGACCGGACCTGTAAACGAGCTACTAAAAATATTGCGAAATACCGCTTCCACAAACA 3244
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QY 4378 TTGCTCAAAAGTATCTCTTTGCTATATATCTCTGCTGCTATATCCCTATATACCTACCCA 4437
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 3243 TTGCTCAAAAGTATCTCTTTGCTATATATCTCTGCTGCTATATCCCTATATACCTACCCA 3184
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 4438 TCGACCTTTTGGCTCCTTGAACCTTGCAATCTAACTCGACCTCTACATTTTTTTATGTTTATC 4497
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 3183 TCCACCTTTTGGCTCCTTGAACCTTGCAATCTAACTCGACCTCTACATTTTTTTATGTTTATC 3124
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 4498 TCTAGTATTTACTCTTTAGACAAAAAATTTGTAGTAAGAACTATTTCATAGAGTGAATCGAA 4557
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 3123 TCTAGTATTTACTCTTTAGACAAAAAATTTGTAGTAAGAACTATTTCATAGAGTGAATCGAA 3064
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 4558 AACAAATACGAAATTTGTAACATTTTCTATACGTATATATAGAGACAAATAGAGAAAC 4617
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 3063 AACAAATACGAAATTTGTAACATTTTCTATACGTATATATAGAGACAAATAGAGAAAC 3004
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 4618 CGTTTCAATAATTTTCTGACCAATGAAGATCATCAACGCTATCACHTTCTGTTTCAAAAGT 4677
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 3003 CGTTTCAATAATTTTCTGACCAATGAAGATCATCAACGCTATCACHTTCTGTTTCAAAAGT 2944
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 4678 ATGCGCAATCCACATCGTATAGAAATATAATCGGGATGCTTTTATCTTGAATAAATGCA 4737
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QY 4738 CCCGAGCTTTCGCTAGTAATCAGTAAACGCGGGAAGTGGAGTCAGGCTTTTTTATGGA 4797
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 2883 CCCGAGCTTTCGCTAGTAATCAGTAAACGCGGGAAGTGGAGTCAGGCTTTTTTATGGA 2824
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 4798 GAGAAATAGACACCAAGTAGCTTCTTTCTAACTTAAACGCACTACAGTCGCAAAAGT 4857
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 2823 GAGAAATAGACACCAAGTAGCTTCTTTCTAACTTAAACGCACTACAGTCGCAAAAGT 2764
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QY 2763 TATCAAGAGACTGCTATATAGAGCGCAAAAGGAGAAAAAGTAACTCTAAGATGCTTTG 2704
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QY 4918 TTAGAAAAATAGCGCTCTCGGATGCAATTTTGTAGAACAAAAAGAGATAGATTCTT 4977
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 2703 TTAGAAAAATAGCGCTCTCGGATGCAATTTTGTAGAACAAAAAGAGATAGATTCTT 2644
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 4978 TGTGTTAAATAGCGCTCTCGGATGCAATTTTGTGTTCTGTAAATAATGAGCTCAGATTTC 5037
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 2643 TGTGTTAAATAGCGCTCTCGGATGCAATTTTGTGTTCTGTAAATAATGAGCTCAGATTTC 2584
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 5038 TTTGTTGAAAAATTAGCGCTCTCGGATGCAATTTTGTGTTCTGTAAATAATGAGCTCAGATTTC 5097
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 2583 TTTGTTGAAAAATTAGCGCTCTCGGATGCAATTTTGTGTTCTGTAAATAATGAGCTCAGATTTC 2524
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 5098 TTTGTTGAAAAATTAGCGCTCTCGGATGCAATTTTGTGTTCTGTAAATAATGAGCTCAGATTTC 5157
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 2523 TTTGTTGAAAAATTAGCGCTCTCGGATGCAATTTTGTGTTCTGTAAATAATGAGCTCAGATTTC 2464
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 5158 GATTCTTTGTTTGAATAATAGCGCTCTCGGATGCAATTTTGTGTTCTGTAAATAATGAGCTCAGATTTC 5217
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 2463 GATTCTTTGTTTGAATAATAGCGCTCTCGGATGCAATTTTGTGTTCTGTAAATAATGAGCTCAGATTTC 2404
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 5218 CAGATGCTTCTGTTTCAAGTGGCACTTTTTCGCGGAAATGTGCGGAAACCCCTATTTTGTGTTT 5277
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 2403 CAGATGCTTCTGTTTCAAGTGGCACTTTTTCGCGGAAATGTGCGGAAACCCCTATTTTGTGTTT 2344
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411
QY 5278 TTTTCTTAAATACATTTCAAAATATGATATCCGCTCATGAGACAAATAACCCCTGATAAATGCTTT 5337
Db |||||-----CTTTTACAGACTTGAAATTTCTTGCNATAACCGGGTCAATGT 4411

Db	2343	CTAATAATGATCCGCTCATGAGCAATAACCCCTGATAAATGCTT	2284
Qy	5338	CAATAATAATTGAAAAAGGAGATAGATGATTAACAACATTTCCGTGTCGCCCTTATTCCC	5397
Db	2283	CAATAATAATTGAAAAAGGAGAGATAGATTAACAACATTTCCGTGTCGCCCTTATTCCC	2224
Qy	5398	TTTTTTGGCGCATTTTGGCCCTTCCTGTTTTGTTGCTCACCCAGAAACGCTGTTGAAAGTAAAA	5457
Db	2223	TTTTTTGGCGCATTTTGGCCCTTCCTGTTTTGTTGCTCACCCAGAAACGCTGTTGAAAGTAAAA	2164
Qy	5458	GATGCTGAAGATCAGTTGGGTGGACAGTGGGTTTACATCGAAGTGCATCTCAACAGGGT	5517
Db	2163	GATGCTGAAGATCAGTTGGGTGGACAGTGGGTTTACATCGAAGTGCATCTCAACAGGGT	2104
Qy	5518	AAGATCCTTTGAGAGTTTTCCGCCCGGAAGAACGTTTTCCAAATGATGAGCACTTTTAAAGTT	5577
Db	2103	AAGATCCTTTGAGAGTTTTCCGCCCGGAAGAACGTTTTCCAAATGATGAGCACTTTTAAAGTT	2044
Qy	5578	CTGCTATGTGGCGGGTATTAATCCCGTAATGACCGCGGGCAAGAGCAACTTCGGTCCCGC	5637
Db	2043	CTGCTATGTGGCGGGTATTAATCCCGTAATGACCGCGGGCAAGAGCAACTTCGGTCCCGC	1984
Qy	5638	ATACACTATTCTCAGATGACTTGGTTGAGTACTACCACTGATCAAGAAAGCATCTTACG	5697
Db	1983	ATACACTATTCTCAGATGACTTGGTTGAGTACTACCACTGATCAAGAAAGCATCTTACG	1924
Qy	5698	GATGGCATGACAGTAAGAGAAATTAATCAGTGTGCCATTAACCATGATGATTAACACTGCG	5757
Db	1923	GATGGCATGACAGTAAGAGAAATTAATCAGTGTGCCATTAACCATGATGATTAACACTGCG	1864
Qy	5758	GCCAACTTACTCTGCAACAGATCGAGGACCGAAGAGCTAACCCGTTTTTGTGCACAAC	5817
Db	1863	GCCAACTTACTCTGCAACAGATCGAGGACCGAAGAGCTAACCCGTTTTTGTGCACAAC	1804
Qy	5818	ATGGGGATCATGTAATCTGCTTGTATCGTTGGGACCGGAGCTGAATGAGCCATACCA	5877
Db	1803	ATGGGGATCATGTAATCTGCTTGTATCGTTGGGACCGGAGCTGAATGAGCCATACCA	1744
Qy	5878	AACGACGAGCGTGACACCAAGATGCTGTAGCAATGGCAACACGTTGGCCAACTATTA	5937
Db	1743	AACGACGAGCGTGACACCAAGATGCTGTAGCAATGGCAACACGTTGGCCAACTATTA	1684
Qy	5938	ACTGGCGAACTACTACTAGCTTCCCGGCAACAAATTAATAGATGGATGGAGCGGAT	5997
Db	1683	ACTGGCGAACTACTACTAGCTTCCCGGCAACAAATTAATAGATGGATGGAGCGGAT	1624
Qy	5998	AAAGTTGCAGGACCACTTCTGGCTCGGCCCTTCCGGCTGGTGTATTGCTGATAAA	6057
Db	1623	AAAGTTGCAGGACCACTTCTGGCTCGGCCCTTCCGGCTGGTGTATTGCTGATAAA	1564
Qy	6058	TCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTTGCAGCACTGGGGCCAGATGGTAAG	6117
Db	1563	TCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTTGCAGCACTGGGGCCAGATGGTAAG	1504
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DEFINITION	Sequence 6 from Patent WO0112796.				
ACCESSION	AX084714				
VERSION	AX084714.1	GI:13274968			
KEYWORDS	synthetic construct				
SOURCE	synthetic construct				
ORGANISM	artificial sequences.				
REFERENCE	1.				
AUTHORS	Kaletha, T., Vangeel, A., Bogaert, T. and van de Craen, M.				
TITLE	Pkd constructs and screening methods				
JOURNAL	Patent: WO 0112796-A 6 22-FEB-2001;				
	Devgen NV (BE)				
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misc_feature	8394..8941				
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ORIGIN					
	Query Match 57.4%; Score 4492.6; DB 6; Length 8941;				
	Best Local Similarity 87.3%; Pred. No. 0;				
	Matches 5104; Conservative 0; Mismatches 629; Indels 114; Gaps 12;				
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RESULT 9
AX054976/c

LOCUS AX054976 9700 bp DNA linear PAT 13-JAN-2001
DEFINITION Sequence 91 from Patent WO0073328.
ACCESSION AX054976
VERSION AX054976.1 GI:12228344

KEYWORDS
SOURCE synthetic construct
ORGANISM synthetic construct
artificial sequences.

REFERENCE

AUTHORS van Crielinge, W., Roelens, I., Bogaert, T. and Verwaerde, P.
TITLE Unc-5 constructs and screening methods
JOURNAL Patent: WO 0073328-A 91 07-DEC-2000;
Devgen NV (BE)

FEATURES

source location/Qualifiers
1. .9700
/organism="synthetic construct"

ORIGIN	Query Match		Best Local Similarity		Matches 5104; Conservative		57.4%; Score 4492.6; DB 6; Length 9700;		/db xref="taxon:32630"		/note="plasmid pGC1037"	
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Db	7263	TCATGTAATAGTATGTCACGCTTACATTCACGCGCTCCGCCACATCCCGCTCTAACCG	7204	7263	TCATGTAATAGTATGTCACGCTTACATTCACGCGCTCCGCCACATCCCGCTCTAACCG	7204	7263	TCATGTAATAGTATGTCACGCTTACATTCACGCGCTCCGCCACATCCCGCTCTAACCG	7204	7263	TCATGTAATAGTATGTCACGCTTACATTCACGCGCTCCGCCACATCCCGCTCTAACCG	7204
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VERSION AX054977.1 GI:12228345
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SOURCE synthetic construct
ORGANISM artificial sequences.
REFERENCE 1
AUTHORS van Criekeinge,W., Roelens,I., Bogaert,T. and Verwaerde,P.
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Devgen NV (BE)
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AUTHORS Bogaert, T., Stringham, E. and Vandekerckhove, J.
TITLE PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR USE IN THE CONTROL OF CELL BEHAVIOUR
JOURNAL Patent: WO 9638555-A 28 05-DEC-1996;
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FEATURES Other publication AU 6123496 961218.
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Query Match 57.4%; Score 4492.6; DB 6; Length 10288;
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ACCESSION AR432922
VERSION AR432922.1 GI:40195525
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 10288)
AUTHORS Peng, J., Hirayama, L. and Lochetto, C.
TITLE Use of the maize X112 mutant has 2 gene and imidazolinone herbicides for selection of transgenic monocots, maize, rice and wheat plants resistant to the imidazolinone herbicides
JOURNAL Patent: US 6653529-A 28 25-NOV-2003;
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RESULT 13

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Sequence 27 from Patent WO9638555.

A58523

A58523.1 GI:3714139

unidentified

unidentified

unclassified.

REFERENCE

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AUTHORS

TITLE

PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH CONTROL CELL
BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND PHARMACEUTICAL COMPOSITIONS
CONTAINING THEM AND THEIR USE IN THE CONTROL OF CELL BEHAVIOUR
Patent: WO 9638555-A 27 05-DEC-1996;

JOURNAL

BOGAERT THIERRY (BE)
Other publication AU 6123496 961218.
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1. 13414
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ORIGIN

Query Match 57.4%; Score 4492.6; DB 6; Length 13414;
Best Local Similarity 87.3%; Pred. No. 0;
Matches 5104; Conservative 0; Mismatches 629; Indels 114; Gaps 12;
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LOCUS Sequence 27 from patent US 6653529.
DEFINITION AR432921
ACCESSION AR432921
VERSION AR432921.1 GI:40195524
KEYWORDS
SOURCE Unknown.
ORGANISM Unclassified.
REFERENCE 1 (bases 1 to 13414)
AUTHORS Peng,J., Hirayama,L., and Lochetto,C.
TITLE Use of the maize Xli2 mutant ahas 2 gene and imidazolinone herbicides for selection of transgenic monocots, maize, rice and wheat plants resistant to the imidazolinone herbicides
JOURNAL Patent: US 6653529-A 27 25-NOV-2003;
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Best Local Similarity 87.3%; Pred. No. 0;
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QY 7318 CTTCCGGCTCCTATCTGTGTGGAATGTCAGCGGATCAACAATTTCAACAGGAAACAGC 7377
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Db 5297 TATGACCATGATTACGCCAAGCTTGCA 5271

RESULT 15
LOCUS PRS426/c
DEFINITION Yeast episomal vector pRS426 with URA3 marker, complete sequence.
ACCESSION U03451
VERSION U03451.1 GI:416322
KEYWORDS Cloning vector pRS426
SOURCE Cloning vector pRS426
ORGANISM artificial sequences; vectors.
REFERENCE 1 (bases 1 to 5726)
AUTHORS Sikorski, R.S. and Hieter, P.
TITLE A system of shuttle vectors and yeast host strains designed for
efficient manipulation of DNA in Saccharomyces cerevisiae
JOURNAL Genetics 122 (1), 19-27 (1989)
MEDLINE 89276910
PUBMED 2659436
REFERENCE 2 (bases 1 to 5726)
AUTHORS Christianson, T.W., Sikorski, R.S., Dante, M., Shero, J.H. and
Hieter, P.
TITLE Multifunctional yeast high-copy-number shuttle vectors
JOURNAL Gene 110 (1), 119-122 (1992)
MEDLINE 92184105
PUBMED 1544568
REFERENCE 3 (bases 1 to 5726)
AUTHORS Stillman, D.J.
TITLE Direct Submission
JOURNAL Submitted (11-NOV-1993) David J. Stillman, Dept. of Cellular, Viral
and Molecular Biology, University of Utah Medical Center, Salt Lake
City, UT 84132 USA
FEATURES
source
1. .5726
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/mol_type="genomic DNA"
/db_xref="taxon:31845"
ORIGIN
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Best Local Similarity 100.0%; Pred. No. 0;
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QY 3880 CTTAGTATGATCCATATCAAGGAATCATAGCAATTCAGAGTCAGACTAATCCAAATG 3939
Db 5666 CTTAGTATGATCCATATCAAGGAATCATAGCAATTCAGAGTCAGACTAATCCAAATG 5607
QY 3940 AGGAGTGGCAGCATATAGAACAGCTAAAGGGTAGTGTGCTGAAGGAGCATACGCCCG 3999
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Qy	7300		CAGCCTTTACACTTTATGCTTCGGCTCCCTATGTTGTGCGAATTGTGAGCGGATTAACAA	7359
Db	2246		CAGCCTTTACACTTTATGCTTCGGCTCCCTATGTTGTGCGAATTGTGAGCGGATTAACAA	2187
Qy	7360		TTTTCACACAGGAACAGCTATGACCATGATTACGCCAAGCGCGCAATTTAACCCCTCACTAA	7419
Db	2186		TTTTCACACAGGAACAGCTATGACCATGATTACGCCAAGCGCGCAATTTAACCCCTCACTAA	2127
Qy	7420		AGGGAACAAAGCTGGAGCTC	7440
Db	2126		AGGGAACAAAGCTGGAGCTC	2106

Search completed: May 16, 2004, 08:37:31
Job time : 19630.2 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 15, 2004, 22:27:02 ; Search time 1826.33 Seconds
(without alignments)
18208.601 Million cell updates/sec

Title: US-10-067-449-9
Perfect score: 7828
Sequence: 1 atgcgcgcgggtcccaaca.....tttttaatttaatacaaaaa 7828

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 3373863 seqs, 2124099041 residues

Total number of hits satisfying chosen parameters: 6747726

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : N_Geneseq_29Jan04:*

- 1: Geneseqn1980s:*
- 2: Geneseqn1990s:*
- 3: Geneseqn2000s:*
- 4: Geneseqn2001as:*
- 5: Geneseqn2001bs:*
- 6: Geneseqn2002s:*
- 7: Geneseqn2003as:*
- 8: Geneseqn2003bs:*
- 9: Geneseqn2003cs:*
- 10: Geneseqn2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match %	Length	DB ID	Description
1	7828	100.0	7828	6	AAL49310 Human Glu
2	6975.2	89.1	7777	6	AAL49312 Human Glu
3	5908	75.5	6360	6	AAL49316 Human HXT
C 4	4492.6	57.4	8749	4	AAC87129 Nucleotid
C 5	4492.6	57.4	8941	4	AAC87131 Nucleotid
C 6	4492.6	57.4	9700	4	AAC87131 Nucleotid
C 7	4492.6	57.4	9749	4	AAC87131 Nucleotid
C 8	4492.6	57.4	10288	2	AAT71322 Plasmid p
C 9	4492.6	57.4	13414	2	AAT71321 Plasmid p
C 10	4469.6	57.1	7210	3	AAX49989 Yeast two
11	3623	46.3	9952	7	ABV77349 Yeast exp
12	3610.2	46.1	7622	5	AAX21455 Human ROM
13	3364	43.0	6671	9	ADC75054 T-cell re
14	3057.4	39.1	5181	2	AAX85877 Nucleotid
15	3045.4	38.9	7063	2	AAX85878 Nucleotid
C 16	2273	29.0	6831	8	ACF57106 pX16 GPD-
C 17	2207.2	28.2	3003	6	AAD46219 pFLC-II v
C 18	2207.2	28.2	7432	2	AAV61459 Vector pp
C 19	2207.2	28.2	20623	3	AAC68294 Lama2/APP
C 20	2206.2	28.2	5534	2	AAT43137 pMIGIT s
21	2205.4	28.2	9072	2	AAX07558 Synthetic
22	2204.6	28.2	6287	6	AAX98923 Human pMS
23	2204.6	28.2	6347	6	AAX98930 Human pMS

ALIGNMENTS

RESULT 1

AAAL49310					
ID	AAAL49310	standard; DNA; 7828 BP.			
XX	AC	AAAL49310;			
XX	XX				
DT	07-NOV-2002	(first entry)			
XX	XX				
DE	Human Glut4	containing vector YEp4H7-HsGLUT4.			
XX	XX				
KW	Human; yeast;	GLUT4; glut transporter; hexose; antidiabetic; anorectic;			
KW	vector; ds.				
XX	OS	Homo sapiens.			
XX	XX				
FN	WO200264784-A2.				
XX	XX				
PD	22-AUG-2002.				
XX	XX				
PF	09-FEB-2002;	2002NO-EP001373.			
XX	XX				
PR	14-FEB-2001;	2001DE-01006718.			
XX	XX				
PA	(AVET)	AVENTIS PHARMA DEUT GMBH.			
PI	Mueller G,	Koller K, Boles E, Wleczorke R, Dlugai S;			
XX	XX				
DR	WPI;	2002-636632/68.			
XX	XX				
PT	New strains of yeast,	useful in screening for modulators of hexose			
PT	transport,	potential antidiabetic and antiobesity agents, lack native			
PT	hexose-transport	function.			
XX	XX				
PS	Claim 10;	Page 34-36; 58pp; German.			
XX	XX				
CC	The present invention	relates to a strain of Saccharomyces cerevisiae			
CC	carbon that cannot	grow on a substrate containing hexose as the only source of			
CC	carbon but the ability	to grow on such substrates is restored when the			
CC	GLUT4 gene is expressed.	A strain transformed to express the GLUT1 or			
CC	GLUT4 genes can be used	to identify compounds that increase/reduce hexose			
CC	transport by these	proteins. These compounds, optionally after			
CC	development, are	potential drugs for treating diabetes and obesity. The			
CC	present sequence is	a vector containing the human Glut4 coding sequence			
CC	as used in the	invention			
XX	XX				
SQ	Sequence	7828 BP; 2009 A; 1928 C; 1771 G; 2120 T; 0 U; 0 Other;			

Query Match				100.0%; Score 7828; DB 6; Length 7828;			
Best Local Similarity				100.0%; Pred. No. 0;			
Matches 7828; Conservative				0; Mismatches 0; Indels 0; Gaps 0;			
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Db	1	ATGCCGTGGGCTTCCAAACAGATAGGCTCCGAAGATGGGAAACCCCTCAGCAGCGAGTG	60				
Qy	61	ACTGGGACCCCTGCTTGGCTGTGTCTCTGGGTGCTTGGCTCCCTGCGAGTTGGGTAC	120				
Db	61	ACTGGGACCCCTGCTTGGCTGTGTCTCTGGGTGCTTGGCTCCCTGCGAGTTGGGTAC	120				
Qy	121	AACATTGGGGTCATCAATGCCCCCTCAGAAGGTGATGAACAGAGCTACAATGAGACGTGG	180				
Db	121	AACATTGGGGTCATCAATGCCCCCTCAGAAGGTGATGAACAGAGCTACAATGAGACGTGG	180				
Qy	181	CTGGGAGGCGAGGCGCTTGAGGACCCAGCTCCATCCCTCCAGGACCCCTCACACCCCTC	240				
Db	181	CTGGGAGGCGAGGCGCTTGAGGACCCAGCTCCATCCCTCCAGGACCCCTCACACCCCTC	240				
Qy	241	TGGGCGCTCTCGTGGCCATCTTTTCCGTGGGGGCATGATTTCTCTCTCAATTGGT	300				
Db	241	TGGGCGCTCTCGTGGCCATCTTTTCCGTGGGGGCATGATTTCTCTCTCAATTGGT	300				
Qy	301	ATCATCTCTCAGTGGCTTGGAGGAAAGGCCATGCTGGTCAACATGTCTCTGGCGGTG	360				
Db	301	ATCATCTCTCAGTGGCTTGGAGGAAAGGCCATGCTGGTCAACATGTCTCTGGCGGTG	360				
Qy	361	CTGGGGGCGAGCTCATGGGCTGGCCAAACGCTGCTCTCTATGAAATGCTCATCCTT	420				
Db	361	CTGGGGGCGAGCTCATGGGCTGGCCAAACGCTGCTCTCTATGAAATGCTCATCCTT	420				
Qy	421	GGACGATTCCTCATTGGGCGCTACTCAGGGGTGACATCAGGGCTGGTGGCCCATGACGTG	480				
Db	421	GGACGATTCCTCATTGGGCGCTACTCAGGGGTGACATCAGGGCTGGTGGCCCATGACGTG	480				
Qy	481	GGGGAGATGTCTCCACATCACTCGGGGGCGCCCTGGGGAGCGCTCAACCAACTGGCCATT	540				
Db	481	GGGGAGATGTCTCCACATCACTCGGGGGCGCCCTGGGGAGCGCTCAACCAACTGGCCATT	540				
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Db	541	GTTATCGGCATCTGATCGCCAGGTGCTGGGCTGGAGTCCCTCTGGGCACTGCCAGC	600				
Qy	601	CTGTGGCACTGCTCTGGGCTCAGTGTCTACTCTGCTGCTGCTGCTGCTGCTGCTGCTG	660				
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Qy	661	CCCTTCTGTCCGAGAGCCCGCTACCTCTACATCATCCAGAACTCTGAGGGCGCTGCC	720				
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Db	781	AAGGATGAGAGCGGAAGCTGAGGCGTGAAGGCGCACTGTCTCTGCTCCAGCTCTGGGC	840				
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Db	1081	TGTGGCTGTGGCATCTGTATGACTGTGGCTGTCTCTCTCTGGAGCGAGTTCCAGCCATG	1140				
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Db	1261	GCTGTGCTGGTTCCTCAACTGACAGAGCAACTTCATCATTTGGCATGGGTTTCAGATAT	1320				
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Db	1321	GTTGCGAGGCTATGGGGCCCTACGTCTTCTCTTCTATTGGGTCTCTCTCTGGGCTTC	1380				
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Db	1681	GTATTAAGAGGTTATTTATTTATTTTCAAAATTTTCTTTTTTCTGTACAGACGCTGTAC	1740				
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Db	1741	GCATGTAACTTATATCTGAAACCTTGTCTGAGAGGTTTTTGGGACGCTCGAAGGCTTTA	1800				
Qy	1801	ATTTGGGCGGCTACCCAAATTTGGCCCTATAGTGTAGTCTATTTACGGGCTCCTCTGCGG	1860				
Db	1801	ATTTGGGCGGCTACCCAAATTTGGCCCTATAGTGTAGTCTATTTACGGGCTCCTCTGCGG	1860				
Qy	1861	TCGTTTTTACACGCTGAGCTGGGAAACCTTGGGTTTACCCAACTTAATCCCTTTCAG	1920				
Db	1861	TCGTTTTTACACGCTGAGCTGGGAAACCTTGGGTTTACCCAACTTAATCCCTTTCAG	1920				
Qy	1921	CACATCCCTCTTTCGCCAGCTGCGTAAATAGCAGAGGCGCGCACCGATCGCCCTTCC	1980				
Db	1921	CACATCCCTCTTTCGCCAGCTGCGTAAATAGCAGAGGCGCGCACCGATCGCCCTTCC	1980				
Qy	1981	AACAGTTGCGCAGCTGAATGGCGGAGATGGCGGAGCGCCCTGTAGCGGCGATTAAGCG	2040				
Db	1981	AACAGTTGCGCAGCTGAATGGCGGAGATGGCGGAGCGCCCTGTAGCGGCGATTAAGCG	2040				
Qy	2041	CGGCGGCTGTGTGTACGCGAGCGTGAACGCTTACACTTTGCCAGCGCCCTTAGCGCCG	2100				
Db	2041	CGGCGGCTGTGTGTACGCGAGCGTGAACGCTTACACTTTGCCAGCGCCCTTAGCGCCG	2100				
Qy	2101	CTCCTTTTCT	2160				

Db 2101 |||||CTCCTTTGCGCTTCTTCCCTTCTCTTCCGACAGTTGCGCGCTTCCCGCTCAAGCTC 2160
Qy 2161 TAAATCGGGGCTCCCTTTAGGGTTCGGAATTAGTCTTTACCGGCACCTCGACCCCAAAA 2220
Db 2161 TAAATCGGGGCTCCCTTTAGGGTTCGGAATTAGTCTTTACCGGCACCTCGACCCCAAAA 2220
Qy 2221 AACTTGATTAGGTGATGGTTCAAGTAGTGGGCATCGGCCCTGATAGACGGTTTTTCGCC 2280
Db 2221 AACTTGATTAGGTGATGGTTCAAGTAGTGGGCATCGGCCCTGATAGACGGTTTTTCGCC 2280
Qy 2281 CTTTGAAGTGGAGTCCACGGTCTTTAAATAGTGGACTCTGTGTTCCAAACTGGAAACACAC 2340
Db 2281 CTTTGAAGTGGAGTCCACGGTCTTTAAATAGTGGACTCTGTGTTCCAAACTGGAAACACAC 2340
Qy 2341 TCAACCTATCTCGGCTCTATCTTTTGAATTAAGGGATTTTGGCGGATTTCCGGCTATT 2400
Db 2341 TCAACCTATCTCGGCTCTATCTTTTGAATTAAGGGATTTTGGCGGATTTCCGGCTATT 2400
Qy 2401 GGTAAATAAATAGCTGATTAAACAAAATTTAAACGGAATTTTAAACAAAATTTAAACGT 2460
Db 2401 GGTAAATAAATAGCTGATTAAACAAAATTTAAACGGAATTTTAAACAAAATTTAAACGT 2460
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Db 2461 TTACAATTTCTGATGGGTATTTTCTCTTACGCACTCTGCGGTATTTTCAACCGCAT 2520
Qy 2521 AGGGTAATTAAGTGAATTAATTAAGTGAAGTCTTAATTTGTGAGTTTGTAGTATACATGCT 2580
Db 2521 AGGGTAATTAAGTGAATTAATTAAGTGAAGTCTTAATTTGTGAGTTTGTAGTATACATGCT 2580
Qy 2581 TTAATTAATAACAGTTTTTGTGTTTGTGGCGCATCTTCTCAAAATGCTTCCAGC 2640
Db 2581 TTAATTAATAACAGTTTTTGTGTTTGTGGCGCATCTTCTCAAAATGCTTCCAGC 2640
Qy 2641 CTGCTTTTCTGTAAGCTTCAACCTCTACCTTAGCATCCCTTCCCTTGGAAATGCTCTC 2700
Db 2641 CTGCTTTTCTGTAAGCTTCAACCTCTACCTTAGCATCCCTTCCCTTGGAAATGCTCTC 2700
Qy 2701 TTCCAAACAAATAAATAGTCAGATCCCTGTAGAGACCAATCATCATCCAGTTTCTATCTGTT 2760
Db 2701 TTCCAAACAAATAAATAGTCAGATCCCTGTAGAGACCAATCATCATCCAGTTTCTATCTGTT 2760
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Db 2761 GACCCAAATGCGTCTCCCTGTGATCTAAACCCACACCGGGTGTCAATAACCAATCGT 2820
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Db 2941 ATGACAAATCTGCTAAACATCAAAAGGCTCTAGGTTCTTTGTTACTTTCTTCCGCGCT 3000
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Db 3001 GCTTCAAAACCGCTAAACATTAACCTTGGGCCCAACACACCGGTGCAATCGTAAATCTTGCCC 3060
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DB |||||

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|||||

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Db 7801 AAAAAAGTTTTTTAAATTTTAAATCAAAA 7828

RESULT 2
AAL49312

ID AAL49312 standard; DNA; 7777 BP.

XX AAL49312;

XX 07-NOV-2002 (first entry)

XX Human Glut1 containing vector YEP4H7-H6GLUT1.

XX Human; yeast; GLUT4; glut transporter; hexose; antidiabetic; anorectic;
KW vector; ds.

XX Homo sapiens.

XX WO200264784-A2.

XX 22-AUG-2002.

XX 09-FEB-2002; 2002WO-BP001373.

XX 14-FEB-2001; 2001DE-01006718.

XX (AVET) AVENTIS PHARMA DEUT GMBH.

XX Mueller G, Koller K, Boles E, Wiczorke R, Dlugai S;

XX WPI; 2002-636632/68.

XX New strains of yeast, useful in screening for modulators of hexose
PT transport, potential antidiabetic and antiobesity agents, lack native
PT hexose-transport function.

XX Example; Page 37-40; 58pp; German.

XX The present invention relates to a strain of *Saccharomyces cerevisiae*
CC that cannot grow on a substrate containing hexose as the only source of
CC carbon but the ability to grow on such substrates is restored when the
CC GLUT4 gene is expressed. A strain transformed to express the GLUT1 or
CC GLUT4 genes can be used to identify compounds that increase/reduce hexose
CC transport by these proteins. These compounds, optionally after
CC development, are potential drugs for treating diabetes and obesity. The
CC present sequence is a vector containing the human Glut1 coding sequence
CC as used in the invention

XX Sequence 7777 BP; 2013 A; 1915 C; 1742 G; 2107 T; 0 U; 0 Other;

Query Match 89.1%; Score 6975.2; DB 6; Length 7777;

Best Local Similarity 93.7%; Pred. No. 0;

Matches 7297; Conservative 0; Mismatches 478; Indels 15; Gaps 2;

Qy 39 GGAACCCCTCAGCAGGAGTGAAGTGGACCTGGCTTCTGCTGTCTCTCGGTGCT 98

Db 3 GGAGCCAGCAGCAAGAGCTGAGGCTCGGCTCATGCTGCTGTGGAGGAGCAGTGTCT 62

Db	2208	CCCTGATAGACGGTCTTTTCGCCCTTTGACGTTGGAGTCCAAGTCTCTTTAATAGTGACATC	2267
Qy	2319	TTGTTCCAAACTGGAAACAACACTCAACCCCTATCTCGGTCTATTCTTTTGATTTATTAAGGG	2378
Db	2268	TTGTTCCAAACTGGAAACAACACTCAACCCCTATCTCGGTCTATTCTTTTGATTTATTAAGGG	2327
Qy	2379	ATTTTGGCCGATTTTCGGCTATTGGTTAAAAAATGAGCTGATTTTAACAAAAATTTAAACGGC	2438
Db	2328	ATTTTGGCCGATTTTCGGCTATTGGTTAAAAAATGAGCTGATTTTAACAAAAATTTAAACGGC	2387
Qy	2439	AAATTTTAAACAAAATATTAAAGTTTACAAATTTCTGTATGCGGTATTTTCTCTTACGCATC	2498
Db	2388	AAATTTTAAACAAAATATTAAAGTTTACAAATTTCTGTATGCGGTATTTTCTCTTACGCATC	2447
Qy	2499	TGTGCGGTATTTTCACACGGCATAGGGTAAATAACTGATATAAATTAATTTGAAGCTCTAAAT	2558
Db	2448	TGTGCGGTATTTTCACACGGCATAGGGTAAATAACTGATATAAATTAATTTGAAGCTCTAAAT	2507
Qy	2559	TGTGAGTTTATGATATACATGCAATTTACTTATAATAACAGTTTTTTAGTTTTGCTGGCCGCAT	2618
Db	2508	TGTGAGTTTATGATATACATGCAATTTACTTATAATAACAGTTTTTTAGTTTTGCTGGCCGCAT	2567
Qy	2619	CTTCTCAAAATATGCTTCCAGCCCTGCTTTTCTGTAAAGTTTACGCTCTACCTTAGCATTC	2678
Db	2568	CTTCTCAAAATATGCTTCCAGCCCTGCTTTTCTGTAAAGTTTACGCTCTACCTTAGCATTC	2627
Qy	2679	CTTCCCTTTGCCAAATAGTCTCTTCCAAACAATAATAATGTACAGATCTGTAGAGACCACA	2738
Db	2628	CTTCCCTTTGCCAAATAGTCTCTTCCAAACAATAATAATGTACAGATCTGTAGAGACCACA	2687
Qy	2739	TCATCCACGGTCTTATACGTGTGACCCAAATGCGCTCTCCCTTGTATCTAAACCCACACCG	2798
Db	2688	TCATCCACGGTCTTATACGTGTGACCCAAATGCGCTCTCCCTTGTATCTAAACCCACACCG	2747
Qy	2799	GGTGTCAATAACCAATCGTAACTTCACTCTTCCACCAATGTCTCTTTGAGCAATA	2858
Db	2748	GGTGTCAATAACCAATCGTAACTTCACTCTTCCACCAATGTCTCTTTGAGCAATA	2807
Qy	2859	AAGCCGATACAAAATCTTTGTGCGCTCTTCGCAATGTCAACAGTACCCCTTAGTATATTCT	2918
Db	2808	AAGCCGATACAAAATCTTTGTGCGCTCTTCGCAATGTCAACAGTACCCCTTAGTATATTCT	2867
Qy	2919	CCAGTAGATAGGAGCCCTTGCATGACAAATCTGCTTAAACATCAAAAGGCCCTCTAGGTTC	2978
Db	2868	CCAGTAGATAGGAGCCCTTGCATGACAAATCTGCTTAAACATCAAAAGGCCCTCTAGGTTC	2927
Qy	2979	TTTGTTACTTCTTTCGCGCTGCTTCAAAACGGCTAACAAATACGTGGGCCACACACCG	3038
Db	2928	TTTGTTACTTCTTTCGCGCTGCTTCAAAACGGCTAACAAATACGTGGGCCACACACCG	2987
Qy	3039	TGTGCATTTCTGTAATGTCTGCCCATTCCTGCTATTCTGTATACACCCGACAGTACTGCAAT	3098
Db	2988	TGTGCATTTCTGTAATGTCTGCCCATTCCTGCTATTCTGTATACACCCGACAGTACTGCAAT	3047
Qy	3099	TTGACTGTATTAACAAATGTACGAAATTTTCTGTCTTCGAAGAGTAAAAAATTTGTACTTG	3158
Db	3048	TTGACTGTATTAACAAATGTACGAAATTTTCTGTCTTCGAAGAGTAAAAAATTTGTACTTG	3107
Qy	3159	GCGGATTAATGCTTTAGGGGTTAACTGTGCGCTTCCATGGAATAAATACGTCAAGATATCC	3218
Db	3108	GCGGATTAATGCTTTAGGGGTTAACTGTGCGCTTCCATGGAATAAATACGTCAAGATATCC	3167
Qy	3219	ACATGCTGTTTTAGTAAACAAAATTTTGGGACCTTAATGCTTCACTAACTCCAGTAATCC	3278
Db	3168	ACATGCTGTTTTAGTAAACAAAATTTTGGGACCTTAATGCTTCACTAACTCCAGTAATCC	3227
Qy	3279	TTGGTGTGACGAACATCCAATGAAGCACACAAAGTTTGTGTTTTGCTGTCATGATATTA	3338
Db	3228	TTGGTGTGACGAACATCCAATGAAGCACACAAAGTTTGTGTTTTGCTGTCATGATATTA	3287
Qy	3339	AATAGCTTGGCAGCAACAGGACTAGGATGAGTACGACGATCTCTTATATGTAGCTTTC	3398

Db	3288	AATAGCTTGGCAGCAACAGGACTAGGATAGTAGCAGCACGTTTCCTTTATATATGTAGCTTC	3347
Qy	3399	GACATGATTTATCTTTCGTTTCCTGCAGGTTTTTGTCTCTGTGCAGTGTGGGTTAAGAAATACT	3458
Db	3348	GACATGATTTATCTTTCGTTTCCTGCAGGTTTTTGTCTCTGTGCAGTGTGGGTTAAGAAATACT	3407
Qy	3459	GGGCAATTTCAATGTTTCTTCAACACCTACATATGCGTATATATACCAATCTAAGTCTGTGC	3518
Db	3408	GGGCAATTTCAATGTTTCTTCAACACCTACATATGCGTATATATACCAATCTAAGTCTGTGC	3467
Qy	3519	TCCTTCCTTCGTTCTTCCTTCGTTTCGGAGATTACCGAATCAAAAAATTTCAAGAANAAC	3578
Db	3468	TCCTTCCTTCGTTCTTCCTTCGTTTCGGAGATTACCGAATCAAAAAATTTCAAGAANAAC	3527
Qy	3579	CGAAATCAAAAAAAGAAATAAAAAAATGATGAATTTGAATTTGAAAGCTGTGGTATGG	3638
Db	3528	CGAAATCAAAAAAAGAAATAAAAAAATGATGAATTTGAATTTGAAAGCTGTGGTATGG	3587
Qy	3639	TGCACTCTCAgTACAATCTCTCTGTATGCGCATAGTTAAAGCCAGCCCCCGACACCCGCCA	3698
Db	3588	TGCACTCTCAgTACAATCTCTCTGTATGCGCATAGTTAAAGCCAGCCCCCGACACCCGCCA	3647
Qy	3699	ACACCCGCTGACGGGCCCTGACGGGCTGTCTGCTCCGGCATCCGCTTACAGACAAGCT	3758
Db	3648	ACACCCGCTGACGGGCCCTGACGGGCTGTCTGCTCCGGCATCCGCTTACAGACAAGCT	3707
Qy	3759	GTGACCGTCTCCGGGAGCTGCATGTGCAGAGTTTTTCACCGTCATCACCGAAACGGCGC	3818
Db	3708	GTGACCGTCTCCGGGAGCTGCATGTGCAGAGTTTTTCACCGTCATCACCGAAACGGCGC	3767
Qy	3819	AGACGAAAGGGCCTCGTGATACGCCATTTTTTATAGGTTAATGTCATGATAATAATGGTT	3878
Db	3768	AGACGAAAGGGCCTCGTGATACGCCATTTTTTATAGGTTAATGTCATGATAATAATGGTT	3827
Qy	3879	TCCTAGTATGATCCAAATATCAAAGEAATAAGTAGCATTGAAGGATGAGACTAATCCAAAT	3938
Db	3828	TCCTAGTATGATCCAAATATCAAAGEAATAAGTAGCATTGAAGGATGAGACTAATCCAAAT	3887
Qy	3939	GAGGAGTGGCAGCATATAGAAACAGCTAAAGGGTAGTGCTCAAGGAGCATACGATACCCC	3998
Db	3888	GAGGAGTGGCAGCATATAGAAACAGCTAAAGGGTAGTGCTCAAGGAGCATACGATACCCC	3947
Qy	3999	GCATGGAAATGGGATAATATCACAGGAGGTACTAGACTACCTTTTCATCCTACATAAAATAGA	4058
Db	3948	GCATGGAAATGGGATAATATCACAGGAGGTACTAGACTACCTTTTCATCCTACATAAAATAGA	4007
Qy	4059	CGCATATAGTAGCATTTAAGCATAAACAAGCAGCTATGCGGTTCTTCTCATGTATATAT	4118
Db	4008	CGCATATAGTAGCATTTAAGCATAAACAAGCAGCTATGCGGTTCTTCTCATGTATATAT	4067
Qy	4119	ATATACAGGCAACACGAGATATAGGTGCGACGTGAACAGTGAAGTCTGTATGTGGCGAGCT	4178
Db	4068	ATATACAGGCAACACGAGATATAGGTGCGACGTGAACAGTGAAGTCTGTATGTGGCGAGCT	4127
Qy	4179	CGCGTTCGATTTTTCGGAAGCGCTCGTTTTTCGGAACGCTTTTGAAGTTCTTATTCGGAAGT	4238
Db	4128	CGCGTTCGATTTTTCGGAAGCGCTCGTTTTTCGGAACGCTTTTGAAGTTCTTATTCGGAAGT	4187
Qy	4239	TCCTATTCTTAGAAAGTATAGGAATTCAGAGGCGTTTTTGAAGAACCAAAAGCGCTCTGA	4298
Db	4188	TCCTATTCTCTAGAAAGTATAGGAATTCAGAGGCGTTTTTGAAGAACCAAAAGCGCTCTGA	4247
Qy	4299	AGACGCACITTTCAAAAAACCAAAACGACCGGAGCTGAACGAGCTACTAAAAATATTGCG	4358
Db	4248	AGACGCACITTTCAAAAAACCAAAACGACCGGAGCTGAACGAGCTACTAAAAATATTGCG	4307
Qy	4359	AATAACCGCTTCCACAAACATTTGCTCAAAGTATCTCTTTCGTATATATCTCTGTGCTATA	4418
Db	4308	AATAACCGCTTCCACAAACATTTGCTCAAAGTATCTCTTTCGTATATATCTCTGTGCTATA	4367
Qy	4419	TCCCTATATAACCTTACCACCTTTCGCTTTCGCTTGAACCTTGAACTTGAACCTTGAACCTT	4478
Db	4368	TCCCTATATAACCTTACCACCTTTCGCTTTCGCTTGAACCTTGAACTTGAACCTTGAACCTT	4427

QY 4479 TACATTTTATGTTTATCTCTAGTATTAATCTTTAGACAAAAAATTTAGTAAGAAT 4538
DB TACATTTTATGTTTATCTCTAGTATTAATCTTTAGACAAAAAATTTAGTAAGAAT 4487
QY 4539 ATTCTAGAGTGAATCGAAAAACAATA CGAAATGTAAACAATTCCTATACGTAGTATA 4598
DB ATTCTAGAGTGAATCGAAAAACAATA CGAAATGTAAACAATTCCTATACGTAGTATA 4547
QY 4599 GAGACAAATAGAGAAACCGTTCATTAATTTCTGACCAATGAAAGATCATCAACGCTAT 4658
DB GAGACAAATAGAGAAACCGTTCATTAATTTCTGACCAATGAAAGATCATCAACGCTAT 4607
QY 4659 CACTTTCTGTTTCAAAAAGTATCGCAATCCACATCGGTATAGAAATAAATCGGGGATGCC 4718
DB CACTTTCTGTTTCAAAAAGTATCGGCAATCCACATCGGTATAGAAATAAATCGGGGATGCC 4667
QY 4719 TTTATCTTGAAAAAATGACCGCGAGCTTCGCTAGTAATCAGTAAACCGCGGAAAGTGAG 4778
DB TTTATCTTGAAAAAATGACCGCGAGCTTCGCTAGTAATCAGTAAACCGCGGAAAGTGAG 4727
QY 4779 TCAGGCTTTTATGGAAGAGAAATAGACACCAAGTAGCCTTCTTAAACCTTAACG 4838
DB TCAGGCTTTTATGGAAGAGAAATAGACACCAAGTAGCCTTCTTAAACCTTAACG 4787
QY 4839 GACCTACAGTCAAAAAGTTATCAAGAGACTGCATTATAGAGCGCACAAAGGAGAAAAA 4898
DB GACCTACAGTCAAAAAGTTATCAAGAGACTGCATTATAGAGCGCACAAAGGAGAAAAA 4847
QY 4899 AGTAATCTAAGATGCTTTGTTAGAAAAATAGCGCTCTCGGATGCAATTTTGTAGAACAA 4958
DB AGTAATCTAAGATGCTTTGTTAGAAAAATAGCGCTCTCGGATGCAATTTTGTAGAACAA 4907
QY 4959 AAAAGAGTATAGATCTTTGTTGTAATAATAGCGCTCTCGGATGCAATTTTGTAGAACAA 5018
DB AAAAGAGTATAGATCTTTGTTGTAATAATAGCGCTCTCGGATGCAATTTTGTAGAACAA 4967
QY 5019 AAAAATGCAAGTCAAGATCTTTGTTGTAATAATAGCGCTCTCGGATGCAATTTTGTAGAACAA 5078
DB AAAAATGCAAGTCAAGATCTTTGTTGTAATAATAGCGCTCTCGGATGCAATTTTGTAGAACAA 5027
QY 5079 TACAAAAATGAAGCAGATCTTCGTTGGTAAATAGCGCTTTTCGGGTGCAATTTCTGT 5138
DB TACAAAAATGAAGCAGATCTTCGTTGGTAAATAGCGCTTTTCGGGTGCAATTTCTGT 5087
QY 5139 TCTGTAAAAATGCAAGTCAAGATCTTTGTTGTAATAATAGCGCTCTCGGATGCAATTTTGTAGAACAA 5198
DB TCTGTAAAAATGCAAGTCAAGATCTTTGTTGTAATAATAGCGCTCTCGGATGCAATTTTGTAGAACAA 5147
QY 5199 TGTCTTACAAAAATGAAGCAGATCTTCGTTGGTAAATAGCGCTTTTCGGGTGCAATTTCTGT 5258
DB TGTCTTACAAAAATGAAGCAGATCTTCGTTGGTAAATAGCGCTTTTCGGGTGCAATTTCTGT 5207
QY 5259 CGGAACCCCTATTTGTTTATTTTCTAAATACATTTCAAAATATGATCGGCTCATGAGACA 5318
DB CGGAACCCCTATTTGTTTATTTTCTAAATACATTTCAAAATATGATCGGCTCATGAGACA 5267
QY 5319 ATAAACCTGATTAATGCTTCAATATATTTGAAAGGAGAGATGATGATTTCAACATTT 5378
DB ATAAACCTGATTAATGCTTCAATATATTTGAAAGGAGAGATGATGATTTCAACATTT 5327
QY 5379 CCGGTGCGCCCTTATTTCCCTTTTTCGGGCAATTTTTCGCTCTCTGTTTTCGCTCAACCCAGA 5438
DB CCGGTGCGCCCTTATTTCCCTTTTTCGGGCAATTTTTCGCTCTCTGTTTTCGCTCAACCCAGA 5387
QY 5439 AACGCTGTGAAAGTAAAGATGCTGAAGATGATGTTGGGTGACAGAGTGGGTTCATCGA 5498
DB AACGCTGTGAAAGTAAAGATGCTGAAGATGATGTTGGGTGACAGAGTGGGTTCATCGA 5447
QY 5499 ACTGGATCTCAACAGCGGTAGATCTCTGAGAGTTTTTCGCCCCGAAAGACGTTTTCCAT 5558
DB ACTGGATCTCAACAGCGGTAGATCTCTGAGAGTTTTTCGCCCCGAAAGACGTTTTCCAT 5507

QY 5559 GATGAGCAGCTTTTAAAGTTCTGCTATCTGCGCGGTATTTATCCCGTATGTAGCGCGGCA 5618
DB GATGAGCAGCTTTTAAAGTTCTGCTATCTGCGCGGTATTTATCCCGTATGTAGCGCGGCA 5567
QY 5619 AGAGCAACTCGGTGCGCGCATACACTATTCTCAGAAATGACTTGGTTGAGTACTCACCAGT 5678
DB AGAGCAACTCGGTGCGCGCATACACTATTCTCAGAAATGACTTGGTTGAGTACTCACCAGT 5627
QY 5679 CACAGAAAAGCATCTTACGGATGGCATGACAGATGAAGAGAAATATGCACTGCTGCCATTAAC 5738
DB CACAGAAAAGCATCTTACGGATGGCATGACAGATGAAGAGAAATATGCACTGCTGCCATTAAC 5687
QY 5739 CATGAGTGAATAACATCGCGGCCAACTTTACTTCTGACAAAGATCGAGAGACCGAAGAGCT 5798
DB CATGAGTGAATAACATCGCGGCCAACTTTACTTCTGACAAAGATCGAGAGACCGAAGAGCT 5747
QY 5799 AACCGCTTTTTCGACAAATGCGGGATCATGTAATCTGCGCTTGTATCGTTGGGAACCGGA 5858
DB AACCGCTTTTTCGACAAATGCGGGATCATGTAATCTGCGCTTGTATCGTTGGGAACCGGA 5807
QY 5859 GCTGAATGAAGCCATACCAACGACGAGCGTGACACACAGATGCTGTAGCAATGGCAAC 5918
DB GCTGAATGAAGCCATACCAACGACGAGCGTGACACACAGATGCTGTAGCAATGGCAAC 5867
QY 5919 AACGTTGCGCAAACTATTTAACTGCGGAACTACTTTACTTCTAGCTTCCCGGCAACAAATTAAT 5978
DB AACGTTGCGCAAACTATTTAACTGCGGAACTACTTTACTTCTAGCTTCCCGGCAACAAATTAAT 5927
QY 5979 AGACTGATGAGGCGGATTAAGTTGACAGACCACTTCTGCGCTGCGGCTTCCCGCTGG 6038
DB AGACTGATGAGGCGGATTAAGTTGACAGACCACTTCTGCGCTGCGGCTTCCCGCTGG 5987
QY 6039 CTGCTTTATTTGCTGATAAACTGAGCGCGGTGAGCGTGGTCTCGCGGTATCATTTGCAGC 6098
DB CTGCTTTATTTGCTGATAAACTGAGCGCGGTGAGCGTGGTCTCGCGGTATCATTTGCAGC 6047
QY 6099 ACTGGGCGCAGATGTTAAGCCCTCCCGTATCGTATGTTATCTACAGCGGGAGTCAAGC 6158
DB ACTGGGCGCAGATGTTAAGCCCTCCCGTATCGTATGTTATCTACAGCGGGAGTCAAGC 6107
QY 6159 AACTATGATGAACGAAATAGACAGATCGCTGAGATGAGTGGCTCCTCAGTATTAAGCATTTG 6218
DB AACTATGATGAACGAAATAGACAGATCGCTGAGATGAGTGGCTCCTCAGTATTAAGCATTTG 6167
QY 6219 GTAACTGTGACAGCAAGTTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTAA 6278
DB GTAACTGTGACAGCAAGTTTACTCATATATACTTTAGATTGATTTAAAACTTCATTTTAA 6227
QY 6279 ATTTAAAGGATCTAGGTGAAGATCTTTTGTGATAATCTCATGACCAAAATCCCTTAAAG 6338
DB ATTTAAAGGATCTAGGTGAAGATCTTTTGTGATAATCTCATGACCAAAATCCCTTAAAG 6287
QY 6339 TGAGTTTTCGTTCCACTGAGCGGTGAGACCGGTAGAAAGATCAAGATCTTCTTTGAGA 6398
DB TGAGTTTTCGTTCCACTGAGCGGTGAGACCGGTAGAAAGATCAAGATCTTCTTTGAGA 6347
QY 6399 TCCCTTTTTCGCGGTAAATCTGCTGCTTGTGCAAAACAAAAAACAACCGCTACCAAGCGGT 6458
DB TCCCTTTTTCGCGGTAAATCTGCTGCTTGTGCAAAACAAAAAACAACCGCTACCAAGCGGT 6407
QY 6459 GGTGTTGTTCCCGGATCAAGAGCTACCAACTCTTTTTCGGAAGGTAACTGGCTTCAGCAG 6518
DB GGTGTTGTTCCCGGATCAAGAGCTACCAACTCTTTTTCGGAAGGTAACTGGCTTCAGCAG 6467
QY 6519 AGGCGATACCAAAATCTGCTTCTAGTGTAGCGGTAGTTAGCCACCACTTCAAGAA 6578
DB AGGCGATACCAAAATCTGCTTCTAGTGTAGCGGTAGTTAGCCACCACTTCAAGAA 6527
QY 6579 CTCTGTAGCAGCGCTACATACCTCGCTCTGCTAATCTGTTTACAGTGGCTGCTGCCAG 6638
DB CTCTGTAGCAGCGCTACATACCTCGCTCTGCTAATCTGTTTACAGTGGCTGCTGCCAG 6587
QY 6639 TGGCGATAAGTGTGCTCTTTACCGGGTTGGACTCAAGACGATAGTTTACCGGATAAGCGGCA 6698

Db 6588 TGGCGATAAGTCGTGCTTTACCGGGTTGGACTCAAGACGATGTTACCGGATTAAGCGCA 6647
Qy 6699 GCGGTGCGGCTGAACGGGGGGTTCGTGCACACAGCCAGCTTCGGAGCGAACGACCTACAC 6758
Db 6648 GCGGTGCGGCTGAACGGGGGGTTCGTGCACACAGCCAGCTTCGGAGCGAACGACCTACAC 6707
Qy 6759 CGAATGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCGAAAGGAGAAA 6818
Db 6708 CGAATGAGATACCTACAGCGTGAGCTATGAGAAAGCGCCACGCTTCCGAAAGGAGAAA 6767
Qy 6819 GCGGACAGGTATCCGCTAGCGGCGAGGTCGAGACAGGAGCGGACGAGGAGCTTCC 6878
Db 6768 GCGGACAGGTATCCGCTAGCGGCGAGGTCGAGACAGGAGCGGACGAGGAGCTTCC 6827
Qy 6879 AGGGGAAACCGCTTGTATCTTATAGTCTCTGTCGGGTTTCGGCCACTCTGACTTGAGCG 6938
Db 6828 AGGGGAAACCGCTTGTATCTTATAGTCTCTGTCGGGTTTCGGCCACTCTGACTTGAGCG 6887
Qy 6939 TCGATTTTGTGATGCTCGTCAGGGGGCGAGCCTATGAAAGAAAGCCAGCAACGCGC 6998
Db 6888 TCGATTTTGTGATGCTCGTCAGGGGGCGAGCCTATGAAAGAAAGCCAGCAACGCGC 6947
Qy 6999 CTTTACGCTTCTGCGCTTTGCTGCGCTTTTGTCTCATGTTCTTCTGCGTTATC 7058
Db 6948 CTTTACGCTTCTGCGCTTTTGTGCGCTTTTGTCTCATGTTCTTCTGCGTTATC 7007
Qy 7059 CCCTGATTTCTGATTAACCGTATTACCGCTTTTGTAGTGAGCTGATACCGCTCGCGCAG 7118
Db 7008 CCCTGATTTCTGATTAACCGTATTACCGCTTTTGTAGTGAGCTGATACCGCTCGCGCAG 7067
Qy 7119 CCAGAACACCGAGCGCAGCGAGTCAGTGACGAGGAGCGAAGAGCGCCCAATACGCAA 7178
Db 7068 CCAGAACACCGAGCGCAGCGAGTCAGTGACGAGGAGCGAAGAGCGCCCAATACGCAA 7127
Qy 7179 ACCGCTTCTCCCGCGGTTGCGCGATTCAATTAATGAGCTGCGACGAGGTTCCCGA 7238
Db 7128 ACCGCTTCTCCCGCGGTTGCGCGATTCAATTAATGAGCTGCGACGAGGTTCCCGA 7187
Qy 7239 CTGGAAGCGGCGAGTGAGCGCAACGCAATTAATGAGTTACTCTACTCATTAGGCACC 7298
Db 7188 CTGGAAGCGGCGAGTGAGCGCAACGCAATTAATGAGTTACTCTACTCATTAGGCACC 7247
Qy 7299 CCAGGCTTTACATTTATGCTTCGGCTCTATGTTGTGGAATTTGTAGCGGATAACA 7358
Db 7248 CCAGGCTTTACATTTATGCTTCGGCTCTATGTTGTGGAATTTGTAGCGGATAACA 7307
Qy 7359 ATTTCACAGGAAACAGCTATGACCATGATTAGCCAGCGGCGCAATTAACCTCACTA 7418
Db 7308 ATTTCACAGGAAACAGCTATGACCATGATTAGCCAGCGGCGCAATTAACCTCACTA 7367
Qy 7419 AAGGGAACAAAGCTGGAGCTCGTAGGAACAATTTGGGGCCCTGCGTGTCTTCTGAGG 7478
Db 7368 AAGGGAACAAAGCTGGAGCTCGTAGGAACAATTTGGGGCCCTGCGTGTCTTCTGAGG 7427
Qy 7479 TTCATCTTTTACATTTGCTTCTGCTGATAATTTTCAGAGGCAACAGGAAAAATTAGAT 7538
Db 7428 TTCATCTTTTACATTTGCTTCTGCTGATAATTTTCAGAGGCAACAGGAAAAATTAGAT 7487
Qy 7539 GGCAGAAAGTCGCTTTCAAGGAAAAATCCCGCCATCTTTTCAGATCCCTGTAACTTA 7598
Db 7488 GGCAGAAAGTCGCTTTCAAGGAAAAATCCCGCCATCTTTTCAGATCCCTGTAACTTA 7547
Qy 7599 TTGCAACTGAAAGATGAAGAGGAGGAAAAATACAAATATCTAGAACTGAAAAAATAA 7658
Db 7548 TTGCAACTGAAAGATGAAGAGGAGGAAAAATACAAATATCTAGAACTGAAAAAATAA 7607
Qy 7659 AAGTATAAATAGACGAGATATATGCCAATCTTTCACAATGTTTCAATTTTCAATTT 7718
Db 7608 AAGTATAAATAGACGAGATATATGCCAATCTTTCACAATGTTTCAATTTTCAATTT 7667
Qy 7719 GCGCTATTGTAATAATTAATAACATCAAGAACAAACAGCTCAACTGTCTTCTTAAG 7778

Db 7668 GCGCTATTGTAATAATAATAAATCAATCAAGAACAAACAGCTCAACTGTCTTCTTAAG 7727
Qy 7779 AACAAAGATAAACACAAAAACAAAAAGTTTTTTTAAATTAATCAAAAA 7828
Db 7728 AACAAAGATAAACACAAAAACAAAAAGTTTTTTTAAATTAATCAAAAA 7777

RESULT 3
AAL49316
ID AAL49316 standard; DNA; 6360 BP.
XX
AC AAL49316;
XX
DT 07-NOV-2002 (first entry)
XX Human HKT7 promoter containing plasmid YEp4H7.
XX Human; yeast; GLUT4; glut transporter; hexose; antidiabetic; anorectic;
XX plasmid; ds.
XX Homo sapiens.
XX WO200264784-A2.
XX
PD 22-AUG-2002.
XX
PF 09-FEB-2002; 2002WO-EP001373.
XX
PR 14-FEB-2001; 2001DE-01006718.
XX
XX (AVET) AVENTIS PHARMA DEUT GMBH.
XX
PI Mueller G, Koller K, Boles E, Wiczorke R, Dlugai S;
XX WPI; 2002-636632/68.
XX
PT New strains of yeast, useful in screening for modulators of hexose
PT transport, potential antidiabetic and antiobesity agents, lack native
PT hexose-transport function.
XX
PS Example; Page 43-45; 58pp; German.
XX
CC The present invention relates to a strain of *Saccharomyces cerevisiae*
CC that cannot grow on a substrate containing hexose as the only source of
CC carbon but the ability to grow on such substrates is restored when the
CC GLUT4 gene is expressed. A strain transformed to express the GLUT1 or
CC GLUT4 genes can be used to identify compounds that increase/reduce hexose
CC transport by these proteins. These compounds, optionally after
CC development, are potential drugs for treating diabetes and obesity. The
CC present sequence is a plasmid described in the invention
XX
SQ Sequence 6360 BP; 1771 A; 1485 C; 1336 G; 1768 T; 0 U; 0 Other;

Query Match 75.5%; Score 5908; DB 6; Length 6360;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 5908; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1532 AGCTTATCGATACCGTCGACCTCGAGTCATGTAATAGTTAGTGTACGCTTACATTCAC 1591
Db 453 AGCTTATCGATACCGTCGACCTCGAGTCATGTAATAGTTAGTGTACGCTTACATTCAC 512
Qy 1592 GCCTTCCCCCAGCATCGCTCTAACCGAAAAAGGAGGTTAGACAACTGGAAGTCTAGG 1651
Db 513 GCCTTCCCCCAGCATCGCTCTAACCGAAAAAGGAGGTTAGACAACTGGAAGTCTAGG 572
Qy 1652 TCCTTATTTATTTTATAGTTATGTTAGTATTAAGACGTTATTTATTTCAATTT 1711
Db 573 TCCTTATTTATTTTATAGTTATGTTAGTATTAAGACGTTATTTATTTCAATTT 632
Qy 1712 TTCTTTTTCGTACAGACGCGTGTACGATGTAACATTATATCTGAAAACTTGTCTG 1771
Db 633 TTCTTTTTCGTACAGACGCGTGTACGATGTAACATTATATCTGAAAACTTGTCTG 692

Db 2853 TCCAAATTGAGGAGTGGCAGCATATAGAACAGCTAAAGGGTAGTGTGTAAGGAAGCATACG 2912
Qy 3992 ATACCCGCGATGGAATGGGATAATATACACAGGAGGTACTAGACTACCTTTTCATCCTACAT 4051
Db 2913 ATACCCGCGATGGAATGGGATAATATACACAGGAGGTACTAGACTACCTTTTCATCCTACAT 2972
Qy 4052 AAATAGACGATATAGTACGCAATTAAGCATAAACACGCACTATGCGGTCTCTCTCATG 4111
Db 2973 AAATAGACGATATAGTACGCAATTAAGCATAAACACGCACTATGCGGTCTCTCTCATG 3032
Qy 4112 TATATATATATACAGGCAACACGAGATATAGTGGACGTGAACAGTGAAGCTGATGTC 4171
Db 3033 TATATATATATACAGGCAACACGAGATATAGTGGACGTGAACAGTGAAGCTGATGTC 3092
Qy 4172 CGCAGCTCGCGTTGCAATTTTCCGAAGCGCTCGTTTTCGAAACGCTTTTGAAGTTCCTATT 4231
Db 3093 CGCAGCTCGCGTTGCAATTTTCCGAAGCGCTCGTTTTCGAAACGCTTTTGAAGTTCCTATT 3152
Qy 4232 CGGAAGTTCCTATCTCTAGAAAGTATAGGAACCTTCAGAGCGCTTTTGAAGCAACCAAGC 4291
Db 3153 CGGAAGTTCCTATCTCTAGAAAGTATAGGAACCTTCAGAGCGCTTTTGAAGCAACCAAGC 3212
Qy 4292 GCTCTGAAGACGCACTTTCAAAAAACCAAAACGCAACGCTGTAAACGCTACTAAAA 4351
Db 3213 GCTCTGAAGACGCACTTTCAAAAAACCAAAACGCAACGCTGTAAACGCTACTAAAA 3272
Qy 4352 TATTGCGAATACCGCTTCCCAAAACATTTGCTCAAAAGTATCTCTTTGCTATATATCTCTG 4411
Db 3273 TATTGCGAATACCGCTTCCCAAAACATTTGCTCAAAAGTATCTCTTTGCTATATATCTCTG 3332
Qy 4412 TGCTATATCCCTATATACCTACCCATCCACCTTTGCTCTTGAACCTTGCACTTAACT 4471
Db 3333 TGCTATATCCCTATATACCTACCCATCCACCTTTGCTCTTGAACCTTGCACTTAACT 3392
Qy 4472 CGACCTCTACATTTTATGTTTATCTCTAGTATTAATCTTTTGAACCAAAAAATTTGAGT 4531
Db 3393 CGACCTCTACATTTTATGTTTATCTCTAGTATTAATCTTTTGAACCAAAAAATTTGAGT 3452
Qy 4532 AAGAACCTATTATAGAGTGAATCGAAACCAATACGAAATGTAAACATTTCTTATACGTA 4591
Db 3453 AAGAACCTATTATAGAGTGAATCGAAACCAATACGAAATGTAAACATTTCTTATACGTA 3512
Qy 4592 GTATATAGACAAAAATAGAAACACCGTTTCATTAATTTTCTGACCAATGAAGATCATCA 4651
Db 3513 GTATATAGACAAAAATAGAAACACCGTTTCATTAATTTTCTGACCAATGAAGATCATCA 3572
Qy 4652 ACCCTATCACTTTCTGTTTCAAAAGTATGCGCAATCCACATCGGTATAGAAATTAATCGG 4711
Db 3573 ACCCTATCACTTTCTGTTTCAAAAGTATGCGCAATCCACATCGGTATAGAAATTAATCGG 3632
Qy 4712 GGATGCCCTTTATCTTGA AAAATGCAACCCGACGCTTCGCTAGTAATCAGTAACGCGGGA 4771
Db 3633 GGATGCCCTTTATCTTGA AAAATGCAACCCGACGCTTCGCTAGTAATCAGTAACGCGGGA 3692
Qy 4772 AGTGGAGTCAGGCTTTTATGGAAGAGAAAAATAGACACCAAGTAGCCTTCTCTTAAC 4831
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Qy 4832 CTTTAAACGACCTACAGTGC AAAAGTTATCAAGAGCTGCATTTATAGAGCGCAAAAGGA 4891
Db 3753 CTTTAAACGACCTACAGTGC AAAAGTTATCAAGAGCTGCATTTATAGAGCGCAAAAGGA 3812
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Qy 5132 TTTCTGTTTCTGTAAAAATGCACTCAGATTTCTTTGTTGTAATAATAGCGCTCTCGCGTT 5191
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Db 4173 ATGTGCGCGAAACCCCTATTTGTTTATTTTCTAAATATCAATCAATATGATATCGGCTCA 4232
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Qy 5432 ACCAGAAACGCTGTTGTAAGATGCTGAAGATCAATTTGGGTGCAAGTGGGTT 5491
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Qy 5492 ACATCGAATGAGTCTCAACAGCGGTAAAGTCTTCTGAGAGTTTTCGCCCGCAAGAGCTT 5551
Db 4413 ACATCGAATGAGTCTCAACAGCGGTAAAGTCTTCTGAGAGTTTTCGCCCGCAAGAGCTT 4472
Qy 5552 TTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTCGCGGTATTTATCCCGTATTGACG 5611
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Qy 5732 CCATAACCATGAGTGATTAACATCTGCGCCAACTTTACTCTGACAAACGATCGAGGACCGA 5791
Db 4653 CCATAACCATGAGTGATTAACATCTGCGCCAACTTTACTCTGACAAACGATCGAGGACCGA 4712
Qy 5792 AGGAGCTAACCGCTTTTTCGCAACATGGGGATCATGTAACCTCGCTTTGATCGTTGGG 5851
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Qy 5852 AACCGAGCTGAATGAAGCCATACCAACGAGCGGTGACACCAAGTCTGCTGATGACAA 5911
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Qy 5912 TGGCAACACGTTGCGCAAACTATTAACTGGCGAACTACTTACTCTAGCTTTCCCGCAAC 5971
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Qy 5972 AATTAAATAGATGGAGCGGATAAAGTTTCAGGAACCACTTCTGCGCTCGGCCCTTC 6031
Db 4893 AATTAAATAGATGGAGCGGATAAAGTTTCAGGAACCACTTCTGCGCTCGGCCCTTC 4952
Qy 6032 CGGCTGGCTGTTTATTTGCTGATAAATCTGAGCCGCTGAGCGGTCTCGCGGTATCA 6091
Db 4953 CGGCTGGCTGTTTATTTGCTGATAAATCTGAGCCGCTGAGCGGTCTCGCGGTATCA 5012
Qy 6092 TTCAGCACTGGGCGCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACACGAGGGA 6151
Db 5013 TTCAGCACTGGGCGCAGATGGTAAGCCCTCCCGTATCGTAGTTATCTACACGAGGGA 5072

QY 6152 GTGAGCACTATGAGTGAACGAAATAGACAGATCGCTGAGATAGGTGCTCACTGATTA 6211
DB 5073 GTGAGCACTATGATGAAACGAAATAGACAGATCGCTGAGATAGGTGCTCACTGATTA 5132
QY 6212 AGCATTTGTAAGTGTGACAGCAAGTTTACTCATATATATCTTATGATTTAAACCTTC 6271
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QY 6272 ATTTTAAATTTAAAGGATCTAGGTGAAGATCTTTTGTAAATCTCATAGCAAAATCC 6331
DB 5193 ATTTTAAATTTAAAGGATCTAGGTGAAGATCTTTTGTAAATCTCATAGCAAAATCC 5252
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QY 6452 CAGCGGTGTTTGTTCGCGGATCAAGAGCTACCAACTCTTTTCCGAGGTAAGTGGCT 6511
DB 5373 CAGCGGTGTTTGTTCGCGGATCAAGAGCTACCAACTCTTTTCCGAGGTAAGTGGCT 5432
QY 6512 TCAGCAGAGCGCAGATACCAAACTACTGCTCTTCTAGTGTAGCGGTAGTTAGGCCACCACT 6571
DB 5433 TCAGCAGAGCGCAGATACCAAACTACTGCTCTTCTAGTGTAGCGGTAGTTAGGCCACCACT 5492
QY 6572 TCAAGAACTCTGTAGCAGCGCTACATACCTGCTCTGCTCTTCTGTTTACCAAGTGGCTG 6631
DB 5493 TCAAGAACTCTGTAGCAGCGCTACATACCTGCTCTGCTCTTCTGTTTACCAAGTGGCTG 5552
QY 6632 CTGCGAGTGGCGATTAAGTGTCTTCTTACCGGGTGGACTCAAGACGATAGTTACCGGATA 6691
DB 5553 CTGCGAGTGGCGATTAAGTGTCTTCTTACCGGGTGGACTCAAGACGATAGTTACCGGATA 5612
QY 6692 AGCGCAGCGGTGCGGGCTGAACGGGGGTTCGTGCACACAGCCGAGCTTGGAGCGAACA 6751
DB 5613 AGCGCAGCGGTGCGGGCTGAACGGGGGTTCGTGCACACAGCCGAGCTTGGAGCGAACA 5672
QY 6752 CTTACACCGAATGAGATACCTTACAGCTGAGCTATGAGAAGCGCCACCGTTCCTCCGAAG 6811
DB 5673 CTTACACCGAATGAGATACCTTACAGCTGAGCTATGAGAAGCGCCACCGTTCCTCCGAAG 5732
QY 6812 CGAGAAAGCGCAGAGTATCCGTAAGCGCAGGTCGGAACAGGAGAGCGCAGAGGG 6871
DB 5733 GGAGAAAGCGCAGAGTATCCGTAAGCGCAGGTCGGAACAGGAGAGCGCAGAGGG 5792
QY 6872 AGCTTCCAGGGGAAACGCTGATCTTTATAGTCTCTGCGGGTTTCGCCACCTCTGAC 6931
DB 5793 AGCTTCCAGGGGAAACGCTGATCTTTATAGTCTCTGCGGGTTTCGCCACCTCTGAC 5852
QY 6932 TTGAGCGTCGATTTTGTGATGCTCGTCAAGGGGGCGGAGCTATGGAATAACGCCAGCA 6991
DB 5853 TTGAGCGTCGATTTTGTGATGCTCGTCAAGGGGGCGGAGCTATGGAATAACGCCAGCA 5912
QY 6992 ACGCGGCTTTTACGTTCTGCGCTTTTCTGCGCTTTTCTGCTCATGTTCTTCTCTG 7051
DB 5913 ACGCGGCTTTTACGTTCTGCGCTTTTCTGCGCTTTTCTGCTCATGTTCTTCTCTG 5972
QY 7052 CGTTATCCCTGATTTCTGTGATACCGTATTTACCGCTTTTGTGAGTGAATGATCCGCTC 7111
DB 5973 CGTTATCCCTGATTTCTGTGATACCGTATTTACCGCTTTTGTGAGTGAATGATCCGCTC 6032
QY 7112 GCCGAGCGGAAACGACCGAGCGCAGTCAAGTGAAGAGCGGAAAGCGGAGCGCCAA 7171
DB 6033 GCCGAGCGGAAACGACCGAGCGCAGTCAAGTGAAGAGCGGAAAGCGGAGCGCCAA 6092
QY 7172 TACGCAAAACCGCTCTCCCGCGCTTCCGCGATTCATTATGAGCTGCAACCAAGT 7231
DB 6093 TACGCAAAACCGCTCTCCCGCGCTTCCGCGATTCATTATGAGCTGCAACCAAGT 6152
QY 7232 TTCCCGACTGGAAAGCGGCGAGTGAGCGCAACGCAATTAATGTGAGTTACCTCACTCATT 7291

RESULT 4
AAC87129/c

ID AAC87129 standard; DNA; 8749 BP.

XX AAC87129;

XX AC AAC87129;

XX 20-APR-2001 (first entry)

XX Nucleotide sequence of plasmid pGB1023.

XX PKD2 gene; *Caenorhabditis elegans*; CEPDK2; polycystin; ADPKD;
XX autosomal dominant polycystic kidney disease; epithelial structure;
XX kidney nephron; circular; cyclic; ss.

XX Synthetic.

XX Aequorea victoria.

XX *Caenorhabditis elegans*.

XX Unidentified.

XX Key Location/Qualifiers

FH CDS 1402..2259

FT /*tag= a

FT /note= "ampicillin resistance sequence"

FT 4243..4944

FT /*tag= b

FT /note= "trp gene"

FT 7153..7891

FT /*tag= d

FT /note= "PADH1 promoter"

FT 7891..8331

FT /*tag= c

FT /note= "GAL4 DNA binding domain"

FT 8401..87486

FT /*tag= e

FT /note= "PKD2 gene"

XX GB2351496-A.

XX 03-JAN-2001.

XX 01-JUN-2000; 2000GB-00013413.

XX 01-JUN-1999; 99GB-00012748.

XX (DEVG-) DEVGEN NV.

XX Kaletta T, Vangeel A, Bogaert T, Van De Craen M;

XX WPI; 2001-105117/12.

XX Novel nucleic acids isolated from the CEPDK2 gene of *Caenorhabditis*
XX *elegans*, used to produce transgenic organisms used to identify compounds
XX for use in the treatment of autosomal dominant polycystic kidney disease.

XX Disclosure; Fig 4; 105pp; English.

XX The present sequence represents a plasmid which was used to express the

CC PKD2 gene of *Caenorhabditis elegans* (designated CEPD2). The PKD2 protein
CC is part of the polycystin family. Defects in the PKD2 gene are
CC responsible for about 15% of autosomal dominant polycystic kidney disease
CC (ADPKD) cases. It is possible that PKD2 proteins perform a general task
CC in maintaining epithelial structure in kidney nephron tubules, especially
CC the maintenance of tubule width. Transgenic *C. elegans* comprising
CC plasmids expressing the PKD2 gene, or deletions thereof, are useful for
CC identifying compounds which may be used to treat ADPKD
XX

SQ Sequence 8749 BP; 2471 A; 1837 C; 1935 G; 2505 T; 0 U; 1 Other;

Query Match 57.4%; Score 4492.6; DB 4; Length 8749;
Best Local Similarity 87.3%; Pred. No. 0;
Matches 5104; Conservative 0; Mismatches 629; Indels 114; Gaps 12;

QY	1559	TCATGTAATAGTATGTCACGCTTACATTCAGCCCTCCGCCACATCCGCTTAACCG	1618
DB	5950	TCATGTAATAGTATGTCACGCTTACATTCAGCCCTCCGCCACATCCGCTTAACCG	5891
QY	1619	AAAGGAAGGAGTTAGACAACTGAAGTCTAGTCCCTATTTATTTTATAGTTATGT	1678
DB	5890	AAAGGAAGGAGTTAGACAACTGAAGTCTAGTCCCTATTTATTTTATAGTTATGT	5831
QY	1679	TAGTATTAAGAACTGTTATTTATTTTCAATTTTCTTTTCTTTTCTGTACAGACGGTGT	1738
DB	5830	TAGTATTAAGAACTGTTATTTATTTTCAATTTTCTTTTCTTTTCTGTACAGACGGTGT	5771
QY	1739	ACGATGTAACTATTAATCAAAACCTTGTCTGAGAGGTTTGGGACGCTCGAAGGCTT	1798
DB	5770	ACGATGTAACTATTAATCAAAACCTTGTCTGAGAGGTTTGGGACGCTCGAAGGCTT	5711
QY	1799	TAAATTCGCGCCGCTACCCAAATTCGCCCTATAGTGTAGTGTATTAACGCGGCTCACTGGC	1858
DB	5710	TAAATTCGCGCCGCTACCCAAATTCGCCCTATAGTGTAGTGTATTAACGCGGCTCACTGGC	5661
QY	1859	CGTCGTTTACACGCTGCTGACCTGGGAAACCTTGGGTTTACCAACTTAATCGCTTGC	1918
DB	5660	CGTCGTTTACACGCTGCTGACCTGGGAAACCTTGGGTTTACCAACTTAATCGCTTGC	5601
QY	1919	AGCACATCCCTTTCGCCAGCTGGGCTAATAGCGAAGGCGCGACCGATCGCCCTTC	1978
DB	5600	AGCACATCCCTTTCGCCAGCTGGGCTAATAGCGAAGGCGCGACCGATCGCCCTTC	5541
QY	1979	CCAAAGTTGCGCAGCTGAATCGCGAATCGCGCAGCGCCCTGTAGCGGCGCATTAAG	2038
DB	5540	CCAAAGTTGCGCAGCTGAATCGCGAATCGCGCAGCGCCCTGTAGCGGCGCATTAAG	5481
QY	2039	CGCGGCGGCTGGTGTAGCGGCGAGCGGTACCGCTACACTTGCAGCGCCCTAGCGCC	2098
DB	5480	CGCGGCGGCTGGTGTAGCGGCGAGCGGTACCGCTACACTTGCAGCGCCCTAGCGCC	5421
QY	2099	CGCTCCTTTTCGCTTCTTCCCTTCTTCGCGACGTTTCGCGGCTTTCCCGTCAAGC	2158
DB	5420	CGCTCCTTTTCGCTTCTTCCCTTCTTCGCGACGTTTCGCGGCTTTCCCGTCAAGC	5361
QY	2159	TCTAAATCGGGGCTCCCTTTAGGGTTCCGATTAGTGTCTTACGCGACCTCGACCCCAA	2218
DB	5360	TCTAAATCGGGGCTCCCTTTAGGGTTCCGATTAGTGTCTTACGCGACCTCGACCCCAA	5301
QY	2219	AAACTTGTAGGGTGAATGGTTTCACTAGTGGGCAATCGCCCTGATAGACGGTTTTCG	2278
DB	5300	AAACTTGTAGGGTGAATGGTTTCACTAGTGGGCAATCGCCCTGATAGACGGTTTTCG	5241
QY	2279	CCCTTTGACGTTGGAGTCCAGCTTCTTTATAGTGGACTCTTCTCCAACTCGAACCAAC	2338
DB	5240	CCCTTTGACGTTGGAGTCCAGCTTCTTTATAGTGGACTCTTCTCCAACTCGAACCAAC	5181
QY	2339	ACTCAACCCCTATCTCGCTCTATTCTTTTGTATTTAAGGGAATTTGCGGCTTA	2398
DB	5180	ACTCAACCCCTATCTCGCTCTATTCTTTTGTATTTAAGGGAATTTGCGGCTTA	5121
QY	2399	TTGGTTAAATAAGCTGATTTTAAACAAATTTTAAACGGAATTTTAAACAAATTTAAC	2458

DB	5120	TTGGTTAAATAAGCTGATTTTAAACAAATTTTAAACGGAATTTTAAACAAATTTAAC	5061
QY	2459	GTTTACAAATTTCTGATGCGGTATTTTCTCTTACGCACTCTGCGGTATTTACACCGC	2518
DB	5060	GTTTACAAATTTCTGATGCGGTATTTTCTCTTACGCACTCTGCGGTATTTACACCGC	5001
QY	2519	ATAGGTAATACTGATATATAATTAATTAAGAGTCTTAATTTGAGTTTATGATACATGC	2578
DB	5000	ATAGATCGGCAAGTGCACAACTACTTAAATAAATACTACTCAGTAATAACCTATTTC	4941
QY	2579	ATTTACTTATATACAGTTTATTTAGTTTCTGCGCGCATCTTCTCAAAATATGTTCCCA	2638
DB	4940	TTAGCAATTTTTCAGCAATTTGCTATTTTGTAGAGTCTTTTACACCAATTTGTTCCACA	4881
QY	2639	GCCTGCTTTTCTGTAACGTTTCAACCTCTACCTTAGCATCCCTTCCCTTTTCAAAATAGTCC	2698
DB	4880	CTTCCGCTTACATCAAC-----ACCAATAACGC 4853	
QY	2699	TCCTTCAACAAATAATATGTTCAGATCCTGTAGAGACCAATCATCCAGGTTCTTATCTG	2758
DB	4852	CATTTAATCTAAGCGCATCACCAATTTTCTGCGCTAGTCCACAGCTAACATAAAT	4793
QY	2759	TTGACCCCAATGCTCTCCCTTGTCTATCAACCCACACCGGGTGTATATCAACCAATC	2818
DB	4792	GTAAGCTTTTGGGGCTCTCTTGCCTT-----CCAACCCAGTCAAGAAATCGAGTTCCAAATC	4738
QY	2819	GTAACCTTCAATCTTCTCCACCCATGCTCTTTGAGCAATAAAGCCGATACAAATCTTT	2878
DB	4737	CANAAGTTCACTGTCCAC-----CTGCTTCTGATCAACAGGGAATAACGNAATG	4684
QY	2879	GTCGCTCTTGGCAATGTCAACAGTACCTTGTATATTTCTCCAGTAGTAGAGGAGCCCTT	2938
DB	4683	AGGTTTCTGTAAGCTGCATGAGTAGTATTTGTCAGTCTTTTGGAAATACGAGTCTTTT	4624
QY	2939	GCATGACAATTTGCTTAACATCAAAAGGCTCTAGGTTCTTTGTTACTTCTTCTCGCGC	2998
DB	4623	-----AATAACTGGCAACCGAGGAATCTTTGTATTTTGGCCAGCATCATCTCCA	4572
QY	2999	CTGCTTCAAAACCGCTAACCAATACCTGGGCCACACACCGGTGCAATCGTAATGTCTGC	3058
DB	4571	TGCAGT-----TGCAGTATCAATGCGTAAATCATTTGACCAAGCCAAACNTCTC	4519
QY	3059	CAATCTGCTATTTCTGTATACACCCGCGAGTACTGCAATTTGATGTATTAACAATGTC	3118
DB	4518	CTTAGGTTGATACGAAACACGCAACCAAGTATTTTGGAGTGCCTGAACTATTTTATA	4459
QY	3119	AGCAAAATTTCTGCTCTTGGAGAGTAAATAATTTGTTACTTTGGCGGATAATGCTTTAGCGG	3178
DB	4458	TG-----CTTTTCAAGACTTGAAATTTTCTTGTCAATAACCGGGTCAATTTGT	4411
QY	3179	CTTAACTGTGCCCTCCATCGAAATAATCAGTCAAGATATCCACATGTGTTTTAGTAAACA	3238
DB	4410	TCTCTTTCTATTGGGCGACATATATATACCCAGCAAGTACGATCGAATCTAG--AGCA	4353
QY	3239	AATTTTGGACCTTAATGCTTCAACTCCAGTAAATCTTGGTGGTAC--GAACATCCA	3297
DB	4352	CATTTCTGGGCTCTGCTCTGCAAGCGCAAACTTTTCAACATGGACCAAGAACCT	4293
QY	3298	ATGAACACACAAAGTTTGTGCTTTTCTGTCATGATATTAATAGTTGGGACCAACAG	3357
DB	4292	GTGAAATTAATAACAGACATATCTCCAAAGCTGCTTTTGTGTGTTAATACAGTATCTAC	4233
QY	3358	GACTAGGATGAGTAGCAGCAGCTTCTTATATGTCAGCTTTCCGACATGATTTATCTCGTT	3417
DB	4232	GTGCTCAATAGTACCAATGCTCTCTCTTGGCCCTCTCC-----TTTCTTTT	4184
QY	3418	TCTGCGAGTTTGTGTCAGTTGGGTGAAGAAATCTGGGCAATTTTCAATGTTTCTT	3477
DB	4183	TTTCGACCGAAATTAATTTCTTAATCGGCAAAAAAGAAAGCTCCGGA-----T	4136
QY	3478	CAACACTACATATGCTATATATACCAATCTAAGTCTGTGCTCTTCTCTCTCTCTCT	3537
DB	4135	CAAGATTGTACGTAAGGTGACAGCTATTTTTCATAAAGAAATATCTTCCACTACTGCCA	4076

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4075 TCTGGGTCATAACTGCGAAAGTACATATATTA-----CGATGCTGTCTATTAAAT 4024
3598 AAAAAAATAATGATGAATTTGAATTTGAAAGCTGTGTATGTGTGTCACCTCTCAGTACAATCT 3657
4023 GCTTCTATATATATATATAGTATGTGCTGTATGTCATGTGTCACCTCTCAGTACAATCT 3964
3658 GCTCTGATCCGCATAGTTAAGCAGCCCGACACCCCGCCAAACACCCGCTGACGGCGCT 3717
3963 GCTCTGATCCGCATAGTTAAGCAGCCCGACACCCCGCCAAACACCCGCTGACGGCGCT 3904
3718 GACGGGCTTGTCTGCTCCCGCATCCGCTTACAGCAAGCTGTGACCGCTCTCCGGAGCT 3777
3903 GACGGGCTTGTCTGCTCCCGCATCCGCTTACAGCAAGCTGTGACCGCTCTCCGGAGCT 3844
3778 GCATGTGTCAGAGGTTTTTACCCTCATCACCGAAACCGCGAGACGAAAGGCGCTCTGTA 3837
3843 GCATGTGTCAGAGGTTTTTACCCTCATCACCGAAACCGCGAGACGAAAGGCGCTCTGTA 3784
3838 TAGGCTATTTTATAGGTTAATGTTCATGATAAATAATGGTTTCTTAGTATGATCAATAT 3897
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3898 CAAAGGAATGATAGCATTTGAAGGATGAGCTTAATCCCAATTTGAGAGTGGCAGCATATAG 3957
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3958 AACAGCTAAAGGTTAGTGTGAAGGAAGCATACGATACCCCGCATGGAATGGGTAATAT 4017
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4198 CGCTGTTTTTCGGAACCGTTTGAAGTTCTTATTCGGAAGTCTCTATCTAGAAAGTA 4257
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4558 AACATACGAAATGTAACATTTTCTTATAGCTAGTATATAGAGCAAAATAGAAAGAAC 4617
3063 AACATACGAAATGTAACATTTTCTTATAGCTAGTATATAGAGCAAAATAGAAAGAAC 3004

4618 CGTTCAATAATTTTCTGACCAATGAAGAAATCATCAACGCTATCATCTTTCTGTTTCAAAAGT 4677
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2523 TTTGTTGAAAAATAGCGCTCTCGGGATGCAATTTTGTGTTTAAATAAAGTAATGAGCTCAG 2464
5158 GATTTCTTTGTTGAAAAATAGCGCTCTCGGGATGCAATTTTGTGTTTAAATAAAGTAATGAG 5217
2463 GATTTCTTTGTTGAAAAATAGCGCTCTCGGGATGCAATTTTGTGTTTAAATAAAGTAATGAG 2404
5218 CAGATGCTTCGTTGAGTGGCACTTTTTCGCGGAAATGTCGCGGAAACCCCTATTTGTTTAA 5277
2403 CAGATGCTTCGTTGAGTGGCACTTTTTCGCGGAAATGTCGCGGAAACCCCTATTTGTTTAA 2344
5278 TTTTCTTAAATACATCTCAAAATATGTCCTGCTATGAGCAATAACCTGATAAATGCTT 5337
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5338 CAATAATATTGAAAAAGGAGATGAGTATCAACATTTCCGTTGCTGCTTATTTCC 5397
2283 CAATAATATTGAAAAAGGAGATGAGTATCAACATTTCCGTTGCTGCTTATTTCC 2224
5398 TTTTCTGCGGATTTTTCGCTTCTTTCCTCACCAGAAACCGCTGTTGAAAGTAAAA 5457
2223 TTTTCTGCGGATTTTTCGCTTCTTTCCTCACCAGAAACCGCTGTTGAAAGTAAAA 2164
5458 GATCTGAAGATCAGTTGGGTGACAGTGGTTCATCGAATCGATCTCAACAGCGGT 5517
2163 GATCTGAAGATCAGTTGGGTGACAGTGGTTCATCGAATCGATCTCAACAGCGGT 2104
5518 AAGATCTCTGAGAGTTTTTCGCCCCGAAAGAAAGTTCCTCAATGATGAGCACTTTTAAAGTT 5577
2103 AAGATCTCTGAGAGTTTTTCGCCCCGAAAGAAAGTTCCTCAATGATGAGCACTTTTAAAGTT 2044
5578 CTGCTATGTCGCGGATTTTATTCGCTATTTGACGCGGCGCAAGCAACTCGTCCGCGC 5637
2043 CTGCTATGTCGCGGATTTTATTCGCTATTTGACGCGGCGCAAGCAACTCGTCCGCGC 1984
5638 ATACATCTTCTCAGAAATGACTTGTGTTGAGTACTCACCAGTCAAGAAAGCATCTTACG 5697
1983 ATACATCTTCTCAGAAATGACTTGTGTTGAGTACTCACCAGTCAAGAAAGCATCTTACG 1924
5698 GATGGCATGACAGTAAGAGAAATTTATGACAGTCTGCCATPAACCATGAGTGAACACTGCG 5757


```
FT FT /*tag= d
FT FT /note= "GAL4 binding domain"
FT CDS 8394..8941
FT FT /*tag= e
FT FT /note= "PKD2 gene"
XX GB2351496-A.
XX 03-JAN-2001.
XX
XX 01-JUN-2000; 2000GB-00013413.
XX
XX 01-JUN-1999; 99GB-00012748.
XX
XX (DEVG-) DEVGEN NV.
XX
XX Kaletta T, Vangeel A, Bogaert T, Van De Craen M;
XX WPI; 2001-105117/12.
XX
XX Novel nucleic acids isolated from the CBPD2 gene of Caenorhabditis
XX elegans, used to produce transgenic organisms used to identify compounds
XX for use in the treatment of autosomal dominant polycystic kidney disease.
XX
XX Disclosure; Fig 6; 105pp; English.
XX
XX The present sequence represents a plasmid which was used to express the
XX PKD2 gene of Caenorhabditis elegans (designated CBPD2). The PKD2 protein
XX is part of the polycystin family. Defects in the PKD2 gene are
XX responsible for about 15% of autosomal dominant polycystic kidney disease
XX (ADPKD) cases. It is possible that PKD2 proteins perform a general task
XX in maintaining epithelial structure in kidney nephron tubules, especially
XX the maintenance of tubule width. Transgenic C. elegans comprising
XX plasmids expressing the PKD2 gene, or deletions thereof, are useful for
XX identifying compounds which may be used to treat ADPKD
XX
XX Sequence 8941 BP; 2544 A; 1854 C; 2009 G; 2533 T; 0 U; 1 Other;
XX
XX Query Match 57.4%; Score 4492.6; DB 4; Length 8941;
XX Best Local Similarity 87.3%; Pred. No. 0;
XX Matches 5104; Conservative 0; Mismatches 629; Indels 114; Gaps 12;
XX
XX 1559 TCATGTAATTAGTATGTCACGCTTACATTCACGCGCTCCGCCACACATCCGCTCTAAACCG 1618
XX 5950 TCATGTAATTAGTATGTCACGCTTACATTCACGCGCTCCGCCACACATCCGCTCTAAACCG 5891
XX
XX 1619 AAAAGAGAGGAGTTAGACAACTGAACTGAGTCTAGTCCCTATTTATTTTATAGTTATGT 1678
XX 5890 AAAAGAGAGGAGTTAGACAACTGAACTGAGTCTAGTCCCTATTTATTTTATAGTTATGT 5831
XX
XX 1679 TAGTATTAGAACGTTATTTATTTATTTTCAAAATTTTCTTTTCTGTACAGACGCGTGT 1738
XX 5830 TAGTATTAGAACGTTATTTATTTTCAAAATTTTCTTTTCTGTACAGACGCGTGT 5771
XX
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XX 5770 AGCATGTAAACATTATCTGAAACCTTGTCTGAGAAGGTTTGGGACGCTCGAAGGCTT 5711
XX
XX 1799 TAAATTGGCGCGGTACCCAAATTCGCCCTA TAGTGAGTGTGATTTACGGCGGCTCACTGGC 1858
XX 5710 TAAATTG-----CAAAGCTCGGATCTCGAGCTCGGAAAGCTTGGACGACTGGC 5661
XX
XX 1859 CGTCGTTTACAACTGCTGAGTGGGAAACCTTGGCGGTACCCAACTTAATTCGCTTGC 1918
XX 5660 CGTCGTTTACAACTGCTGAGTGGGAAACCTTGGCGGTACCCAACTTAATTCGCTTGC 5601
XX
XX 1919 AGCACATCCCCCTTTCCGCGAGTGGCGTAATAGCGAAGAGCGCCGACCGATCGCCCTTC 1978
XX 5600 AGCACATCCCCCTTTCCGCGAGTGGCGTAATAGCGAAGAGCGCCGACCGATCGCCCTTC 5541
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XX 1979 CCAACAGTTGCGCAGCTGAATGGGGAATGGCGCAACCGGCGCTGTAGCGCGCATTAAG 2038
XX 5540 CCAACAGTTGCGCAGCTGAATGGGGAATGGCGCAACCGGCGCTGTAGCGCGCATTAAG 5481
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QY 3179 CTTAACTGTGCCCTCCATGGAATAATCAGTCAAGATATCCACATGTGTTTTAGTAAACA 3238
Db 4410 TCTCTTCTATTGGGCACATATATATACCAGCAAGTCAGCATCGGAATCTAG--AGCA 4353
QY 3239 AATTTTGGGACCTAATGCTTTCACTAATCTCAGTAAATTCCTTGGTGGTAC-GAACAATCCA 3297
Db 4352 CATTTCTGGCCCTCTGTGCTCTGCAAGCGCAAACTTTTACCATAATGGACCAAGTACCT 4293
QY 3298 ATGAAGCAACAAGTTGTTGTTTCTTTCGTGCGATGATATTAATATAGCTTGGCAGCAACAG 3357
Db 4292 GTGAATTAATAACAGACATACTCCAGCTGCGCTTTGTGTGCTTAATACAGTATCTCAC 4233
QY 3358 GACTAGGATGAGTACAGCAGCTTCTTATATATGATGATCTTCGACATGATTTATCTCGTT 3417
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QY 3418 TCCTGCAGGTTTGTGCTGTGCAGTTGGGTAAAGAACTACTGGGCAATTTTCATGTTCTT 3477
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QY 3478 CAACACTACATATGCGTATATATACCAATCTAAGTCTGTGCTCTCTCTTCTGTTCTTCT 3537
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QY 3538 TCTGTTCCGAGATTAACCGAATCAAAAATTTCAAAGAACCCGAAATCAAAAAGAAAT 3597
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QY 3598 AAAAAAATAATGATGAATTTGAATTTGAAAGCTGTGTATGTTGTCACCTCTCAGTACAATCT 3657
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QY 3658 GCTCTGATGCGGATAGTTAAGCAGCCCGCAGACCCCGCAACACCCGCTGAGCGCCCT 3717
Db 3963 GCTCTGATGCGGATAGTTAAGCAGCCCGCAGACCCCGCAACACCCGCTGAGCGCCCT 3904
QY 3718 GACGGGCTCTGCTCCCGCATCCGCTTACAGCAAGCTGTGACCGCTCTCCGGGAGCT 3777
Db 3903 GACGGGCTTGTCTGCTCCCGCATCCGCTTACAGCAAGCTGTGACCGCTCTCCGGGAGCT 3844
QY 3778 GCATGTGTACAGAGTTTTCACCGTCATCACCGAAAACCGCGAGACGAAAGGGCTCGTGA 3837
Db 3843 GCATGTGTACAGAGTTTTCACCGTCATCACCGAAAACCGCGAGACGAAAGGGCTCGTGA 3784
QY 3838 TAGCCCTATTTTATAGGTTAATGTCAATGATAATATGTTTCTTAGTATGATCCAAAT 3897
Db 3783 TAGCCCTATTTTATAGGTTAATGTCAATGATAATATGTTTCTTAATATGATCCAAAT 3724
QY 3898 CAAAGGAATGATAGCAATTCAGGATGAGACTAATCCAATTTGAGGAGTGGCAGCATATAG 3957
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QY 4138 ATATAGTGGCAGGTGAACAGTGAAGTGTATGTGCGCAGCTCCGCTTGCATTTTTCGGAAG 4197
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Db 3423 CGCTCGTTTTTCGGAACCGCTTTTGAAGTTCCTATTTCCGAAGTTCCTATTTCTTAGAAAGTA 3364
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Db 3363 TAGGAACTTTCAGAGCGCTTTTGAATAACCAAGCGCTCTGGAAGCGCACTTTCAAAAAAC 3304
QY 4318 CAAAAACGCAACCGGACTGTAAAGAGCTACTAAATAATTCGAATAACCGCTTCCACAAACA 4377
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QY 5218 CAGATGCTTCGTTTTCAGGTGCACTTTTTCGCGGGAATGTGCGCGGAACCCCTATTTGTTTA 5277
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Db 2343 TTTTCTAAATCAATTCAAATATGATATCGCTCATGAGCAATAACCCGTGATAAATGCTT 2284
QY 5338 CAATAATATTGAAAGAGAGATGATGAGTATCAACATTTCCGGTGTCCCTTATTCCC 5397
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QY 5518 AAGATCCCTTGAGAGTTTTCGCCCGCAAGAACGTTTCCAAATGATGAGCACTTTTAAAGTT 5577
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QY 5578 CTGCTATGTGGCGCGGTATTATCCCGTATTGACGCGCGGCAAGAGCAACTCGGTCCGCGC 5637
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QY 6298 AAGATCCCTTTTGAATATCTCATGACCAAAATCCCTTAAACGTCAGTCTTCCCTGCACTGA 6357
Db 1323 AAGATCCCTTTTGAATATCTCATGACCAAAATCCCTTAAACGTCAGTCTTCCCTGCACTGA 1264
QY 6358 GGTGACAGCCCGTGAAGAAAGATCAAGATCTTCTTGAGATCCCTTTTCTGCGCGTA 6417
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RESULT 6
AAC90958/c
ID AAC90958 standard; cdna; 9700 BP.

QY 6418 ATCTGCTGCTTGCAAAACAAAAAACACACCGCTACACCGTGGTGTGTTGTTGCGCGATCAA 6477
Db 1203 ATCTGCTGCTTGCAAAACAAAAAACACACCGCTACACCGTGGTGTGTTGTTGCGCGATCAA 1144
QY 6478 GAGTACCAACTCTTTTCCGAAGGTAACTGGCTTTCAGCAGAGCGCAGATACCAAAATCT 6537
Db 1143 GAGTACCAACTCTTTTCCGAAGGTAACTGGCTTTCAGCAGAGCGCAGATACCAAAATCT 1084
QY 6538 GTCCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCAGCGCTACA 6597
Db 1083 GTCCCTTCTAGTGTAGCCGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCAGCGCTACA 1024
QY 6598 TACCTCCCTCTGCTAACTCTGTTTACCACTGCTGCTGCACTGGCAGTAAAGTCTGTCTT 6657
Db 1023 TACCTCCCTCTGCTAACTCTGTTTACCACTGCTGCTGCACTGGCAGTAAAGTCTGTCTT 964
QY 6658 ACCGGTGTGAATCTCAAGACGATAGTTACCGATTAAGCGCAGCGGTCCGGGTGAACGGGG 6717
Db 963 ACCGGTGTGAATCTCAAGACGATAGTTACCGATTAAGCGCAGCGGTCCGGGTGAACGGGG 904
QY 6718 GGTTCGTGCACACAGCCCGAGCTTGGAGGGAACCTTACACCGAACTGAGATACCTACAG 6777
Db 903 GGTTCGTGCACACAGCCCGAGCTTGGAGGGAACCTTACACCGAACTGAGATACCTACAG 844
QY 6778 CGTGAGCTATGAGAAAGCGCCACGCTTCCGAAAGGAGAAAGGCGACAGGTATCCGGTA 6837
Db 843 CGTGAGCTATGAGAAAGCGCCACGCTTCCGAAAGGAGAAAGGCGACAGGTATCCGGTA 784
QY 6838 AGCGCAGGCTCGGAAACAGGAGCGCAAGAGGAGCTTCCAGGGGGAAACGCCCTGGTAT 6897
Db 783 AGCGCAGGCTCGGAAACAGGAGCGCAAGAGGAGCTTCCAGGGGGAAACGCCCTGGTAT 724
QY 6898 CTTTATAGTCTGCTCGGTTTCGCCACTCTGACTGAGCGTCAATTTTGTGATGCTCG 6957
Db 723 CTTTATAGTCTGCTCGGTTTCGCCACTCTGACTGAGCGTCAATTTTGTGATGCTCG 664
QY 6958 TCAGGGGGCGGAGCTTATGGAATAACGCGCAACGCGGCTTTTACGGTTCCTGGCC 7017
Db 663 TCAGGGGGCGGAGCTTATGGAATAACGCGCAACGCGGCTTTTACGGTTCCTGGCC 604
QY 7018 TTTTGTGCGCTTTTGTCTACATGTTCTTCTCCTGCTTATCCCTGATTTCTGTGATTAAC 7077
Db 603 TTTTGTGCGCTTTTGTCTACATGTTCTTCTCCTGCTTATCCCTGATTTCTGTGATTAAC 544
QY 7078 GGTATTAACCGCTTTGAGTGTGCTGATACCGCTCGCGCAGCGCAACGACGAGCGCAGC 7137
Db 543 GGTATTAACCGCTTTGAGTGTGCTGATACCGCTCGCGCAGCGCAACGACGAGCGCAGC 484
QY 7138 GAGTCAGTGTAGCGAGGAAGCGGAAGAGCGCCCAATACGCAAAACCGCTTCTCCCGCGCT 7197
Db 483 GAGTCAGTGTAGCGAGGAAGCGGAAGAGCGCCCAATACGCAAAACCGCTTCTCCCGCGCT 424
QY 7198 TGGCCGATTCATTAATCAGCTGCGACGAGTGTTCCTGATTCGGAACGCGGCGAGTAG 7257
Db 423 TGGCCGATTCATTAATCAGCTGCGACGAGTGTTCCTGATTCGGAACGCGGCGAGTAG 364
QY 7258 GCGAACCAATTAATGTGAGTTACTCTACTATTAGGCAACCCAGGCTTACACTTTATG 7317
Db 363 GCGAACCAATTAATGTGAGTTACTCTACTATTAGGCAACCCAGGCTTACACTTTATG 304
QY 7318 CTTCCGCTCTCTATGTTGTGGAAATGTGAGCGGATAACAAATTTTCAACAGGAACAGC 7377
Db 303 CTTCCGCTCTCTATGTTGTGGAAATGTGAGCGGATAACAAATTTTCAACAGGAACAGC 244
QY 7378 TATGACCATGATTAACGCAAGCGCGCA 7404
Db 243 TATGACCATGATTAACGCAAGCGCTTGCA 217

XX AAC90958;
 XX DT 19-MAR-2001 (first entry)
 XX DE Plasmid pGC1037 nucleotide sequence SEQ ID NO:91.
 XX KW Human; Caenorhabditis elegans; UNC-5; splice variant; nematode worm;
 XX KW protein-protein interaction; identification; ss.
 XX OS Synthetic.
 XX PN WO200073328-A2.
 XX PD 07-DEC-2000.
 XX PF 02-JUN-2000; 2000WO-EP005108.
 XX PR 01-JUN-1999; 99GB-00012755.
 XX (DEVG-) DEVGEN NV.
 XX PA Van Criekeinge W, Roelens I, Bogaert T, Verwaerde P;
 XX PI WPI; 2001-016508/02.
 XX DR Three variants of human unc-5C cDNAs (unc-5Cb, unc-5Cc and unc-5C8) and a
 XX PT human unc-5HS1 cDNA, useful in yeast two hybrid experiments for
 XX PT identifying unknown human cDNAs which encode proteins that interact with
 XX PT the human unc-5C protein.
 XX PS Example 4; Page 228-230; 246pp; English.
 XX CC The present invention describes 3 variants of human unc-5C cDNAs (unc-
 CC 5Cb, unc-5Cc and unc-5C8) which correspond to alternatively spliced unc-
 CC 5C transcripts, and a human unc-5HS1 cDNA which shares homology with the
 CC Rattus norvegicus unc-5HS1 cDNA. Also described are assays based on
 CC protein-protein-interactions between the unc-5 protein and a variety of
 CC different interacting proteins. The unc-5C variant cDNAs and unc-5HS1
 CC cDNA are useful in methods for identifying compounds which reduce or
 CC inhibit the lethal phenotype associated with the expression of the unc-5
 CC death domain in yeast. They are also useful in yeast two hybrid
 CC experiments for identifying unknown human cDNAs which encode proteins
 CC that interact with the human unc-5C protein. AAC90914 to AAC90971 and
 CC AAB50646 to AAB50693 represent sequences used in the exemplification of
 CC the present invention
 XX Sequence 9700 BP; 2604 A; 2193 C; 2236 G; 2666 T; 0 U; 1 Other;
 XX
 Query Match 57.4%; Score 4492.6; DB 4; Length 9700;
 Best Local Similarity 87.3%; Pred. No. 0;
 Matches 5104; Conservative 0; Mismatches 629; Indels 114; Gaps 12;
 QY 1559 TCATGTAATTAGTATGTCACGCTTACATTCACGCGCTCCGCCACATCGGCTCTAACCG 1618
 DB 7263 TCATGTAATTAGTATGTCACGCTTACATTCACGCGCTCCGCCACATCGGCTCTAACCG 7204
 QY 1619 AAAAGGAAGGAGTTAGACAACTGAACTCTAGTCTCCCTATTTATTTTATAGTTATGT 1678
 DB 7203 AAAAGGAAGGAGTTAGACAACTGAACTCTAGTCTCCCTATTTATTTTATAGTTATGT 7144
 QY 1679 TAGTATTAGAAAGCTTATTTATTTTCAAAATTTTCTTTTCTGTACAGACGGGTGT 1738
 DB 7143 TAGTATTAGAAAGCTTATTTATTTTCAAAATTTTCTTTTCTGTACAGACGGGTGT 7084
 QY 1739 ACCATGTATACATTAATCTGAAACCTTGTCTGAGAGGTTTGGGACCGCTCGAAGGCTT 1798
 DB 7083 ACGCATGTATACATTAATCTGAAACCTTGTCTGAGAGGTTTGGGACCGCTCGAAGGCTT 7024
 QY 1799 TAATTTGGCGCGGTACCCCAATTCGCCCTATAGTGTATGATTTACGCGGCTCACTGGC 1858
 DB 7023 TAATTTG-----CAAAGCTCGGGATCTCGAGCTCGGAAAGCTTGGACGACTGGC 6974

QY 1859 CGTCGTTTACAAACGTCGTGACCTGGGAAACCCCTGGCGTTACCCAACTTAATCGCCTTGC 1918
 DB 6973 CGTCGTTTACAAACGTCGTGACCTGGGAAACCCCTGGCGTTACCCAACTTAATCGCCTTGC 6914
 QY 1919 AGCACATCCCTTTTCGCCAGCTGGCGTAATAGCGAAGGCGCGCACCGATCGCCCTTC 1978
 DB 6913 AGCACATCCCTTTTCGCCAGCTGGCGTAATAGCGAAGGCGCGCACCGATCGCCCTTC 6854
 QY 1979 CCAACAGTTTGGCAGCTGAAATGGCGAATGGCGGCGGCGGCTGTAGCGCGCATTAAG 2038
 DB 6853 CCAACAGTTTGGCAGCTGAAATGGCGGCGGCGGCGGCTGTAGCGCGCATTAAG 6794
 QY 2039 CGCGCGGGTGTGGTGTACGCGCAGCGTACCGCTACACTTTGCGCAGCGCCCTAGCGCC 2098
 DB 6793 CGCGCGGGTGTGGTGTACGCGCAGCGTACCGCTACACTTTGCGCAGCGCCCTAGCGCC 6734
 QY 2099 CGCTCCTTTTCGCTTCTTCCCTTCTCCCTTCTCGCACGTTGCGCGGCTTTCCCGCTCAAGC 2158
 DB 6733 CGCTCCTTTTCGCTTCTTCCCTTCTTCCCTTCTCGCACGTTGCGCGGCTTTCCCGCTCAAGC 6674
 QY 2159 TCTAAATCGGGGCTCCCTTTAGGGTTCCGATTTAGTGTCTTTACGGCACCCTCGACCCCAA 2218
 DB 6673 TCTAAATCGGGGCTCCCTTTAGGGTTCCGATTTAGTGTCTTTACGGCACCCTCGACCCCAA 6614
 QY 2219 AAAAATTGATAGGTGATGGTTACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTCG 2278
 DB 6613 AAAAATTGATAGGTGATGGTTACGTAGTGGGCCATCGCCCTGATAGACGGTTTTTCG 6554
 QY 2279 CCCTTTGAGTTGGAGTCCACGTTCTTTTAAATAGTGCACCTCTGTTCCAACTCGGAACAC 2338
 DB 6553 CCCTTTGAGTTGGAGTCCACGTTCTTTTAAATAGTGCACCTCTGTTCCAACTCGGAACAC 6494
 QY 2339 ACTCAACCTCTATCTCGTCTATTCTTTTGAATTTATAAGGATTTTGGCGGCTA 2398
 DB 6493 ACTCAACCTCTATCTCGTCTATTCTTTTGAATTTATAAGGATTTTGGCGGCTA 6434
 QY 2399 TTGGTTAAAAAATAGCTGATTTAAACAAAATTTTAAACGGAAATTTTAAACAAAATTTAAC 2458
 DB 6433 TTGGTTAAAAAATAGCTGATTTAAACAAAATTTTAAACGGAAATTTTAAACAAAATTTAAC 6374
 QY 2459 GTTTACAAATTTCTGATGTCGGTATTTTCTTCTTACGCATCTGCGGTATTTTACACCGC 2518
 DB 6373 GTTTACAAATTTCTGATGTCGGTATTTTCTTCTTACGCATCTGCGGTATTTTACACCGC 6314
 QY 2519 ATAGGGTAATAACTGATATAATTAATTAATTAATTAATTAATTAATTAATTAATTAATTA 2578
 DB 6313 ATAGATCGGCAAGTGCACAACTACTTAAATAATAATAATAATAATAATAATAATAATA 6254
 QY 2579 ATTTACTTATAATACAGTTTTTTTGTGTCGGCGCATCTTCTCAAAATATGCTTCCCA 2638
 DB 6253 TTAGCATTTTTCACGAAATTTTGTCTATTTTGTAGAGTCTTTTACACCAATTTGTCTCACA 6194
 QY 2639 GCCTGCTTTTCTGTAAGTTTCAACCTCTACCTTAGCATCCCTTCCCTTTTGCATATAGTCC 2698
 DB 6193 CCTCCGCTTACATCAAC-----ACCAATAACGC 6166
 QY 2699 TCTTCCAACTAAATAATGTCTAGATCTCTGTAGAGACCAATCATCATCCGGTCTCTACTG 2758
 DB 6165 CATTTAATCTAGCGCATCACCAATTTTCTGGGTCTAGTCCACGAGTAACTAAAT 6106
 QY 2759 TTGACCCAATGCTCTCCCTTGTCTATTAACCCACACCGGGTGTCTAATCAACCAATC 2818
 DB 6105 GTAAGCTTTTCGGGGCTCTCTTGCCTT-----CCAACTAGTCAAGAAATCGAGTTCCAATC 6051
 QY 2819 GTAACCTTCTCTCTTCCACCCATGTCTTTTGAGCAATAAAGCCGATTAACAAATCTTT 2878
 DB 6050 CAAAAGTTTCACTGTCTCCAC-----CTGCTTCTGAAATCAACAGGGAATTAACGAATG 5997
 QY 2879 GTGCTCTTTTCGCAATGTCAACAGTACCTCTTAGTATATTTCTCCAGTAGATAGGAGCCCT 2938
 DB 5996 AGGTTTCTGTGAAGCTGCACTGAGTAGTATGTTGAGTCTTTTGGAAATAGAGTCTTTT 5937
 QY 2939 GCATGCAATTTCTGCTTAACATCAAAAGGCTCTAGGTTCTTTTGTACTTTCTTCTCCGC 2998

Db 5936 -----AATAACTGGCAACCGAGGAACCTTGGTATTCTTGCCACGACTCATCTCCA 5885
QY 2999 CTGCTTCAACCGCTTAACNATACCTGGGCCCAACACCGGTGTGCATTCGTAAATGTCTGC 3058
Db 5884 TGCAGT-----TGGACGATATCAATCCGCTTAATCATTTACCGAGAGCAAAACATCCTC 5832
QY 3059 CCATTCTGCTATTCTGTATACACCCGACAGAGTACTGCAATTTGACTGTATTACCAATGTC 3118
Db 5831 CTTAGGTTGATTTACGAAACACGCCCAACCAAGTATTTCCGAGTGCCTGAACTATTTTATA 5772
QY 3119 AGCAAAATTTCTGTCTTCCGAGAGTAAATAATGTAATGTCGGGTAATGCTTTAGCGG 3178
Db 5771 TG-----CTTTTACAAGACTTGAAATTTCTTGCAATAAACCGGGTCAATGTT 5724
QY 3179 CTTAACTGTCCTCCATGGAATAATCAGTCAAGATATCCACATGTGTGTTTTAGTAAACA 3238
Db 5723 TCTCTTTCTATTGGGCACACATATAATACCCAGCAAGTCAGCATGGGAATCTAG--AGCA 5666
QY 3239 AATTTTGGGACCTAATGCTTCAACTAAGTCCAGTAATTTCTTGGTGGTAC--GAACATCCA 3297
Db 5665 CATTCGCGGCTCTGTGCTGTGAAGCGGCAAACTTTACCAATGGACCAAACTACCT 5606
QY 3298 ATGAAGCACACAAGTTTGTGCTTTTTCGTGATGATATTAATAGCTTTGGCAGCAACAG 3357
Db 5605 GTGAATTAATAACAGACATACCTCAAGCTGCCITTTGTGCTTAATCAAGTATACTCAC 5546
QY 3358 GACTAGGATGAGTAGACGACGCTTCTTATATGATGCTTTGACATGATTTATCTTGCTT 3417
Db 5545 GTGCTCAATAGTCACCAATAGCCCTCCCTCTTGGCCCTCTCC-----TTTTCTTT 5497
QY 3418 TCCCTCAGGTTTTTGTCTGTGACGTGGGTAGAACTAGGCAATTTTCATGTTTCTT 3477
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QY 3478 CAACACTACATAGCGGTATATACCAATCTAAGTCTGTGCTCTCTTCTGTTCTTCTCT 3537
Db 5448 CAAGATTGACGTAAAGTGACAAGCTATTTTCAATAAAGAAATCTTTCCACTACTGCCA 5389
QY 3538 TCTGTTCCGAGATTACCGAATCAAAAATTTCAAGAAACCGAAATCAAAAAAAGNAT 3597
Db 5388 TCTGGCGTCATAACTGCAAGTACACATATATTA-----CGATGCTGTCTATTAAAT 5337
QY 3598 AAAAAAATAATCATGAATTTGAATTCGAAAGCTGTGGTATGTCGACTCTCAGTACAACTCT 3657
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Db 5276 GCTCTGATGCGCATAGTTAAGCCAGCCCGACACCCGCCCAACACCCGCTGACGCGCCT 5217
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Db 5216 GACGGGCTGTCTGCTCCGGGATCCGCTTACAGCAAGCTGTGACCGTCTCCGGGAGCT 5157
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Db 5156 GCATGTGTACAGAGTTTTCACCGTCAATCACGAAACGCGGAGAGCAAGGCGCTCGTGA 5097
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Db 5096 TACGCGCTATTTTATAGGTTAAATGTCATGATAAATGTTTTCTTAGTATGATCCAATAT 5037
QY 3898 CAAAGGAATGATAGCATTTGAAGATGAGATTAATCCAAATTTGAGGAGTGGCAGCATATAG 3957
Db 5036 CAAAGGAATGATAGCATTTGAAGATGAGATTAATCCAAATTTGAGGAGTGGCAGCATATAG 4977
QY 3958 AACAGCTAAGGTTAGTGTGAGGAGACATACGATACCCGCAATGGAATGGGATAATAT 4017
Db 4976 AACAGCTAAGGTTAGTGTGAGGAGACATACGATACCCGCAATGGAATGGGATAATAT 4917
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Db 4916 CACAGGAGTACTAGACTACCTTTTCATCTACATAAAATAGACGCATATAAGTACGCAATTT 4857
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Db 4856 AAGCATAAACACGCACTATCGCTTCTTCTCATGTATATATATACAGGAAACACGAG 4797
QY 4138 ATATAGTGTGGACCTGAAACAGTGAAGTGTATGTGCGCAGCTCGGCTTGCATTTTCGGAAG 4197
Db 4796 ATATAGTGTGGACCTGAAACAGTGAAGTGTATGTGCGCAGCTCGGCTTGCATTTTCGGAAG 4737
QY 4198 CGCTCGTTTTTCGGAACGCTTTTGAAGTTCCTATTTCCGAAAGTTCCTATTTCTCTAGAAAGTA 4257
Db 4736 CGCTCGTTTTTCGGAACGCTTTTGAAGTTCCTATTTCCGAAAGTTCCTATTTCTCTAGAAAGTA 4677
QY 4258 TAGGAACCTTCAGAGCGCTTTTGAACCCAAAGCGCTCTGAAGAGCACTTTTCAAAACAC 4317
Db 4676 TAGGAACCTTCAGAGCGCTTTTGAACCCAAAGCGCTCTGAAGAGCACTTTTCAAAACAC 4617
QY 4318 CAAAAACGCAACCGGACTGTAAACGAGCTACTAAAAATTTGCGAATAACCGCTTCCACAAAACA 4377
Db 4616 CAAAAACGCAACCGGACTGTAAACGAGCTACTAAAAATTTGCGAATAACCGCTTCCACAAAACA 4557
QY 4378 TTGCTCAAAAGTATCTCTTTGCTATATATCTCTGTGCTATATCCCTATATAACCTACCCA 4437
Db 4556 TTGCTCAAAAGTATCTCTTTGCTATATATCTCTGTGCTATATCCCTATATAACCTACCCA 4497
QY 4438 TCCACCTTTGCTCTTGAACCTTGCATCTAAACCTCGACCTCTACATTTTATGTTTATC 4497
Db 4496 TCCACCTTTGCTCTTGAACCTTGCATCTAAACCTCGACCTCTACATTTTATGTTTATC 4437
QY 4498 TCTAGTATTACTCTTTTAGACAAAAAATTTGTAGTAAGAACTATTTCATAGAGTGAATCGAA 4557
Db 4436 TCTAGTATTACTCTTTTAGACAAAAAATTTGTAGTAAGAACTATTTCATAGAGTGAATCGAA 4377
QY 4558 AACAAATACGAAATGTAAACATTTCCCTATACGTAGTATATAGAGACAAATAAGAGAAAC 4617
Db 4376 AACAAATACGAAATGTAAACATTTCCCTATACGTAGTATATAGAGACAAATAAGAGAAAC 4317
QY 4618 CGTTCATAATTTCTGACCAATGAAGAACTCAACCGCTATCACCTTCTGTTTCACAAAGT 4677
Db 4316 CGTTCATAATTTCTGACCAATGAAGAACTCAACCGCTATCACCTTCTGTTTCACAAAGT 4257
QY 4678 ATGCGCAATCCACATCGGTATAGAAATAAATTAATTCGGGATGTCCTTTATCTTGAATAATGCA 4737
Db 4256 ATGCGCAATCCACATCGGTATAGAAATAAATTAATTCGGGATGTCCTTTATCTTGAATAATGCA 4197
QY 4738 CCGCAGCTTCGCTAGTAAATCAGTAAACGCGGAAAGTGGAGTCAGGCTTTTTTATGGA 4797
Db 4196 CCGCAGCTTCGCTAGTAAATCAGTAAACGCGGAAAGTGGAGTCAGGCTTTTTTATGGA 4137
QY 4798 GAGAAATAGACACCAAGTAGCCCTTCTTAACCTTAACCGACCTACAGTGCAGAAAGT 4857
Db 4136 GAGAAATAGACACCAAGTAGCCCTTCTTAACTTAACCGACCTACAGTGCAGAAAGT 4077
QY 4858 TATCAAGAGACTGCATTTATAGCGGCAAAAGGAGAAAAAAGTAATCTAAGATGCTTTG 4917
Db 4076 TATCAAGAGACTGCATTTATAGCGGCAAAAGGAGAAAAAAGTAATCTAAGATGCTTTG 4017
QY 4918 TTAGAAAAATAGCGCTCTCGGGATGCAATTTTGTAGAAACAAAAAGAGATATAGATCTT 4977
Db 4016 TTAGAAAAATAGCGCTCTCGGGATGCAATTTTGTAGAAACAAAAAGAGATATAGATCTT 3957
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QY 5038 TTTGTTTCAAAAAATAGCGCTCTCGCGTTCGATTTTCTTTTCAAAAAATGAAGCACAGA 5097
Db 3896 TTTGTTTCAAAAAATAGCGCTCTCGCGTTCGATTTTCTTTTCAAAAAATGAAGCACAGA 3837
QY 5098 TTTCTGTTGTAATAATAGCGCTTTCCGTTGCAATTTCTGTTCTGTAAATAAGCAGCTCA 5157
Db 3836 TTTCTGTTGTAATAATAGCGCTTTCCGTTGCAATTTCTGTTCTGTAAATAAGCAGCTCA 3777

QY 5158 GATCTTTGTTGAAATATAGCGCTCTCCGGTGTGAATTTTGTCTCAAAAATGAAGCA 5217
Db 3776 GATCTTTGTTGAAATATAGCGCTCTCCGGTGTGAATTTTGTCTCAAAAATGAAGCA 3717
QY 5218 CAGATGCTTGGTTCAGTGGCACTTTTCGGGGAAATGTGCGCGAAACCCCTATTGTTTA 5277
Db 3716 CAGATGCTTGGTTCAGTGGCACTTTTCGGGGAAATGTGCGCGAAACCCCTATTGTTTA 3657
QY 5278 TTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCCTGATAAATGCTT 5337
Db 3656 TTTTCTAAATACATTCAAATATGTATCCGCTCATGAGACAATAACCCCTGATAAATGCTT 3597
QY 5338 CAATAATATTGAAAGAGAGATATGAGTATTCAACATTTCCGTGTGCGCCCTATTGCC 5397
Db 3596 CAATAATATTGAAAGAGAGATATGAGTATTCAACATTTCCGTGTGCGCCCTATTGCC 3537
QY 5398 TTTTTCGGCGCATTTTTCGGCGTTCCTGTTTTCGTCACCCAGAAACGCTGGTGAAGTAAA 5457
Db 3536 TTTTTCGGCGCATTTTTCGGCGTTCCTGTTTTCGTCACCCAGAAACGCTGGTGAAGTAAA 3477
QY 5458 GATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTTACATCGAACTGGATCTCAACAGCGT 5517
Db 3476 GATGCTGAAGATCAGTTGGGTGCACGAGTGGGTTTACATCGAACTGGATCTCAACAGCGT 3417
QY 5518 AAGATCTTGAGAGTTTTCGCCCGGAAAGACGTTTTCCAATGATGAGCACTTTTAAAGTT 5577
Db 3416 AAGATCTTGAGAGTTTTCGCCCGGAAAGACGTTTTCCAATGATGAGCACTTTTAAAGTT 3357
QY 5578 CTGCTATGTCGGCGGTATTATCCGTTATTGACCGCGGCAAGGCAACTCGTCCGCG 5637
Db 3356 CTGCTATGTCGGCGGTATTATCCGTTATTGACCGCGGCAAGGCAACTCGTCCGCG 3297
QY 5638 ATACACTATTCTCAGAACTGACTGGTTGAGTACTCACAGTCAAGAAAGCATCTTACG 5697
Db 3296 ATACACTATTCTCAGAACTGACTGGTTGAGTACTCACAGTCAAGAAAGCATCTTACG 3237
QY 5698 GATGGCATGACGTAAGAGAAATATGCACTGCTGCCATACCATGATGATGATAACACTGCG 5757
Db 3236 GATGGCATGACGTAAGAGAAATATGCACTGCTGCCATACCATGATGATGATAACACTGCG 3177
QY 5758 GCCAACTTCTTGACACGATCGGAGGACGAGGCTAACCGCTTTTTCGACAAAC 5817
Db 3176 GCCAACTTCTTGACACGATCGGAGGACGAGGCTAACCGCTTTTTCGACAAAC 3117
QY 5818 ATGGGGATCATGTAACTCCGCTTGATGCTGGGAACCGGAGCTGAATGAAGCCATACCA 5877
Db 3116 ATGGGGATCATGTAACTCCGCTTGATGCTGGGAACCGGAGCTGAATGAAGCCATACCA 3057
QY 5878 AACGACGAGGTGACACACGATGCTGTAGCAATGGCAACAAAGTTGCGCAAACTATTA 5937
Db 3056 AACGACGAGGTGACACACGATGCTGTAGCAATGGCAACAAAGTTGCGCAAACTATTA 2997
QY 5938 ACTGGGAACTTACTACTCTAGCTTCCCGCAACATTAATAGACTGGATGGAGCGGAT 5997
Db 2996 ACTGGGAACTTACTACTCTAGCTTCCCGCAACATTAATAGACTGGATGGAGCGGAT 2937
QY 5998 AAAGTTGACGACCACTTCTGCGCTCGCGCTTCCGCTGGCTGTTTATTGCTGATAAA 6057
Db 2936 AAAGTTGACGACCACTTCTGCGCTCGCGCTTCCGCTGGCTGTTTATTGCTGATAAA 2877
QY 6058 TCTGGAGCCGTTGAGCTGGGTCTCGCGGTATCATNTGACACTTGGGGCCAGATGGTAAAG 6117
Db 2876 TCTGGAGCCGTTGAGCTGGGTCTCGCGGTATCATNTGACACTTGGGGCCAGATGGTAAAG 2817
QY 6118 CCCTCCGCTATCTAGTATTCTACACGACGGGAGTCAAGCAACTATGGATGAACGAAT 6177
Db 2816 CCCTCCGCTATCTAGTATTCTACACGACGGGAGTCAAGCAACTATGGATGAACGAAT 2757
QY 6178 AGACAGATCGCTGAGATAGGTGCTCACTGATTAAAGCATTTGTAAGTGTGAGCAAGTT 6237
Db 2756 AGACAGATCGCTGAGATAGGTGCTCACTGATTAAAGCATTTGTAAGTGTGAGCAAGTT 2697

QY 6238 TACTCATATATATCTTTAGATTGATTTAAACCTTCATTTTAAATTTAAAGATCTAGGTG 6297
Db 2696 TACTCATATATATCTTTAGATTGATTTAAACCTTCATTTTAAATTTAAAGATCTAGGTG 2637
QY 6298 AAGATCCTTTTGTATATCTCATGACCAAAATCCCTTAAGCTGAGTTTTCGTTCCACTGA 6357
Db 2636 AAGATCCTTTTGTATATCTCATGACCAAAATCCCTTAAGCTGAGTTTTCGTTCCACTGA 2577
QY 6358 GCGTCAGACCCCGTAGAAAAGATCAAAAGGATCTTCTTGAGATCCTTTTCTGCGCGTA 6417
Db 2576 GCGTCAGACCCCGTAGAAAAGATCAAAAGGATCTTCTTGAGATCCTTTTCTGCGCGTA 2517
QY 6418 ATCTGCTGCTTGCAAAACAAAACCAACCGCTACACGCGTGTGTTGTTGCGGATCAA 6477
Db 2516 ATCTGCTGCTTGCAAAACAAAACCAACCGCTACACGCGTGTGTTGTTGCGGATCAA 2457
QY 6478 GAGCTACCAACTCTTTTTCGAAAGTAACTGGCTTCAGACAGCGAGATACCAATACT 6537
Db 2456 GAGCTACCAACTCTTTTTCGAAAGTAACTGGCTTCAGACAGCGAGATACCAATACT 2397
QY 6538 GTCCTTCTAGTGTAGCCGCTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCTTACA 6597
Db 2396 GTCCTTCTAGTGTAGCCGCTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCTTACA 2337
QY 6598 TACTCGCTCTGCTAATCTCTGTTTACAGTGGCTGTGCTGAGTGGCGATTAAGTGTCTT 6657
Db 2336 TACTCGCTCTGCTAATCTCTGTTTACAGTGGCTGTGCTGAGTGGCGATTAAGTGTCTT 2277
QY 6658 ACCGGTGTGAGCTCAAGACGATAGTTTACCGGATAAGCGCAGCGCTCGGCTGAACGGGG 6717
Db 2276 ACCGGTGTGAGCTCAAGACGATAGTTTACCGGATAAGCGCAGCGCTCGGCTGAACGGGG 2217
QY 6718 GGTTCGTGCACACAGCCGCTTGGAGCGAAACGACCTTACACCGAACTGAGATACCTACAG 6777
Db 2216 GGTTCGTGCACACAGCCGCTTGGAGCGAAACGACCTTACACCGAACTGAGATACCTACAG 2157
QY 6778 CGTGAAGTATGAGAAACGCGCTTCCGAAAGGAGAAAGCGGAGACGATTCGGTA 6837
Db 2156 CGTGAAGTATGAGAAACGCGCTTCCGAAAGGAGAAAGCGGAGACGATTCGGTA 2097
QY 6838 AGCGGAGGCTCGGAAACAGGAGAGCGACGAGGAGCTTCCAGGGGAAACGCTGTAT 6897
Db 2096 AGCGGAGGCTCGGAAACAGGAGAGCGACGAGGAGCTTCCAGGGGAAACGCTGTAT 2037
QY 6898 CTTTATAGTCTCTGCGGCTTCCGCTACCTCTGCTGAGCTGATTTTGTGATGCTCG 6957
Db 2036 CTTTATAGTCTCTGCGGCTTCCGCTACCTCTGCTGAGCTGATTTTGTGATGCTCG 1977
QY 6958 TCAGGGGGCGGAGCGCTATGGAACAAACGCGCAGCAACGCGGCTTTTTCAGGTTCTGCGC 7017
Db 1976 TCAGGGGGCGGAGCGCTATGGAACAAACGCGCAGCAACGCGGCTTTTTCAGGTTCTGCGC 1917
QY 7018 TTTTGTGCGCTTTTCTCATGTTCTTCTGCGTTATCCCTGATTCCTGTGGATTAAC 7077
Db 1916 TTTTGTGCGCTTTTCTCATGTTCTTCTGCGTTATCCCTGATTCCTGTGGATTAAC 1857
QY 7078 CGTATTAACCGCTTTGAGTGTGATGATACCGCTGCGCGACGCGAAACGAGCGGAGC 7137
Db 1856 CGTATTAACCGCTTTGAGTGTGATGATACCGCTGCGCGACGCGAAACGAGCGGAGC 1797
QY 7138 GAGTCAGTGTGAGGAGCGGAGAGCGGCAATACGCAACCGGCTCTCCCGCGCGT 7197
Db 1796 GAGTCAGTGTGAGGAGCGGAGAGCGGCAATACGCAACCGGCTCTCCCGCGCGT 1737
QY 7198 TGCGCGATTCATTAATGAGCTGCGACGAGCTTTCCGACTGGAAAGCGGAGTGAG 7257
Db 1736 TGCGCGATTCATTAATGAGCTGCGACGAGCTTTCCGACTGGAAAGCGGAGTGAG 1677
QY 7258 CGCAACGCAATTAATGTGAGTTACCTCACTCATTAGGACCCCGGCTTTACATTTATG 7317
Db 1676 CGCAACGCAATTAATGTGAGTTACCTCACTCATTAGGACCCCGGCTTTACATTTATG 1617
QY 7318 CTTCCGCGCTCCTATGTTGTGGAATTTGTGAGCGGATTAACAAATTTTTCACAGGAAACAGC 7377

DB 1616 CTTCCGGCTGATGTTGTGGAATTGTAGCGGATACAAATTTCCACAGGAACAGC 1557
 QY 7378 TATGACCATGATTACGCCAAGCGCCA 7404
 DB 1556 TATGACCATGATTACGCCAAGCTTGCA 1530

RESULT 7
 AAC90959/c
 ID AAC90959 standard; cDNA; 9749 BP.
 AC AAC90959;
 XX
 DT 19-MAR-2001 (first entry)
 XX
 DE Plasmid pGC1003 nucleotide sequence SEQ ID NO:92.
 XX
 KW Human; Caenorhabditis elegans; UNC-5; splice variant; nematode worm;
 XX protein-protein interaction; identification; ss.
 OS Synthetic.
 XX
 PN W0200073328-A2.
 PD 07-DEC-2000.
 XX
 PF 02-JUN-2000; 2000WO-EP005108.
 PR 01-JUN-1999; 99GB-00012755.
 XX (DEVG-) DEVGEN NV.
 PA
 PI Van Criekinge W, Roelens I, Bogaert T, Verwaerde P;
 DR WPI; 2001-016508/02.
 PT Three variants of human unc-5C cDNAs (unc-5Cb, unc-5Cc and unc-5C8) and a
 PT human unc-5HS1 cDNA, useful in yeast two hybrid experiments for
 PT identifying unknown human cDNAs which encode proteins that interact with
 PT the human unc-5C protein.
 XX
 PS Example 4; Page 231-233; 246pp; English.
 CC The present invention describes 3 variants of human unc-5C cDNAs (unc-
 CC 5Cb, unc-5Cc and unc-5C8) which correspond to alternatively spliced unc-
 CC 5C transcripts, and a human unc-5HS1 cDNA which shares homology with the
 CC Rattus norvegicus unc-5HS1 cDNA. Also described are assays based on
 CC protein-protein-interactions between the unc-5 protein and a variety of
 CC different interacting proteins. The unc-5C variant cDNAs and unc-5HS1
 CC cDNA are useful in methods for identifying compounds which reduce or
 CC inhibit the lethal phenotype associated with the expression of the unc-5
 CC death domain in yeast. They are also useful in yeast two hybrid
 CC experiments for identifying unknown human cDNAs which encode proteins
 CC that interact with the human unc-5C protein. AAC90914 to AAC90971 and
 CC AAB50646 to AAB50693 represent sequences used in the exemplification of
 CC the present invention
 SQ Sequence 9749 BP; 2764 A; 2006 C; 2176 G; 2802 T; 0 U; 1 Other;

Query Match 57.4%; Score 4492.6; DB 4; Length 9749;
 Best Local Similarity 87.3%; Pred. No. 0;
 Matches 5104; Conservative 0; Mismatches 629; Indels 114; Gaps 12;

QY 1559 TCATGTAATTAGTTATGTCACGCTTACATTCACGCCCTCCGCCACATCCGCTCTAACCG 1618
 DB 8560 TCATGTAATTAGTTATGTCACGCTTACATTCACGCCCTCCGCCACATCCGCTCTAACCG 8501
 QY 1619 AAAAGGAGGAGTTAGACAACTGAAGTCTAGGTCCTCTATTTATTTTATAGTTATGT 1678
 DB 8500 AAAAGGAGGAGTTAGACAACTGAAGTCTAGGTCCTCTATTTATTTTATAGTTATGT 8441
 QY 1679 TAGTATTAAGAACGTTATTTATATTTTCAAAATTTTCTTTTCTGTGACAGCGCGTGT 1738

DB 8440 TAGTATTAAGAACGTTATTTATATTTTCAAAATTTTCTTTTCTGTGACAGCGGTGT 8381
 QY 1739 ACGCATGTAACTATATCTGAAACCTTGTGTAGAGGTTTGGGACGCTCGAAGGCTT 1798
 DB 8380 ACGCATGTAACTATATCTGAAACCTTGTGTAGAGGTTTGGGACGCTCGAAGGCTT 8321
 QY 1799 TAATTTGCGGCGGTACCCCAATTCGCCCTATAGTGAGTCGTATTACGCGCGCTCACTGGC 1858
 DB 8320 TAATTTG-----CAAAGCTCGGGAATCTGAGCTCGGAAAGCTTGAACGACTGGC 8271
 QY 1859 CGTCGTTTTTCAACGTCGTGATCGGGAACCTCTGGCGTTTACCCAACTTAATTCGCTTGC 1918
 DB 8270 CGTCGTTTTTCAACGTCGTGATCGGGAACCTCTGGCGTTTACCCAACTTAATTCGCTTGC 8211
 QY 1919 AGCACATCCCGCTTTCCGCGAGCTGGCGTAATAGCGAAGAGCGCCGACGATCGCGCTTC 1978
 DB 8210 AGCACATCCCGCTTTCCGCGAGCTGGCGTAATAGCGAAGAGCGCCGACGATCGCGCTTC 8151
 QY 1979 CCAACAGTTGCGCAGCTGAAATGCGGGAATGCGGCGAGCGCCCTGTAGCGGCGCATTAAG 2038
 DB 8150 CCAACAGTTGCGCAGCTGAAATGCGGGAATGCGGCGAGCGCCCTGTAGCGGCGCATTAAG 8091
 QY 2039 CGCGCGGGTGTGTTGTTTACGCGCAGCGTGACCGCTACACTTGCACGCGCCTTAGCGCC 2098
 DB 8090 CGCGCGGGTGTGTTGTTTACGCGCAGCGTGACCGCTACACTTGCACGCGCCTTAGCGCC 8031
 QY 2099 CGCTCCTTTCCGCTTTCTTCCCTTCTTCGCCACAGTTTCGCGGCTTTCGCGCTCAAGC 2158
 DB 8030 CGCTCCTTTCCGCTTTCTTCCCTTCTTCGCCACAGTTTCGCGGCTTTCGCGCTCAAGC 7971
 QY 2159 TCTAAATCGGGGCTCCCTTTTAGGGTTCCGATTTAGTGTCTTTTACGCGACCTCGACCCCAA 2218
 DB 7970 TCTAAATCGGGGCTCCCTTTTAGGGTTCCGATTTAGTGTCTTTTACGCGACCTCGACCCCAA 7911
 QY 2219 AAAACTTTGATTAGGGTGTGATGTTTCAAGGGAATTTTTCGCGATTTTCGCGCTTA 2278
 DB 7910 AAAACTTTGATTAGGGTGTGATGTTTCAAGGGAATTTTTCGCGATTTTCGCGCTTA 7851
 QY 2279 CCCTTTGACGTTGAGTCCAGCTTCTTTAATAGTGGACTCTTGTTCGAACCTGGACACAC 2338
 DB 7850 CCCTTTGACGTTGAGTCCAGCTTCTTTAATAGTGGACTCTTGTTCGAACCTGGACACAC 7791
 QY 2339 ACTCAACCTTATCTCGTCTATTTCTTTTATTAAGGGAATTTTCGCGATTTTCGCGCTTA 2398
 DB 7790 ACTCAACCTTATCTCGTCTATTTCTTTTATTAAGGGAATTTTCGCGATTTTCGCGCTTA 7731
 QY 2399 TTGCTTAAAAAATGAGCTGATTTTAAACAAAAATTTTAAACGGAATTTTAAACAAATATTAC 2458
 DB 7730 TTGCTTAAAAAATGAGCTGATTTTAAACAAAAATTTTAAACGGAATTTTAAACAAATATTAC 7671
 QY 2459 GTTTTACAAATTTCTGATCGGCTATTTTCTCTTACGCACTGTGCGGTATTTTCACACCGC 2518
 DB 7670 GTTTTACAAATTTCTGATCGGCTATTTTCTCTTACGCACTGTGCGGTATTTTCACACCGC 7611
 QY 2519 ATAGGTAATAACCTGATATTAATAAATGAAGCTCTAATTTGTGAGTTTAGTATATACATGC 2578
 DB 7610 ATAGTACGCGAAGTGCACAAACATATCTTAATAAATACTACTAGTAATAACCTATTTC 7551
 QY 2579 ATTTTACTTATAATACAGTTTATTTTGTGCGCGCATCTTCTCAAAATATGCTTCCCA 2638
 DB 7550 TTAGCAATTTTACGAAATTTGCTATTTTGTGTAGAGTCTTTTACACCATTTTGTCTCCACA 7491
 QY 2639 GCCTGCTTTTCTGTAAAGTTTCAACCTCTACCTTAGCATCCCTTCCCTTTGCAAAATAGTCC 2698
 DB 7490 CCTCCGCTTACATCAAC-----ACCAATTAACCG 7463
 QY 2699 TCTTCCAAACATAATATGTGATCTGTAGAGACCAATCATCATCGGTTCTATACATG 2758
 DB 7462 CATTTATCTAAGCGCATCAACAATTTTCTGCGGTGAGTCCACGAGTACATAAAT 7403
 QY 2759 TTGACCAATGCGGTCTCCCTTGTGATCTTAACCAACCGCGGTGTCATAATCAACCAATC 2818

Db 7402 GTAAAGCTTTGCGGCTCTCTTGGCTT-----CCAAACCAGTCAGAAATCGAGTTCCTAATC 7348
Qy 2819 GTAAACCTTCATCTCTTCCACCCATGCTCTTTGAGCAATAAAGCCGTAACAATAATCTTT 2878
Db 7347 CAAAAGTTACCTGTGCCAC-----CTGCTTCTGAATCAACAAGGGAATAAAGCAATG 7294
Qy 2879 GTGCTCTTCGCAATGTCACAGTACCCCTTAGTATATCTTCCAGTAGATAGAGGCCCTT 2938
Db 7293 AGGTTTCTGTGAAGCTGCACTGAGTAGTATGTTGCGAGTCTTTTGGAAATACGAGTCTTTT 7234
Qy 2939 GCATGACAAATCTGCTAAACATCAAAAGCCCTCTAGGTTCTTGTGTACTTCTTCTGCGGC 2998
Db 7233 -----ATAACTGCGAAACCGAGGAATCTTGTGTTCTTGGCCAGCACTCATCCCA 7182
Qy 2999 CTGCTTCAAAACCGCTAACAACTCTGGGCCCAACACACCGGTGCAATCTGTAATGTGTC 3058
Db 7181 TGCAGT-----TGGAGCATATCAATGCGGTAACTCATTCAGCAGAGCCAAACATCCTC 7129
Qy 3059 CCATTCTGCTATCTGTATACACCGCAGAGTACTGCAATTTGACTGTATATACCAATGTC 3118
Db 7128 CTTAGGTTGATTACGAAACACGCCAACCAAGTATTTCCGAGTGCCTGAACTATTTTATA 7069
Qy 3119 AGCAAAATTTCTGCTTCGAAGAGTAAATAATGTTACTTTCGCGGATAATCCTTTAGCGG 3178
Db 7068 TG-----CTTTAAGACTTGAATTTTCTTGCATTAACCGGGTCAATGT 7021
Qy 3179 CTTAACTGTGCCCTCCATGGAATAATCAGTCAAGATATCACATGTGTTTTTATAGTAAACA 3238
Db 7020 TCTCTTCTATTTGGGCACACATATAATACCAGCAAGTCAGCATCGGAATCTAG--AGCA 6963
Qy 3239 AATTTGGGACCTAAAGCTTCAACTCACTCACTCACTCACTCACTCACTCACTCACTCACT 3297
Db 6962 CATTTGCGGCTCTGTGCTCTGCAAGCGCAAACTTTCCACCAATGCAACCAAGTACCT 6903
Qy 3298 ATGAAGCACACAAGTTTGTGCTTTTGTGCGATGATATTAATAGCTTGCAGCAACAG 3357
Db 6903 GTGAAATTAATACAGACATCTCCAAAGCTGCTTTGTGCTTAACTACGATATCTAC 6843
Qy 3358 GACTAGATGAGTAGCAGACGTTTCTTATATGATGATGCTTTGACATGATTTATCTTGTT 3417
Db 6842 GTGCTCAATAGTCACCAATGCCCTCCCTCTTGGCCCTCTCC-----TTTCTTTT 6794
Qy 3418 TCTGCGAGTTTGTGTTCTGTGAGTTGGGTTAAGAACTAGGGCAATTTTCATGTTCTTT 3477
Db 6793 TTTGCGACGAATTAATCTTAAATCGGCAAAAAAAGAAAGCTCCGGA-----T 6746
Qy 3478 CAACACTACATATGCGTATATATACCAATCTAAGTCTGCTCTCTCTCTCTCTCTCTCT 3537
Db 6745 CAAGATTGTCGTAAGTGCAAGCTATTTTCAATAAAGAAATCTTCCACTACTGCCA 6886
Qy 3538 TCTGTTGCGAGATTACCGAATCAAAAAATTTCAAAGAAACCGAAATCAAAAAAAGAAAT 3597
Db 6885 TCTGGGCTCAACTGCAAGTAGTACACATATTA-----CGATGCTGCTCTATTAAAT 6634
Qy 3598 AAAAAAATATGATGAAATGAAATGAAAGCTGTGATGCTGATGCTGCTGCTGCTGCTGCT 3657
Db 6633 GCTTCTATATATATATATAGTAAATGCTGTGATCTAATGCTGCACTCTCAGTACAACT 6574
Qy 3658 GCTCTGATGCGCATAGTTAAGCAGCCCGACACCGCCCAACACCGCTGACCGCCCT 3717
Db 6573 GCTCTGATGCGCATAGTTAAGCAGCCCGACACCGCCCAACACCGCTGACCGCCCT 6514
Qy 3718 GAGGGCTGCTGCTCCCGCATCCGCTTACAGACAAGCTGTGACCGCTCTCCGGGAGCT 3777
Db 6513 GACGGCTGCTGCTCCCGCATCCGCTTACAGACAAGCTGTGACCGCTCTCCGGGAGCT 6454
Qy 3778 GCATGTCAGAGTTTTCACCGTCACTCAACGAAACCGCGAGACGAAAGGGCTCTGTGA 3837
Db 6453 GCATGTCAGAGTTTTCACCGTCACTCAACGAAACCGCGAGACGAAAGGGCTCTGTGA 6394
Qy 3838 TAGCCCTATTTTATAGTTATGTCATGATATATAGTTTCTTAGTATGATCCATAT 3897
Db 6393 TAGCCCTATTTTATAGTTATGTCATGATATATAGTTTCTTAGTATGATCCATAT 6334

Qy 3898 CAAAGGAAATGATAGCATTTGAAGATGAGACTAATCAATTTGAGGAGTGCAGCATATAG 3957
Db 6333 CAAAGGAAATGATAGCATTTGAAGATGAGACTAATCAATTTGAGGAGTGCAGCATATAG 6274
Qy 3958 ACAGCTAAAGGTTAGTGTGAGGAAAGCATACGATACCCCGCATGGAATGGGATATAT 4017
Db 6273 ACAGCTAAAGGTTAGTGTGAGGAAAGCATACGATACCCCGCATGGAATGGGATATAT 6214
Qy 4018 CACAGAGGTACTAGACTACCTTTTCATCTACATAAATAGACGATATAGTAGTCGCAATTT 4077
Db 6213 CACAGAGGTACTAGACTACCTTTTCATCTACATAAATAGACGATATAGTAGTCGCAATTT 6154
Qy 4078 AAGCATAAACACGCACTATGCCCTTCTCTCATGTATATATATACAGCAACACGCAAG 4137
Db 6153 AAGCATAAACACGCACTATGCCCTTCTCTCATGTATATATATACAGCAACACGCAAG 6094
Qy 4138 ATATAGTGGGAGCTGAACAGTGAGCTGTATGTGCGCAGCTCGCGTTGCAATTTTCCGAAG 4197
Db 6093 ATATAGTGGGAGCTGAACAGTGAGCTGTATGTGCGCAGCTCGCGTTGCAATTTTCCGAAG 6034
Qy 4198 CGCTCGTTTTCGGAACGCTTTTGAAGTTCCTATTTCGAAAGTTCCTATTCTCTAGAAAGTA 4257
Db 6033 CGCTCGTTTTCGGAACGCTTTTGAAGTTCCTATTTCGAAAGTTCCTATTCTCTAGAAAGTA 5974
Qy 4258 TAGGAACTTCAGAGCGCTTTTGAACACCAAAAGCGCTCTGAAAGCAGCACTTTCAAAAAC 4317
Db 5973 TAGGAACTTCAGAGCGCTTTTGAACACCAAAAGCGCTCTGAAAGCAGCACTTTCAAAAAC 5914
Qy 4318 CAAAAACGCGGACGTGAACGAGCTACTAAATATGCGAATACCGCTTCCACAACA 4377
Db 5913 CAAAAACGCGGACGTGAACGAGCTACTAAATATGCGAATACCGCTTCCACAACA 5854
Qy 4378 TTGCTCAAAAGTATCTCTTTGCTATATATCTCTGCTATATCTCTGCTATATCCCTATATACTACCCA 4437
Db 5853 TTGCTCAAAAGTATCTCTTTGCTATATATCTCTGCTATATCTCTGCTATATCCCTATATACTACCCA 5794
Qy 4438 TCCACTTTTGGCTCTTGAACTTTGCATCTAAACTCGACCTCTACATTTTATGTTTATC 4497
Db 5793 TCCACTTTTGGCTCTTGAACTTTGCATCTAAACTCGACCTCTACATTTTATGTTTATC 5734
Qy 4498 TCTAGTATTACTCTTTTAGACAAAAAATTTGTAGTAGAAGTATTCATAGAGTAAATCGAA 4557
Db 5733 TCTAGTATTACTCTTTTAGACAAAAAATTTGTAGTAGAAGTATTCATAGAGTAAATCGAA 5674
Qy 4558 AACAAACGAAATGTAACATTTCTCTATACGTAGTATATAGAGACAAAAATAGAGAAAC 4617
Db 5673 AACAAACGAAATGTAACATTTCTCTATACGTAGTATATAGAGACAAAAATAGAGAAAC 5614
Qy 4618 CGTTCTAAATTTTCTGACCAATGAAGAATCATCAACGCTATCATCTTTCTGTTTCAAAAGT 4677
Db 5613 CGTTCTAAATTTTCTGACCAATGAAGAATCATCAACGCTATCATCTTTCTGTTTCAAAAGT 5554
Qy 4678 ATGCGCAATCCCATCGGTATAGAAATATATTCGGGATGCTTTTATGAAAAATGCA 4737
Db 5553 ATGCGCAATCCCATCGGTATAGAAATATATTCGGGATGCTTTTATGAAAAATGCA 5494
Qy 4738 CCGCAGCTTTGCTAGTAAATCAGTAAACGCGGAAGTGGAGTCAGGCTTTTATGCGAA 4797
Db 5493 CCGCAGCTTTGCTAGTAAATCAGTAAACGCGGAAGTGGAGTCAGGCTTTTATGCGAA 5434
Qy 4798 GAGAAATAGACACCAAGTAGCTTTCTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 4857
Db 5433 GAGAAATAGACACCAAGTAGCTTTCTTAACTTAACTTAACTTAACTTAACTTAACTTAACT 5374
Qy 4858 TATCAAGAGCTGCTATATAGCGGACCAAGAGAGAAAAAAGTAATCTAGATGCTTTG 4917
Db 5373 TATCAAGAGCTGCTATATAGCGGACCAAGAGAGAAAAAAGTAATCTAGATGCTTTG 5314
Qy 4918 TTAGAAAAATAGCGCTCTCGGATGCAATTTTCTAGAAACAAAAAAGATATAGATCTTT 4977
Db 5313 TTAGAAAAATAGCGCTCTCGGATGCAATTTTCTAGAAACAAAAAAGATATAGATCTTT 5254

Qy	4978	TGTTGGTAAATAATAGCGCTCTCGCGGTTGCATTTCTGTGTTCTGTATAAAATGACAGCTCAGATTCC	5033
Db	5253	TGTTGGTAAATAATAGCGCTCTCGCGGTTGCATTTCTGTGTTCTGTATAAAATGACAGCTCAGATTCC	5194
Qy	5038	TTTGTGTTGAAATAATAGCGCTCTCGCGGTTGCATTTTGTGTTTACAAAAATGAAGACACAGA	5097
Db	5193	TTTGTGTTGAAATAATAGCGCTCTCGCGGTTGCATTTTGTGTTTACAAAAATGAAGACACAGA	5134
Qy	5098	TTCTTCCTGTTGGTAAATAATAGCGCTTTCCGCTTGCAATTTCTCTCTGTAAAAATGCAGCTCA	5157
Db	5133	TTCTTCCTGTTGGTAAATAATAGCGCTTTCCGCTTGCAATTTCTCTCTGTAAAAATGCAGCTCA	5074
Qy	5158	GATTCTTTGTTGAAAAAATAGCGCTCTCGGTTGCATTTTGTCTACAAAATGAAGACA	5217
Db	5073	GATTCTTTGTTGAAAAAATAGCGCTCTCGGTTGCATTTTGTCTACAAAATGAAGACA	5014
Qy	5218	CAGATGCTTCGTTCAGGTGGCACTTTTTCGGGGGAAATGTGCGCGGAAACCCCTATTTCGTTTA	5277
Db	5013	CAGATGCTTCGTTCAGGTGGCACTTTTTCGGGGGAAATGTGCGCGGAAACCCCTATTTCGTTTA	4954
Qy	5278	TTTTTCTAAATACATTTCAAAATATGATATGCCCTCATGAGACAAATAACCCCTGATATAATGCCTT	5337
Db	4953	TTTTTCTAAATACATTTCAAAATATGATATGCCCTCATGAGACAAATAACCCCTGATATAATGCCTT	4894
Qy	5338	CAATPAAATATTGAAAAAGAAAGATGATGAGTATTCAACATTTCCGTTGCGCCCTTATTTCCTCC	5397
Db	4893	CAATPAAATATTGAAAAAGAAAGATGATGAGTATTCAACATTTCCGTTGCGCCCTTATTTCCTCC	4834
Qy	5398	TTTTTTTCGGGCAATTTTCGCTTCTCTGTTTTTGTCTCACCAGAAAACGCTGCTGAAAGTAAAA	5457
Db	4833	TTTTTTTCGGGCAATTTTCGCTTCTCTGTTTTTGTCTCACCAGAAAACGCTGCTGAAAGTAAAA	4774
Qy	5458	GATCCTGAAGATCAGTTGGGTGACGAGTGGTTTTACATCGAACTGGATCTCAACACAGCGGT	5517
Db	4773	GATCCTGAAGATCAGTTGGGTGACGAGTGGTTTTACATCGAACTGGATCTCAACACAGCGGT	4714
Qy	5518	AAGATCCTTGAGAGTTTTTCGCCCCCGAAGAACGTTTTTCCAAATGATGAGCACTTTTAAAGTT	5577
Db	4713	AAGATCCTTGAGAGTTTTTCGCCCCCGAAGAACGTTTTTCCAAATGATGAGCACTTTTAAAGTT	4654
Qy	5578	CTGCTATGTGCGCGGTTATTATCCGTTATTGACGCGCGGGCAAGAGCAACTCGGTCGCGCGC	5637
Db	4653	CTGCTATGTGCGCGGTTATTATCCGTTATTGACGCGCGGGCAAGAGCAACTCGGTCGCGCGC	4594
Qy	5638	ATACACTATTCTCAGAAATGACTTGGTTGAGTACTCACGAGTCAAGAAAAAGCATCTTACG	5697
Db	4593	ATACACTATTCTCAGAAATGACTTGGTTGAGTACTCACGAGTCAAGAAAAAGCATCTTACG	4534
Qy	5698	GATGGCATGACAGTAAGAGAAATTATGAGTGTCTGCCATAAACCATGATGATGATAACACTGCG	5757
Db	4533	GATGGCATGACAGTAAGAGAAATTATGAGTGTCTGCCATAAACCATGATGATGATAACACTGCG	4474
Qy	5758	GCCAACTTACTTCTGACAAACGATCGGAGGACCGNAGAGCTAACCGCTTTTTTTCGCAACAC	5817
Db	4473	GCCAACTTACTTCTGACAAACGATCGGAGGACCGNAGAGCTAACCGCTTTTTTTCGCAACAC	4414
Qy	5818	ATGGGGGATCATGTAACTCGCCTTTGATCGTTGGGAAACCGGAGCTGAAATGAAGCCATACCA	5877
Db	4413	ATGGGGGATCATGTAACTCGCCTTTGATCGTTGGGAAACCGGAGCTGAAATGAAGCCATACCA	4354
Qy	5878	AACGACGAGCGTGACACCAACGATGCCCTGTAGCAATGCGCAACAAAGTTTGCACAACTATTTA	5937
Db	4353	AACGACGAGCGTGACACCAACGATGCCCTGTAGCAATGCGCAACAAAGTTTGCACAACTATTTA	4294
Qy	5938	ACTGGGGAACATACTTACTATCTAGCTTCCGGGCAACAATTATAGACTGGATGGAGGCGGAT	5997
Db	4293	ACTGGGGAACATACTTACTATCTAGCTTCCGGGCAACAATTATAGACTGGATGGAGGCGGAT	4234
Qy	5998	AAAGTTCGAGGACCACTTCTCGCTCGGCGCTTCCGCGCTCGCTGTTTATTGCTGATPAAA	6057
Db	4233	AAAGTTCGAGGACCACTTCTCGCTCGGCGCTTCCGCGCTCGCTGTTTATTGCTGATPAAA	4174
Qy	6058	TCTGGAGCCGGTGACGCTGGGTTCTCGCGGTTATCAATTGACAGCACTGGGGGCGAGATGGTAAG	6117

4173	TCTGGAGCCGGTGAGCGTGGGTCTCGCGGTATCATTTGCAGCACTGGGGCCAGATGTAAG	4114
6118	CCCTCCCGGTATCGTAGTTATCTACACGACGGGGAGTCAGGCAACTATGATGAACGAAT	6177
4113	CCCTCCCGGTATCGTAGTTATCTACGACGGGGAGTCAGGCAACTATGATGAACGAAT	4054
6178	AGACAGATCGCTGAGATAGGTGCCCTCACATGATTAAAGCATTTGGTAACTGTACGACCAGTT	6237
4053	AGACAGATCGCTGAGATAGGTGCCCTCACATGATTAAAGCATTTGGTAACTGTACGACCAGTT	3994
6238	TACTCATAATATCTTTAGATTGATTTAAAACCTTCATTTTTAATTTAAAGGATCTAGGTG	6297
3993	TACTCATAATATCTTTAGATTTGATTTAAAACCTTCATTTTTAATTTAAAGGATCTAGGTG	3934
6298	AAGATCCTTTTGTATTAATCTCATGACAAAAATCCCTTTAACGTGAGTTTTCGTTCCA CTGA	6357
3933	AAGATCCTTTTGTATTAATCTCATGACAAAAATCCCTTTAACGTGAGTTTTCGTTCCA CTGA	3874
6358	GCGTCAGACCCGTAGAAAAGATCAAAGATCTTTCTTGAGATCCTTTTTTTCTGCGGTA	6417
3873	GCGTCAGACCCGTAGAAAAGATCAAAGATCTTTCTTGAGATCCTTTTTTTCTGCGGTA	3814
6418	ATCTGCTGCTTGCAAA CAAAAAACAACCGCTACACGCGTGGTTGTTTGC CGGATCAA	6477
3813	ATCTGCTGCTTGCAAA CAAAAAACAACCGCTACACGCGTGGTTGTTTGC CGGATCAA	3754
6478	GACCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGACAGCGCAGATACCAATACT	6537
3753	GACCTACCAACTCTTTTTCCGAAGGTAACTGGCTTCAGACAGCGCAGATACCAATACT	3694
6538	GTCTTTCTAGTGTAGCGGTAGTTTAGGCCACCACTTCAAGAATCTCTGTAGCACCGCTTACA	6597
3693	GTCTTTCTAGTGTAGCGGTAGTTTAGGCCACCACTTCAAGAATCTCTGTAGCACCGCTTACA	3634
6598	TACCTCGCTCTGCTAATCTGTTTACAGTGTGCTGTCGACGTGGCGATAGTCTGTCTTT	6657
3633	TACCTCGCTCTGCTAATCTGTTTACAGTGTGCTGTCGACGTGGCGATAGTCTGTCTTT	3574
6658	ACCGGGTTGACCTCAAGACGATAGTTACCGGATAAGCGCGAGCGGTCTGGGCTCAACCGGG	6717
3573	ACCGGGTTGACCTCAAGACGATAGTTACCGGATAAGCGCGAGCGGTCTGGGCTCAACCGGG	3514
6718	GGTTCTGTGCACACAGCCCCAGCTTTGGACGAAACGACCTTACACCGAACTGAGATACCTACAG	6777
3513	GGTTCTGTGCACACAGCCCCAGCTTTGGACGAAACGACCTTACACCGAACTGAGATACCTACAG	3454
6778	CGTGAGCTATGAAAAAGCGCCAGCTTTCCGAAAGGAGAAAGCGGCACAGGTATCCGGTA	6837
3453	CGTGAGCTATGAAAAAGCGCCAGCTTTCCGAAAGGAGAAAGCGGCACAGGTATCCGGTA	3394
6838	AGCGCAGGTCGGAAACAGAGAGCGCACAGGGAGCTTCCAGGGGAAACGCTCGGTAT	6897
3393	AGCGCAGGTCGGAAACAGAGAGCGCACAGGGAGCTTCCAGGGGAAACGCTCGGTAT	3334
6898	CTTTATAGTCTCTCGGGTTTCGCCACCTCTGACTTTGAGCGTCEATTTTTGTGATGCTCG	6957
3333	CTTTATAGTCTCTCGGGTTTCGCCACCTCTGACTTTGAGCGTCEATTTTTGTGATGCTCG	3274
6958	TCAGGGGGCGGAGCCTATGAAAAAAGCGCAGCAACGCGGCCCTTTTTTACGGTTCTTGCC	7017
3273	TCAGGGGGCGGAGCCTATGAAAAAAGCGCAGCAACGCGGCCCTTTTTTACGGTTCTTGCC	3214
7018	TTTTTGCTGGCTTTTGCTCACAATGTTCTTTCTCGCGTTATCCCTCGATTCTGTGGATAAC	7077
3213	TTTTTGCTGGCTTTTGCTCACAATGTTCTTTCTCGCGTTATCCCTCGATTCTGTGGATAAC	3154
7078	CGTATTACCGCCTTTTGAGTGAGCTGATACCGCTTCGCGCAGCGCAACGACCGAGCGCAGC	7137
3153	CGTATTACCGCCTTTTGAGTGAGCTGATACCGCTTCGCGCAGCGCAACGACCGAGCGCAGC	3094
7138	GAGTCA GTGACGAGGAGCGGAAAGCGCCCAATACGCAAAACCGCTCTTCCC GCGGT	7197

Db 3093 GAGTCACTGAGCGAGGAGCGGAGCGCCCAATACGAAACGGCTCTCCCGCGCGT 3034
Qy 7198 TGGCCGATTCATTAATGACAGTGGCAGCAGAGTTTCCCGAGCTGGAAGCGGCGAGTGAG 7257
Db 3033 TGGCCGATTCATTAATGACAGTGGCAGCAGAGTTTCCCGAGCTGGAAGCGGCGAGTGAG 2974
Qy 7258 GCGACGCAATTAATGAGTGTACCTCACTCATTTAGGACCCCGAGGCTTTACACTTTATG 7317
Db 2973 GCGACGCAATTAATGAGTGTACCTCACTCATTTAGGACCCCGAGGCTTTACACTTTATG 2914
Qy 7318 CTTCGGGCTCTATGTTGTGTGGAAATTTGTAGCGGATAACAAATTTACACAGAAACAGC 7377
Db 2913 CTTCGGGCTCTATGTTGTGTGGAAATTTGTAGCGGATAACAAATTTACACAGAAACAGC 2854
Qy 7378 TATGACCATGATTACGCCAAGCGCGCA 7404
Db 2853 TATGACCATGATTACGCCAAGCTTGCA 2827

RESULT 8

AAT71322/c
ID AAT71322 standard; DNA; 10288 BP.
XX AC AAT71322;
XX DT 11-SEP-1997 (first entry)
XX DE Plasmid pCB51 encoding partial UNC-53 protein used as bait vector.
XX KW UNC-53; neuronal regeneration; revascularisation; wound healing;
XX KW neurodegenerative disease; Alzheimer's disease; Huntington's;
XX KW peripheral neuropathies; metastasis inhibition; cancer; circular;
XX KW Caenorhabditis elegans; ds.
XX OS Synthetic.
XX XX W09638555-A2.
XX PD 05-DEC-1996.
XX PF 31-MAY-1996; 96WO-EP002311.
XX PR 31-MAY-1995; 95GB-00010944.
XX PA (BOGA/) BOGAERT T.
XX PA (STRI/) STRINGHAM E.
XX PA (VAND/) VANDEKERCKHOVE J.
XX PI Bogaert T, Stringham E, Vandekerckhove J;
XX WPI; 1997-034369/03.

Caenorhabditis elegans UNC-53 protein 8A and 7A variants - useful to promote neuronal regeneration, revascularisation or wound healing.

Example 15; Page 139-145; 278pp; English.

AAT71321 and AAT71322 are plasmids pCB50 and pCB51, respectively. They are used as bait vectors in a yeast two hybrid system. pCB50 encodes the full length UNC-53 protein variant 7A of Caenorhabditis elegans and pCB51 encodes a C-terminal portion of this protein. Both vectors were constructed by cloning the appropriate cDNA fragment into pAS1-CYH2 (Clontech). The yeast two hybrid system was set up for identifying proteins that interact with UNC-53. UNC-53 protein 8A and 7A variants and nucleic acids encoding them are useful as medicaments to promote neuronal regeneration, revascularisation or wound healing, or for treatment of chronic neurodegenerative diseases (e.g. Alzheimer's or Huntington's disease) or acute traumatic injuries. Transgenic cells and organisms transfected with UNC-53 cDNA can be used to determine whether a substance is an inhibitor or enhancer of the regulation of cell shape or motility or the direction of cell migration by screening for a phenotypic change in the cell. Inhibitors can be used to alleviate the spread of disease inducing cells or metastasis. Probes derived from the cDNA sequences can

CC be used to identify homologues of the C. elegans unc-53 gene. The UNC-53 protein can be used to identify proteins which are active in the signal transduction pathway that can be used as mentioned above
CC
XX
SQ Sequence 10288 BP; 2909 A; 2218 C; 2242 G; 2918 T; 0 U; 1 Other;

Query Match 57.4%; Score 4492.6; DB 2; Length 10288;
Best Local Similarity 87.3%; Pred. No. 0;
Matches 5104; Conservative 0; Mismatches 629; Indels 114; Gaps 12;

Qy 1559 TCATGTAATTTAGTGTATGTCACGCTTACATTTACGCGCTCCCGACATCCGCTCTAACCG 1618
Db 7878 TCATGTAATTTAGTGTATGTCACGCTTACATTTACGCGCTCCCGACATCCGCTCTAACCG 7819
Qy 1619 AAAAGGAAGGAGTTAGACAACTGAAGTCTAGGTCCCTATTTATTTTATATAGTTATGT 1678
Db 7818 AAAAGGAAGGAGTTAGACAACTGAAGTCTAGGTCCCTATTTATTTTATATAGTTATGT 7759
Qy 1679 TAGTATTAAGAACGTTATTTATATTTTCAATTTTCTTTTCTTTTCTGTACAGAGCGTGT 1738
Db 7758 TAGTATTAAGAACGTTATTTATATTTTCAATTTTCTTTTCTTTTCTGTACAGAGCGTGT 7699
Qy 1739 ACGCATGTACATTATATCTGAAACCTTGTCTGAGAGGTTTGGGACGCTCGAAGGCTT 1798
Db 7698 ACGCATGTACATTATATCTGAAACCTTGTCTGAGAGGTTTGGGACGCTCGAAGGCTT 7639
Qy 1799 TAATTTGCGGCGGTATCCCAATTCGCGCTATATAGTGTCTATTTATTCGCGGCTCACCTGC 1858
Db 7638 TAATTTG-----CAAGCTCGGATCTCGAGCTCGGAAAGCTTGGAGACTGC 7589
Qy 1859 CGTCGTTTACAACGTCGTGACCTGGGAAACCTTGGGTTACCGAATTTAATGCGCTTGC 1918
Db 7588 CGTCGTTTACAACGTCGTGACCTGGGAAACCTTGGGTTACCGAATTTAATGCGCTTGC 7529
Qy 1919 AGCACATCCCGCTTCCGCGAGCTGGGTAATAGCGAGGCGCGACCGATCGCCCTTC 1978
Db 7528 AGCACATCCCGCTTCCGCGAGCTGGGTAATAGCGAGGCGCGACCGATCGCCCTTC 7469
Qy 1979 CCAACAGTTGCGCAGCGCTGAATGCGGAAATGCGCGAGCGCCCTGTAGCGCGCGCATTAAG 2038
Db 7468 CCAACAGTTGCGCAGCGCTGAATGCGGAAATGCGCGAGCGCCCTGTAGCGCGCGCATTAAG 7409
Qy 2039 CGCGCGGCTGTGTGTTACGCGAGCGTGACCGCTACACTTGCAGCGCGCTTAGCGCC 2098
Db 7408 CGCGCGGCTGTGTGTTACGCGAGCGTGACCGCTACACTTGCAGCGCGCTTAGCGCC 7349
Qy 2099 CGCTCCTTTGCGCTTCTTCCCTTCTGCGCAGGTTGCGCGGCTTCCCGCTCAAGC 2158
Db 7348 CGCTCCTTTGCGCTTCTTCCCTTCTGCGCAGGTTGCGCGGCTTCCCGCTCAAGC 7289
Qy 2159 TCTAAATCGGGGCTCCCTTTAGGGTTCCGATTTAGTGTCTTTACGGCACCTCGACCCCAA 2218
Db 7288 TCTAAATCGGGGCTCCCTTTAGGGTTCCGATTTAGTGTCTTTACGGCACCTCGACCCCAA 7229
Qy 2219 AAAACTGTAGTGGGTGATGGTTCACTAGTGGGCAATCGCCCTGTAGACGGTTTTTCG 2278
Db 7228 AAAACTGTAGTGGGTGATGGTTCACTAGTGGGCAATCGCCCTGTAGACGGTTTTTCG 7169
Qy 2279 CCCTTTGACGTTGAGTCCACGTTCTTTAATAGTGAAGTCTTGTTCGAACTGGAACAAC 2338
Db 7168 CCCTTTGACGTTGAGTCCACGTTCTTTAATAGTGAAGTCTTGTTCGAACTGGAACAAC 7109
Qy 2339 ACTCAACCCCTATCTCGGTCTATTTCTTTGATTTTAAAGGAGTTTTCGGGCTA 2398
Db 7108 ACTCAACCCCTATCTCGGTCTATTTCTTTGATTTTAAAGGAGTTTTCGGGCTA 7049
Qy 2399 TTGGTTAAAAAATGAGCTGATTTAAACAAATTTAAACGCGAATTTTAAACAAATTTAAC 2458
Db 7048 TTGGTTAAAAAATGAGCTGATTTAAACAAATTTTAAACGCGAATTTTAAACAAATTTAAC 6989
Qy 2459 GTTTACAAATTTCTGATGCGGTATTTCTCTTACGCATCTGTGCGGTATTTTACACCGC 2518
Db 6988 GTTTACAAATTTCTGATGCGGTATTTCTCTCTTACGCATCTGTGCGGTATTTTACACCGC 6929

QY 6898 CTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTGTGATGCTCG 6957
 DB |||||
 QY 2651 CTTTATAGTCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTCGATTTTGTGATGCTCG 2592
 DB |||||
 QY 6958 TCAGGGGGCGGAGCCTATGAAAAACCCAGCAACCGCGGCTTTTACGGTTCTCGGCC 7017
 DB |||||
 QY 2591 TCAGGGGGCGGAGCCTATGAAAAACCCAGCAACCGCGGCTTTTACGGTTCTCGGCC 2532
 DB |||||
 QY 7018 TTTTCTGGCCTTTTGGCTCACATGTTCTTCTCTGGTTATCCCTGATTCTGTGATAAC 7077
 DB |||||
 QY 2531 TTTTCTGGCCTTTTGGCTCACATGTTCTTCTCTGGTTATCCCTGATTCTGTGATAAC 2472
 DB |||||
 QY 7078 CGTATTACCGCTTTTGGTGTAGCTCATACCGCTCGCCGACCGCAACGACGCGGAGC 7137
 DB |||||
 QY 2471 CGTATTACCGCTTTTGGTGTAGCTCATACCGCTCGCCGACCGCAACGACGCGGAGC 2412
 DB |||||
 QY 7138 GAGTCAGTGAGCGAGAAAGCGGAGAGCGCCCAATACGCAACCGCTCTCCCGCGGT 7197
 DB |||||
 QY 2411 GAGTCAGTGAGCGAGAAAGCGGAGAGCGCCCAATACGCAACCGCTCTCCCGCGGT 2352
 DB |||||
 QY 7198 TGGCGGATTCATTATGAGCTGGGACGACAGAGTTTCCGACTGGAAAGCGGCGAGTGAG 7257
 DB |||||
 QY 2351 TGGCGGATTCATTATGAGCTGGGACGACAGAGTTTCCGACTGGAAAGCGGCGAGTGAG 2292
 DB |||||
 QY 7258 CGCAACGCAATTAATGTGAGTTACCTCACTCATTAGGCAACCCAGGCTTTACACTTTATG 7317
 DB |||||
 QY 2291 CGCAACGCAATTAATGTGAGTTACCTCACTCATTAGGCAACCCAGGCTTTACACTTTATG 2232
 DB |||||
 QY 7318 CTTCCGGCTCCTATGTTGTGTGAAATTGTGAGCGGATTAACAATTTACACAGGAAACAGC 7377
 DB |||||
 QY 2231 CTTCCGGCTCCTATGTTGTGTGAAATTGTGAGCGGATTAACAATTTACACAGGAAACAGC 2172
 DB |||||
 QY 7378 TATGACCATGATTACGCCAGCGGCCA 7404
 DB |||||
 QY 2171 TATGACCATGATTACGCCAAGCTTGCA 2145
 DB |||||

RESULT 9

AAT71121/c
 ID AAT71321 standard; DNA; 13414 BP.

AC AAT71321;

DT 11-SEP-1997 (firet entry)

XX Plasmid pCB50 encoding UNC-53 protein variant 7A used as bait vector.

KW UNC-53; neuronal regeneration; revascularisation; wound healing;

KW neurodegenerative disease; Alzheimer's disease; Huntington's;

KW peripheral neuropathies; metastasis inhibition; cancer; circular;

KW Caenorhabditis elegans; ds.

XX Synthetic.

OS WO9638555-A2.

XX 05-DEC-1996.

XX 31-MAY-1996; 96WO-EP002311.

XX 31-MAY-1995; 95GB-00010944.

XX (BOGAERT) BOGAERT T.

PA (STRI/) STRINGHAM E.

PA (VAND/) VANDEKERCKHOVE J.

XX Bogaert T, Stringham E, Vandekerckhove J;

XX WPI; 1997-034369/03.

XX Caenorhabditis elegans UNC-53 protein 8A and 7A variants - useful to

PT promote neuronal regeneration, revascularisation or wound healing.

XX PS Example 15; Page 132-139; 270pp; English.
 CC AAT71321 and AAT71322 are plasmids pCB50 and pCB51, respectively. They
 CC are used as bait vectors in a yeast two hybrid system. pCB50 encodes the
 CC full length UNC-53 protein variant 7A of *Caenorhabditis elegans* and pCB51
 CC encodes a C-terminal portion of this protein. Both vectors were
 CC constructed by cloning the appropriate cDNA fragment into pAS1-CYH2
 CC (Clontech). The yeast two hybrid system was set up for identifying
 CC proteins that interact with UNC-53. UNC-53 protein 8A and 7A variants and
 CC nucleic acids encoding them are useful as medicaments to promote neuronal
 CC regeneration, revascularisation or wound healing, or for treatment of
 CC chronic neurodegenerative diseases (e.g. Alzheimer's or Huntington's
 CC disease) or acute traumatic injuries. Transgenic cells and organisms
 CC transfected with UNC-53 cDNA can be used to determine whether a substance
 CC is an inhibitor or enhancer of the regulation of cell shape or motility
 CC or the direction of cell migration by screening for a phenotypic change
 CC in the cell. Inhibitors can be used to alleviate the spread of disease
 CC inducing cells or metastasis. Probes derived from the cDNA sequences can
 CC be used to identify homologues of the *C. elegans* unc-53 gene. The UNC-53
 CC protein can be used to identify proteins which are active in the signal
 CC transduction pathway that can be used as mentioned above

XX SQ Sequence 13414 BP; 3854 A; 3072 C; 2884 G; 3603 T; 0 U; 1 Other;

	Query Match	Best Local Similarity	Score	DB 2;	Length
	57.4%;	87.3%;	4492.6;	13414;	
	Matches 5104;	Conservative 0;	Mismatches 629;	Indels 114;	Gaps 12;
Qy	1559	TCATGTAATAGTATGTCACGCTTACATTCACGCCCTCCGCCACATCCGCTCTAAACCG	1618		
Db	11004	TCATGTAATAGTATGTCACGCTTACATTCACGCCCTCCGCCACATCCGCTCTAAACCG	10945		
Qy	1619	AAAAGGAAGAGTTAGCAACCTGAACTAGGTCCTTATTTATTTTATAGTATGCT	1678		
Db	10944	AAAAGGAAGAGTTAGCAACCTGAACTAGGTCCTTATTTATTTTATAGTATGCT	10885		
Qy	1679	TAGTATTAAAGAACGTTATTTATATTTTCAAAATTTTCTTTTCTGTACAGACGCTGT	1738		
Db	10884	TAGTATTAAAGAACGTTATTTATATTTTCAAAATTTTCTTTTCTGTACAGACGCTGT	10825		
Qy	1739	ACGCATGTAAACATTATATCTGAAAACCTTGTGTGAGAGGTTTGGAGCGCTCGAAGGCTT	1798		
Db	10824	ACGCATGTAAACATTATATCTGAAAACCTTGTGTGAGAGGTTTGGAGCGCTCGAAGGCTT	10765		
Qy	1799	TAATTTTCGGCGCGGTACCCATTCGCCCTATAGTACGTCGATTTACGCGCGCTCACTGCG	1858		
Db	10764	TAATTTTCGGCGCGGTACCCATTCGCCCTATAGTACGTCGATTTACGCGCGCTCACTGCG	10715		
Qy	1859	CGTCGTTTACACGCTGCTGACTGGGAAAACCCCTGGCGTTACCCAACTTAATCGCCTTGC	1918		
Db	10714	CGTCGTTTACACGCTGCTGACTGGGAAAACCCCTGGCGTTACCCAACTTAATCGCCTTGC	10655		
Qy	1919	AGCACATCCCGCTTTTCGCCAGCTGGCGTAATAGCGAAGAGCGCCGACGATCGCCCTTC	1978		
Db	10654	AGCACATCCCGCTTTTCGCCAGCTGGCGTAATAGCGAAGAGCGCCGACGATCGCCCTTC	10595		
Qy	1979	CCACACGTCGCGAGCGCTGATGCGGATGCGGACGCGCGCTCTAGCGGCGCATTAAG	2038		
Db	10594	CCACACGTCGCGAGCGCTGATGCGGATGCGGACGCGCGCTCTAGCGGCGCATTAAG	10535		
Qy	2039	CGCGCGGCTGTGTTGGTTACGCGCAGCGCTGACCGCTACACTTTCGACGCGCCTTAGCGGC	2098		
Db	10534	CGCGCGGCTGTGTTGGTTACGCGCAGCGCTGACCGCTACACTTTCGACGCGCCTTAGCGGC	10475		
Qy	2099	CGCTCCTTTTCGCTTTCTTCCCTTCTCTTCTCGCACAGTTCGCGCGCTTCCCGCTCAAGC	2158		
Db	10474	CGCTCCTTTTCGCTTTCTTCCCTTCTCTTCTCGCACAGTTCGCGCGCTTCCCGCTCAAGC	10415		
Qy	2159	TCTAAATCGGGGCTCCCTTTAGGGTTCCGATTTAGTCTTTTACGCGACCTCGACCCCAA	2218		
Db	10414	TCTAAATCGGGGCTCCCTTTAGGGTTCCGATTTAGTCTTTTACGCGACCTCGACCCCAA	10355		

QY 2219 AAAAATTGATGGGTGATCGGTTCAAGTGGGGCAATCGCCCTGATAGACGGTTTTTCG 2278
DB 10354 AAAAATTGATGGGTGATCGGTTCAAGTGGGGCAATCGCCCTGATAGACGGTTTTTCG 10295
QY 2279 CCCTTTGACGTTGAGTCCAGGTTCTTAATAGTGGACCTCTTCCAACTCGGAACAC 2338
DB 10294 CCCTTTGACGTTGAGTCCAGGTTCTTAATAGTGGACCTCTTCCAACTCGGAACAC 10235
QY 2339 ACTCAACCCCTATCTCGGTCTATTTCTTTGATTTTAAAGGATTTTGCAGTTTTCGGCCTA 2398
DB 10234 ACTCAACCCCTATCTCGGTCTATTTCTTTGATTTTAAAGGATTTTGCAGTTTTCGGCCTA 10175
QY 2399 TTGGTTAAAAAATAGAGCTGATTTAAACAAAATTTAAACGCAATTTTAAACAAAATTTAAC 2458
DB 10174 TTGGTTAAAAAATAGAGCTGATTTAAACAAAATTTAAACGCAATTTTAAACAAAATTTAAC 10115
QY 2459 GTTTTCAATTTCTCGATGGGATTTTCTCTTACGATCTGCGGTATTTTACACACCGC 2518
DB 10114 GTTTTCAATTTCTCGATGGGATTTTCTCTTACGATCTGCGGTATTTTACACACCGC 10055
QY 2519 ATAGGGTAATPAACTGATATTAATTAATTTGAAGCTCTAAATTTGTGAGTTTAGTATACATGC 2578
DB 10054 ATAGATCGGCAAGTGACAAACAATCTTAATTAATTAATTAATTAATTAATTAATTAAT 9995
QY 2579 ATTTACTTAAATPACAGTTTTTTAGTTTTTGTCTGGCGCATCTTCTCAAAATATGCTTCCCA 2638
DB 9994 TTAGCATTTTGTAGCAAAATTTGCTATTTTGTAGAGTCTTTTACACCAATTTGTCTCCACA 9935
QY 2639 GCCTGCTTTCTGTAGAGTTTCAACCTTACCTTACCTTACCTTCCCTTTTGCATATAGTCC 2698
DB 9934 CCTCCGCTTACATCAAC-----ACCAATTAACGC 9907
QY 2699 TCTTCCAAACAATAATATGTAGATCTGTGAGAGCCACATCATCAAGGTTCTATAGTCTG 2758
DB 9906 CATTTAATCTAAGGGATCAACAATTTTCTGGCGTCACTCAGCTAAATTAAT 9847
QY 2759 TTGACCCAATTCGTCTCCCTTGTGATCTAAACCAACACCGGTTGTATTAATCAACCAATC 2818
DB 9846 GTAAAGCTTTTGGGGCTCTCTTGGCTT-----CCAAACCAAGTCAAGATTCGAATC 9792
QY 2819 GTAACTTCTATCTTTCCACCATGTTCTTTGAGCAATAAAGCCGATTAACAAATCTTT 2878
DB 9791 CAAAAGTTTCACTTGTCCAC-----CTGCTTCTGAATCAAAACAGGGAATAACGAATG 9738
QY 2879 GTGCTCTTTCGCAATGTCAACAGTACCTTATGATATTTCTCCAGTATAGTAGGAGGCCCT 2938
DB 9737 AGTTTCTGTGAGCTGCATGAGTAGTAGTTGCTAGTCTTTTGGAAATACAGTCTTTT 9678
QY 2939 GCATGCAATTTCTGTAACATCAAAAGGCTCTAGGTTCTTTGTTATCTTTCTGCGGC 2998
DB 9677 -----AATAACTGGCAACCGAGAACTCTTTGGTATTTCTTCCACGACTCATCTCCA 9626
QY 2999 CTGCTTCAACCCGCTAACATATCTGGGGCCCAACACCGGTGCAATCTGATATGCTGC 3058
DB 9625 TGCACT-----TGCAAGATATCAATGCGGTAATCATTTGACAGAGCCCAAAACATCTCT 9573
QY 3059 CCATTTCTGCTATCTGTATACACCGCAGAGTAGTGCATTTTGCATGTAATTAACAATGTC 3118
DB 9572 CTTAGGTTGATAGCAACACCGCAACCAAGTATTTTGGAGTGCCTGAACTATTTTATA 9513
QY 3119 AGCAAAATTTTCTGCTTCGAGAGTAAATAATTTGTACTTTGGCGGATTAATGCTTTAGCGG 3178
DB 9512 TG-----CTTTTACAAGACTTGAATTTTCTTGTCAATAAACCGGGTCAATTTGT 9465
QY 3179 CTTAACTGTCCCTCCATGGAATAATCAGTCAAGATATCAACATGTTTATTAGTAACA 3238
DB 9464 TCTCTTTCTATTGGGCACACATATAATACCAGCAAGTCAAGTCAAGTCTAG--AGCA 9407
QY 3239 AATTTTGGGACCTTAATGCTTCAACTTCACTTCACTTCACTTCTTGTGTGATC--GAACATCCA 3297
DB 9406 CATTTCTGGGCGCTCTGTGCTCTGAGCGGCAAACTTTACCAATGACCAAGAACTACCT 9347
QY 3298 ATGAAGCACACAAGTTTGTGCTTTTCTGTCATGATATTAATATAGCTTGGCAGCAACAG 3357

DB 9346 GTCAAAATTAATAACACACATATCTCAAGCTGCCTTTTGTGCTTAATACAGTATCTAC 9287
QY 3358 GACTAGGATGAGTAGCAGACGCTTCTTATATAGTATAGCTTTTCGACATGATTTATCTTCTGTT 3417
DB 9286 GTGCTCAATAGTACCAATGCTCTCTTGGCCCTCTCC-----TTTCTTTT 9238
QY 3418 TCTGTCAGGTTTTTGTGTCAGTTGGTTAAGAAATCTGGGCAATTTTCATGTTTCTT 3477
DB 9237 TTTTCGACCGAATTTAAATCTTAATCGCAAAAAGAAAGCTCCGGA-----T 9190
QY 3478 CAACACTCATATGCGTATATATACCAATCTAAGTCTGTGCTCTCTCTTCTGTTCTTCTTCT 3537
DB 9189 CRAAGATTGTAAGTAAGGTCAGTATTTTCAATAAAGAAATATCTTCCACTACTGCCA 9130
QY 3538 TCTGTTTCGGAGATTACCGAATCAAAAATTTTCAAGAAACCGAAATCAAAAAGAAAT 3597
DB 9129 TCTGGGCTCATTAATCTGCAAGTACATATATTA-----CGATGCTGCTATTAAT 9078
QY 3598 AAAAAAATAATGATGAATTTGAATTTGAAGCTGTGGTATGGTGCACTCTCAGTACAACTCT 3657
DB 9077 GCTTCTCTATATATATATATATAGTAAATGCTGTTGATCTATGTTGCACTCTCAGTACAACTCT 9018
QY 3658 GCTCTGATGCGCATAGTTAAGCCAGCCCGCAACACCCGCAACACCCGCTGACGCGCCT 3717
DB 9017 GCTCTGATGCGCATAGTTAAGCCAGCCCGCAACACCCGCTGACGCGCCT 8958
QY 3718 GACGGCTTGTCTGCTCCGCAATCGCTTTACAGCAAGCTGAGCCGCTCTCCGGAGCT 3777
DB 8957 GACGGCTTGTCTGCTCCGCAATCGCTTTACAGCAAGCTGAGCCGCTCTCCGGAGCT 8898
QY 3778 GCATGCTCAGAGGTTTTTCAACCGTCAACCGAAGCCGCGAGACGAAAGGCTCTCGTGA 3837
DB 8897 GCATGCTCAGAGGTTTTTCAACCGTCAACCGAAGCCGCGAGACGAAAGGCTCTCGTGA 8838
QY 3838 TAGCCTATTTTATAGTTAATGTCATGATATAATAGTTTCTTAGTATGATCCAAATAT 3897
DB 8837 TAGCCTATTTTATAGTTAATGTCATGATATAATAGTTTCTTAGTATGATCCAAATAT 8778
QY 3898 CAAAGCAATATGATGATGAGGATGAGATCAATCCAAATGAGGAGTGGCAGCATATAG 3957
DB 8777 CAAAGCAATATGATGATGAGGATGAGATCAATCCAAATGAGGAGTGGCAGCATATAG 8718
QY 3958 AACAGCTAAAGGTTAGTGTGAGGAGGATACGATACCCCGCATGGAATGGGATATAT 4017
DB 8717 AACAGCTAAAGGTTAGTGTGAGGAGGATACGATACCCCGCATGGAATGGGATATAT 8658
QY 4018 CACAGAGGATCTAGACTACCTTTTCACTTATATATATATATATATATATATATATATAT 4077
DB 8657 CACAGAGGATCTAGACTACCTTTTCACTTATATATATATATATATATATATATATATAT 8598
QY 4078 AAGCATAAACACGCTATGCGGCTTCTCTCATGATATATATATATATATATATATATATAT 4137
DB 8597 AAGCATAAACACGCTATGCGGCTTCTCTCATGATATATATATATATATATATATATATAT 8538
QY 4138 ATATAGTGTGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAG 4197
DB 8537 ATATAGTGTGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAGGATGAG 8478
QY 4198 CGCTGTTTTTGGAAACGCTTTTGAAGTCTTATATATATATATATATATATATATATATATAT 4257
DB 8477 CGCTGTTTTTGGAAACGCTTTTGAAGTCTTATATATATATATATATATATATATATATATAT 8418
QY 4258 TAGGAATTTTCAAGCGCTTTTGAAGACCAAGCGCTCTGAAGACCAAGCGCTTTCAAAAAC 4317
DB 8417 TAGGAATTTTCAAGCGCTTTTGAAGACCAAGCGCTCTGAAGACCAAGCGCTTTCAAAAAC 8358
QY 4318 CAAAACGCAACGCACTGTAACGAGCTACTTAAATATTTGGAATATCGGCTTTCCACAAACA 4377
DB 8357 CAAAACGCAACGCACTGTAACGAGCTACTTAAATATTTGGAATATCGGCTTTCCACAAACA 8298
QY 4378 TTGCTCAAAAGTATCTTTTGTGATATATCTCTGTCATATATCTCTGTCATATATATATATATAT 4437


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QY 6417 AATCTGCTGCTGCAAAACAAAAAACCCACCGCTACAGCGGTGTTGTTGTTGCGGATCA 6476
DB |||||
DB 1236 AATCTGCTGCTGCAAAACAAAAAACCCACCGCTACAGCGGTGTTGTTGTTGCGGATCA 1177
QY 6477 AGAGTACCAACTCTTTTTCGAAGGTAACTGGCTTACAGAGCGGAGATACCAAAATAC 6536
DB |||||
DB 1176 AGAGTACCAACTCTTTTTCGAAGGTAACTGGCTTACAGAGCGGAGATACCAAAATAC 1117
QY 6537 TGTCTCTTCTAGTGTAGCGTGTAGGCGACACACTTCAAGAACTCTGTAGCAGCGCTTAC 6596
DB |||||
DB 1116 TGTCTCTTCTAGTGTAGCGTGTAGGCGACACACTTCAAGAACTCTGTAGCAGCGCTTAC 1057
QY 6597 ATACCTCGCTCTGCTTAATCTGTTTACAGTGGCTGCTGCCAGTGGCGATAGTGTGTCT 6656
DB |||||
DB 1056 ATACCTCGCTCTGCTTAATCTGTTTACAGTGGCTGCTGCCAGTGGCGATAGTGTGTCT 997
QY 6657 TACCGGGTGGACTCAAGACGATAGTTTACCGGATAGGCGCGAGCGGTGGCTGAAACGGG 6716
DB |||||
DB 996 TACCGGGTGGACTCAAGACGATAGTTTACCGGATAGGCGCGAGCGGTGGCTGAAACGGG 937
QY 6717 GGGTTCGTGCACACAGCCCGCTTGGAGCGAACGACCTTACACCGAATGAGATACCTACA 6776
DB |||||
DB 936 GGGTTCGTGCACACAGCCCGCTTGGAGCGAACGACCTTACACCGAATGAGATACCTACA 877
QY 6777 GGGTTCGTGCATCAGAAAGCGCCACGCTTCCGAGAGGAGAGCGGACAGGTATCCGGT 6836
DB |||||
DB 876 GGGTTCGTGCATCAGAAAGCGCCACGCTTCCGAGAGGAGAGCGGACAGGTATCCGGT 817
QY 6837 AAGCGGAGGGTGGAAACGAGAGCGGACGAGGAGCTTCCAGGGGAAACGGCTGTGTA 6896
DB |||||
DB 816 AAGCGGAGGGTGGAAACGAGAGCGGACGAGGAGCTTCCAGGGGAAACGGCTGTGTA 757
QY 6897 TCTTTATAGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 6956
DB |||||
DB 756 TCTTTATAGTCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 697
QY 6957 GTCCAGGGGGGGGAGCTATGAAAAAGCCAGCAACCGCGCTTTTTCAGGTTCTCGGC 7016
DB |||||
DB 696 GTCCAGGGGGGGGAGCTATGAAAAAGCCAGCAACCGCGCTTTTTCAGGTTCTCGGC 637
QY 7017 CTTTTCGCTGGCTTTTGTCTCAATGTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 7076
DB |||||
DB 636 CTTTTCGCTGGCTTTTGTCTCAATGTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 577
QY 7077 CGGTATTACCGCTTTTGTGAGCTGATACGCTCGCGCAGCGCAACGAGCGAGCGAG 7136
DB |||||
DB 576 CGGTATTACCGCTTTTGTGAGCTGATACGCTCGCGCAGCGCAACGAGCGAGCGAG 517
QY 7137 CGAGTCAAGTGAAGGAGCGGAGCGGCGCAATAGCGCAACCGCGCTTCTCCCGCGCG 7196
DB |||||
DB 516 CGAGTCAAGTGAAGGAGCGGAGCGGCGCAATAGCGCAACCGCGCTTCTCCCGCGCG 457
QY 7197 TTGGCCGATTTAATGAGCTGGACGACAGGTTTCCGACTGGAAAGCGGGCAGTGA 7256
DB |||||
DB 456 TTGGCCGATTTAATGAGCTGGACGACAGGTTTCCGACTGGAAAGCGGGCAGTGA 397
QY 7257 GCGCAACGAAATTAATGAGTACTCTCACTATTAGGACCCCGAGCTTTTACACTTTAT 7316
DB |||||
DB 396 GCGCAACGAAATTAATGAGTACTCTCACTATTAGGACCCCGAGCTTTTACACTTTAT 337
QY 7317 GCTTCGGGCTCTATGTTGTGGAAATGTGAGCGGATAACAAATTTTACACAGGAAACAG 7376
DB |||||
DB 336 GCTTCGGGCTCTATGTTGTGGAAATGTGAGCGGATAACAAATTTTACACAGGAAACAG 277
QY 7377 CTATGACCAATGATTACGCCAAGCGGCA 7404
DB |||||
DB 276 CTATGACCAATGATTACGCCAAGCGTGA 249
```

RESULT 11
ABV77349
ID ABV77349 standard; DNA; 9952 BP.
XX

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AC ABV77349;
XX 24-FEB-2003 (first entry)
XX Yeast expression vector for the E. coli glucuronidase gene.
XX
XX Gender-sorting; ligand dependent transactivation; sex separation;
XX poultry industry; glucuronidase gene; ds.
XX
XX Saccharomyces cerevisiae.
XX Escherichia coli.
XX Homo sapiens.
XX Synthetic.
XX W0200286446-A2.
XX
XX 31-OCT-2002.
XX
XX 23-APR-2002; 2002WO-US012590.
XX
XX 23-APR-2001; 2001US-0286010P.
XX (LIFE-) LIFESENSORS INC.
XX
XX Butt T, Tran HT;
XX WPI; 2003-075636/07.
XX
XX New ligand dependent transactivation system, useful for accurate and
XX efficient gender sorting in mammalian and avian species, and for
XX assessing patient populations for their susceptibility to drugs and
XX predisposition to disease.
XX
XX Disclosure; Fig 12; 79pp; English.
XX
XX The invention relates to a new ligand dependent transactivation system
XX for gender-sorting in a test animal. The ligand dependent transactivation
XX system is useful for accurate and efficient gender sorting in mammalian
XX and avian species. The method may also be used to advantage to gender
XX sort other animal species, and to assess patient populations for their
XX susceptibility to drugs and predisposition to disease. The method of the
XX invention may be useful in the poultry industry. Unlike previous methods
XX (e.g. radioimmunoassays), which are cumbersome, expensive and not readily
XX adaptable to high throughput formats, the new method provides robustness,
XX cost-effectiveness, and is 100% accurate. The yeast transactivation is
XX 100-fold more sensitive to 17-beta estradiol when compared to mammalian
XX cell assays and no transactivation was observed with the indicated
XX concentration of oestrogen glucuronides. The current sequence represents
XX the yeast expression vector for the E. coli glucuronidase gene - pRS425-
XX GPD-Ub-GUS
XX
XX Sequence 9952 BP; 2823 A; 2246 C; 2243 G; 2640 T; 0 U; 0 Other;
XX
XX Query Match 46.3%; Score 3623; DB 7; Length 9952;
XX Best Local Similarity 100.0%; Pred. No. 0;
XX Matches 3623; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
XX
QY 3820 GACGAAAGGGCCTCGTATACGCTATTTTATAGGTTAATGTCATGATAATAGTGT 3879
DB |||||
DB 1 GACGAAAGGGCCTCGTATACGCTATTTTATAGGTTAATGTCATGATAATAGTGT 60
QY 3880 CTTAGTATGATCCCAATATCAAGGAAATGATAGCATTCGAAGGATGAGACTAATCCAATG 3939
DB |||||
DB 61 CTTAGTATGATCCCAATATCAAGGAAATGATAGCATTCGAAGGATGAGACTAATCCAATG 120
QY 3940 AGGAGTGGCAGCATATAGAACAGCTAAGGGTAGTGTGTAAGGAAGCATACATACCCCG 3999
DB |||||
DB 121 AGGAGTGGCAGCATATAGAACAGCTAAGGGTAGTGTGTAAGGAAGCATACATACCCCG 180
QY 4000 CATGGAATGGGATATATCAAGGAGGTACTAGACTCTTTCATCCTACATAATAGAC 4059
DB |||||
DB 181 CATGGAATGGGATATATCAAGGAGGTACTAGACTCTTTCATCCTACATAATAGAC 240
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QY 4060 GCATATAAGTACGCAATTAAGCATATAACACGCACTATGCCGTTCTTCTCATGTATATATA 4119
Db 241 GCATATAAGTACGCAATTAAGCATATAACACGCACTATGCCGTTCTTCTCATGTATATATA 300
QY 4120 TATACAGGCAACACGCAATATAGTGCAGCTGCAAGTGAAGTGTATGTGCGAGCTC 4179
Db 301 TATACAGGCAACACGCAATATAGTGCAGCTGCAAGTGAAGTGTATGTGCGAGCTC 360
QY 4180 GCGTGTGCAATTTCCGAAAGCGCTCGTTTTCCGAAACGCTTTGAAAGTTCCTATTCCGAAGTT 4239
Db 361 GCGTGTGCAATTTCCGAAAGCGCTCGTTTTCCGAAACGCTTTGAAAGTTCCTATTCCGAAGTT 420
QY 4240 CCTATTCTCTAGAAAGTATAGGAACCTTCAGAGCGCTTTTGAAACCAAAAGCGCTCGAA 4299
Db 421 CCTATTCTCTAGAAAGTATAGGAACCTTCAGAGCGCTTTTGAAACCAAAAGCGCTCGAA 480
QY 4300 GAGCAGCTTTCAAAAAACCAAAACGCAACGCACTGTAACGAGCTACTTAAATAATTCCGA 4359
Db 481 GAGCAGCTTTCAAAAAACCAAAACGCAACGCACTGTAACGAGCTACTTAAATAATTCCGA 540
QY 4360 ATACCGCTTCCACAAACATTTGCTCAAAAGTATCTCTTTGCTATATATCTCTGTGCTATAT 4419
Db 541 ATACCGCTTCCACAAACATTTGCTCAAAAGTATCTCTTTGCTATATATCTCTGTGCTATAT 600
QY 4420 CCTATATAACCTTACCCATCCACTTTTCGCTCTTGAACCTTGATCTTAAACTCGACCTCT 4479
Db 601 CCTATATAACCTTACCCATCCACTTTTCGCTCTTGAACCTTGATCTTAAACTCGACCTCT 660
QY 4480 ACATTTTTTATGTTTACTCTAGTATTACTCTTTAGACAAAAAATTTGTAAGAACTA 4539
Db 661 ACATTTTTTATGTTTACTCTAGTATTACTCTTTAGACAAAAAATTTGTAAGAACTA 720
QY 4540 TTCTATAGAGTGAATCGAAAAACAATFACGAAATGTAAACATTTTCTATACGTAGTATATAG 4599
Db 721 TTCTATAGAGTGAATCGAAAAACAATFACGAAATGTAAACATTTTCTATACGTAGTATATAG 780
QY 4600 AGACAAATATAGAAACCGTTTCAATATTTTCTGACCAATGAAGATCATCAACGCTATC 4659
Db 781 AGACAAATATAGAAACCGTTTCAATATTTTCTGACCAATGAAGATCATCAACGCTATC 840
QY 4660 ACTTTCTGTTTCAAAAAGTATGCGCAATCCACATCGGTATAGAAATATAATCGGGAGTGCCT 4719
Db 841 ACTTTCTGTTTCAAAAAGTATGCGCAATCCACATCGGTATAGAAATATAATCGGGAGTGCCT 900
QY 4720 TTATCTTGAAAAATGACACCGGAGCTTCGCTAGTATCAGTAAACCGCGGAAAGTGAGT 4779
Db 901 TTATCTTGAAAAATGACACCGGAGCTTCGCTAGTATCAGTAAACCGCGGAAAGTGAGT 960
QY 4780 CAGCCTTTTTTATGGAAGAAATAAGACACCAAGTAGCCTTCTTCTAACCTTAAACGG 4839
Db 961 CAGCCTTTTTTATGGAAGAAATAAGACACCAAGTAGCCTTCTTCTAACCTTAAACGG 1020
QY 4840 ACCTACAGTCNAAAAGTATCAAGAGCTGCATTATAGAGCCGACACAAAGGAGAAAAA 4899
Db 1021 ACCTACAGTCNAAAAGTATCAAGAGCTGCATTATAGAGCCGACACAAAGGAGAAAAA 1080
QY 4900 GTAATCTAAGAGTCTTTGTTAGAAAAATAGCGCTCTCGGATGCAATTTTGTAGAAACAA 4959
Db 1081 GTAATCTAAGAGTCTTTGTTAGAAAAATAGCGCTCTCGGATGCAATTTTGTAGAAACAA 1140
QY 4960 AAAGAAGTATAGATCTTTGTTGTAATAATAGCGCTCTCGGTTGCAATTTCTGTTCTGTA 5019
Db 1141 AAAGAAGTATAGATCTTTGTTGTAATAATAGCGCTCTCGGTTGCAATTTCTGTTCTGTA 1200
QY 5020 ABAATGAGCTCAGATCTTTGTTGTAATAATAGCGCTCTCGGTTGCAATTTTGTGTTT 5079
Db 1201 ABAATGAGCTCAGATCTTTGTTGTAATAATAGCGCTCTCGGTTGCAATTTTGTGTTT 1260
QY 5080 ACAAATATGAAGCAGATCTTCTGTTGTAATAATAGCGCTCTCGGTTGCAATTTCTGTT 5139
Db 1261 ACAAATATGAAGCAGATCTTCTGTTGTAATAATAGCGCTCTCGGTTGCAATTTCTGTT 1320
QY 5140 CTGTAAAAATGCAAGCTCAGATCTTTGTTGTAATAATAGCGCTCTCGGTTGCAATTTT 5199

Db 1321 CTGTAAAAATGCAAGCTCAGATCTTTGTTGTAATAATAGCGCTCTCGGTTGCAATTTT 1380
QY 5200 GTTCTCAAAAATGAAGCAGATCTTCTGTTCAAGTGGCACTTTTCCGGGAAATGTGCGC 5259
Db 1381 GTTCTCAAAAATGAAGCAGATCTTCTGTTCAAGTGGCACTTTTCCGGGAAATGTGCGC 1440
QY 5260 GGAACCCCTATTGTTTCTAAATAATCTTCAAAATATGATCGGCTCATGAGACAA 5319
Db 1441 GGAACCCCTATTGTTTCTAAATAATCTTCAAAATATGATCGGCTCATGAGACAA 1500
QY 5320 TAACCCCTGATAAATGCTTCAATAATATGAAAAGGAGAGTATGAGTATTTCAACATTC 5379
Db 1501 TAACCCCTGATAAATGCTTCAATAATATGAAAAGGAGAGTATGAGTATTTCAACATTC 1560
QY 5380 CGTGTGCGCCCTTATTTCCCTTTTGGGCACTTTTGCCTCTCTGTTTGTCTCACCCAGAA 5439
Db 1561 CGTGTGCGCCCTTATTTCCCTTTTGGGCACTTTTGCCTCTCTGTTTGTCTCACCCAGAA 1620
QY 5440 ACCTGCTGAAAGTAAAGATGCTGAAGATCAGTTGGGTGCAAGAGTGGTTACATCGAA 5499
Db 1621 ACCTGCTGAAAGTAAAGATGCTGAAGATCAGTTGGGTGCAAGAGTGGTTACATCGAA 1680
QY 5500 CTGGATCTCAACAGCGGTAAAGTCTTGAAGTCTTGGGCGGAAAGAACTTTTCCAATG 5559
Db 1681 CTGGATCTCAACAGCGGTAAAGTCTTGAAGTCTTGGGCGGAAAGAACTTTTCCAATG 1740
QY 5560 ATGAGCACATTTTAAAGTCTGCTATGTTGGCGGCTATTTATCCGCTATTTGACCGCGGCA 5619
Db 1741 ATGAGCACATTTTAAAGTCTGCTATGTTGGCGGCTATTTATCCGCTATTTGACCGCGGCA 1800
QY 5620 GAGCAACTCGGTGCGCGCATACACTATTTCTCAGAAATGACTTGGTTGAGTACTCACAGTC 5679
Db 1801 GAGCAACTCGGTGCGCGCATACACTATTTCTCAGAAATGACTTGGTTGAGTACTCACAGTC 1860
QY 5680 ACAGAAAGCATCTTACGGATGCGATGACAGTAAAGAAATTAAGCACTGCTGCCATAAACC 5739
Db 1861 ACAGAAAGCATCTTACGGATGCGATGACAGTAAAGAAATTAAGCACTGCTGCCATAAACC 1920
QY 5740 ATGAGTGAATAAATCTCGGCAACTTACTTCTGACAAACGATCGAGGACCGGAGAGCTA 5799
Db 1921 ATGAGTGAATAAATCTCGGCAACTTACTTCTGACAAACGATCGAGGACCGGAGAGCTA 1980
QY 5800 ACCGCTTTTTTGCAACAATGCGGATCATGTAACTCGCTTGCCTTGCCTGCGGAAACCGAG 5859
Db 1981 ACCGCTTTTTTGCAACAATGCGGATCATGTAACTCGCTTGCCTTGCCTGCGGAAACCGAG 2040
QY 5860 CTGAATGAAGCCATACCAAAACGAGCGGTGACACCAACGATGCTGTAGCAATGGCAACA 5919
Db 2041 CTGAATGAAGCCATACCAAAACGAGCGGTGACACCAACGATGCTGTAGCAATGGCAACA 2100
QY 5920 ACCTTGGCGCAACTTATTAACTGGCGAACTACTTACTTACTAGCTTCCCGGCAACAATTAATA 5979
Db 2101 ACCTTGGCGCAACTTATTAACTGGCGAACTACTTACTTACTAGCTTCCCGGCAACAATTAATA 2160
QY 5980 GACTGATGAGCGGATAAAGTTGAGGACCACTTCTGCGCTGCGGCTTCCGCTGCGC 6039
Db 2161 GACTGATGAGCGGATAAAGTTGAGGACCACTTCTGCGCTGCGGCTTCCGCTGCGC 2220
QY 6040 TGGTTTATGCTCATTAATCTGAGCGGTTGAGGTTGGGTCTCGCGGTATCATTTGACGA 6099
Db 2221 TGGTTTATGCTCATTAATCTGAGCGGTTGAGGTTGGGTCTCGCGGTATCATTTGACGA 2280
QY 6100 CTGGGCGCAGATGTTAAGCCCTCCCGTATCTGATTTACTTACTAGCTTCCCGGCAACAATTAATA 6159
Db 2281 CTGGGCGCAGATGTTAAGCCCTCCCGTATCTGATTTACTTACTAGCTTCCCGGCAACAATTAATA 2340
QY 6160 ACTATGATGAACGAAATAGACAGATGCTGAGATAGGTCCTCATGATTAAGCATGG 6219
Db 2341 ACTATGATGAACGAAATAGACAGATGCTGAGATAGGTCCTCATGATTAAGCATGG 2400
QY 6220 TAACTGTGACACCAAGTTTACTCATATATATTTAGATTGATTTAAACTTCAATTTTAA 6279

3940 AGAGTGGCAGCATATATAGAACAGCTAAAGGGTAGTGTCTGAAGGAGCATACGATACCCCG 3999
Db
120 AGAGTGGCAGCATATATAGAACAGCTAAAGGGTAGTGTCTGAAGGAGCATACGATACCCCG 179
Qy
4000 CATGGAATGGATATATACAGAGGAGTACTAGACTACCTTTTCATCTACATATAAGAC 4059
Db
180 CATGGAATGGATATATACAGAGGAGTACTAGACTACCTTTTCATCTACATATAAGAC 239
Qy
4060 GCATATAGTACGATTTAAGCATATAACAGCGACTATGCGGTTCTTCTCATGTATATATA 4119
Db
240 GCATATAGTACGATTTAAGCATATAACAGCGACTATGCGGTTCTTCTCATGTATATATA 299
Qy
4120 TATACAGGCAACGAGATATAGTGGAGCTGAGAGTGAACAGTGTATGTGCGAGCTC 4179
Db
300 TATACAGGCAACGAGATATAGTGGAGCTGAGAGTGAACAGTGTATGTGCGAGCTC 359
Qy
4180 GCGTTGCAATTTTCGGAAGCGCTCGTTTTCGGAACGCTTTGGAAGTCTCTAATCCGAGTT 4239
Db
360 GCGTTGCAATTTTCGGAAGCGCTCGTTTTCGGAACGCTTTGGAAGTCTCTAATCCGAGTT 419
Qy
4240 CCTATTCTCTAGAAAGTATAGGAACCTTCAGAGCGCTTTTGAAACCAAAAAGCGCTCTGAA 4299
Db
420 CCTATTCTCTAGAAAGTATAGGAACCTTCAGAGCGCTTTTGAAACCAAAAAGCGCTCTGAA 479
Qy
4300 GACGCACTTTCAAAAACCAAAAACGCAACGCGACTGTAACGAGTACTAAAAATATTGCGA 4359
Db
480 GACGCACTTTCAAAAACCAAAAACGCAACGCGACTGTAACGAGTACTAAAAATATTGCGA 539
Qy
4360 ATACCGCTTCCACAAACATTTGCTCAAAAGTATCTTTGCTATATATCTCTGTGCTATAT 4419
Db
540 ATACCGCTTCCACAAACATTTGCTCAAAAGTATCTTTGCTATATATCTCTGTGCTATAT 599
Qy
4420 CCCTATATAACCTACCCATCCACTTTTCGCTCTCTGAACTTGCACTTGCACTTAACCTCGACTCT 4479
Db
600 CCCTATATAACCTACCCATCCACTTTTCGCTCTCTGAACTTGCACTTGCACTTAACCTCGACTCT 659
Qy
4480 ACATTTTATAGTTTATCTCTAGTATTAATCTCTTTAGACAAAAAATTTGTAAGAACTA 4539
Db
660 ACATTTTATAGTTTATCTCTAGTATTAATCTTTTAGACAAAAAATTTGTAAGAACTA 719
Qy
4540 TTCTATAGAGTGAATCGAAACAATACGAAATGTAACATTTTCTATACGTAGTATATAG 4599
Db
720 TTCTATAGAGTGAATCGAAACAATACGAAATGTAACATTTTCTATACGTAGTATATAG 779
Qy
4600 AGACAAAATAGAGAAACCGTTTCATATTTTCTGACCAATGAAGAATCATCAACGCTATC 4659
Db
780 AGACAAAATAGAGAAACCGTTTCATATTTTCTGACCAATGAAGAATCATCAACGCTATC 839
Qy
4660 ACTTCTGTTTCAAAAGTATGCGGAATCCACATCGGTATAGAAATATAATCGGGGATGCCT 4719
Db
840 ACTTCTGTTTCAAAAGTATGCGGAATCCACATCGGTATAGAAATATAATCGGGGATGCCT 899
Qy
4720 TTATCTTGAATAATGCACCCGAGCTTCGCTAGTAACTAGTAAACGCGGAATGCGAGT 4779
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900 TTATCTTGAATAATGCACCCGAGCTTCGCTAGTAACTAGTAAACGCGGAATGCGAGT 959
Qy
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Db
960 CAGGCTTTTATTTAGGAAGAAAAATAGACACCAAAAGTAGCTTCTTCTAAACCTTAACGG 1019
Qy
4840 ACTTACAGTCAAAAAGTTTATCAAGAGACTGCAATTTAGAGCGCAAAAAGGAGAAAAAA 4899
Db
1020 ACTTACAGTCAAAAAGTTTATCAAGAGACTGCAATTTAGAGCGCAAAAAGGAGAAAAAA 1079
Qy
4900 GTAATCTAGATGCTTTGTTAGAAAAATAGCGCTCTCGGATGCAATTTTGTAGAACAA 4959
Db
1080 GTAATCTAGATGCTTTGTTAGAAAAATAGCGCTCTCGGATGCAATTTTGTAGAACAA 1139
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4960 AAAAGAGTATAGATTTCTTTGTTGTAATAATAGCGCTCTCGGTTGCAATTTCTGTTGTA 5019
Db
1140 AAAAGAGTATAGATTTCTTTGTTGTAATAATAGCGCTCTCGGTTGCAATTTCTGTTGTA 1199
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Db
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Qy
5140 CTGTAAAAATGCAGCTCAGATTTCTTTGTTGTAATAATAGCGCTCTCGGTTGCAATTTT 5199
Db
1320 CTGTAAAAATGCAGCTCAGATTTCTTTGTTGTAATAATAGCGCTCTCGGTTGCAATTTT 1379
Qy
5200 GTTCTAAAAATGAAGCAGACAGATTTCTTTGTTGTAATAATAGCGCTCTCGGTTGCAATTTT 5259
Db
1380 GTTCTAAAAATGAAGCAGACAGATTTCTTTGTTGTAATAATAGCGCTCTCGGTTGCAATTTT 1439
Qy
5260 GGAACCCCTATTGTTGTTTATTTTCTAAAAATACATTTCAAAATGATGATCGCTCATGAGACAA 5319
Db
1440 GGAACCCCTATTGTTGTTTATTTTCTAAAAATACATTTCAAAATGATGATCGCTCATGAGACAA 1499
Qy
5320 TAAACCTGATAAATGCTTCAATAATATTGAAAAAGGAGATGATGATTTCAACATTTT 5379
Db
1500 TAAACCTGATAAATGCTTCAATAATATTGAAAAAGGAGATGATGATTTCAACATTTT 1559
Qy
5380 CGTGTGCGCCCTTATTTCCCTTTTGTGGGCAATTTTGTGCTCTCTGTTTGTCTCACCCAGAA 5439
Db
1560 CGTGTGCGCCCTTATTTCCCTTTTGTGGGCAATTTTGTGCTCTCTGTTTGTCTCACCCAGAA 1619
Qy
5440 ACSCTGCTGAAGTAAAGATGCTGAAGATGCTGAGATGCTGAGATGCTGAGTGGGTATACATCGAA 5499
Db
1620 ACSCTGCTGAAGTAAAGATGCTGAAGATGCTGAGATGCTGAGATGCTGAGTGGGTATACATCGAA 1679
Qy
5500 CTGGATCTCAACAGCGGTAAAGTCTTTGAGAGTCTTTCGCCCCGAAAGAACCTTTTCCAATG 5559
Db
1680 CTGGATCTCAACAGCGGTAAAGTCTTTGAGAGTCTTTCGCCCCGAAAGAACCTTTTCCAATG 1739
Qy
5560 ATGAGCACTTTTAAAGTCTGCTATGTTGGGCGGTATTTATCCCGTATTTGACGCGGGCAA 5619
Db
1740 ATGAGCACTTTTAAAGTCTGCTATGTTGGGCGGTATTTATCCCGTATTTGACGCGGGCAA 1799
Qy
5620 GAGCAACTCGGTGCGCGCATACACTATTTCTCAGAAATGACTTGTGAGTACTCACAGTC 5679
Db
1800 GAGCAACTCGGTGCGCGCATACACTATTTCTCAGAAATGACTTGTGAGTACTCACAGTC 1859
Qy
5680 ACAGAAAAGCATCTTACGGATGCGATGACAGATGAAGAGATTTATGCACTGTGTCATAAACC 5739
Db
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Qy
5740 ATGAGTGAATAACCTGCGGCAACCTTATCTTCTGACAAACGATCGGAGAACCGAGAGCTA 5799
Db
1920 ATGAGTGAATAACCTGCGGCAACCTTATCTTCTGACAAACGATCGGAGAACCGAGAGCTA 1979
Qy
5800 ACCGCTTTTTCACAACTGCGGGATCATGTAACCTCGCTTCATCGTTCGTTGGAACCGGAG 5859
Db
1980 ACCGCTTTTTCACAACTGCGGGATCATGTAACCTCGCTTCATCGTTCGTTGGAACCGGAG 2039
Qy
5860 CTGAATGAAGCCATACCAAAACGAGCGGTGACACCAAGTGTCTGTAGCAATGGCAACA 5919
Db
2040 CTGAATGAAGCCATACCAAAACGAGCGGTGACACCAAGTGTCTGTAGCAATGGCAACA 2099
Qy
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Db
2100 ACCTTTCGCAAACTATTAATCTGCGAACTAATTTATCTTCTAGTCTTCCCGGCAACAAATTAATA 2159
Qy
5980 GACTGATGAGGCGGATAAAGTTGAGGACCACTTCTGCGCTCGGCTTCCGCTGCG 6039
Db
2160 GACTGATGAGGCGGATAAAGTTGAGGACCACTTCTGCGCTCGGCTTCCGCTGCG 2219
Qy
6040 TGGTTTATTTGCTGATAAATCTGAGCGCGGTGAGCGTGGGTCTCGCGTATCATTTGACGCA 6099
Db
2220 TGGTTTATTTGCTGATAAATCTGAGCGCGGTGAGCGTGGGTCTCGCGTATCATTTGACGCA 2279
Qy
6100 CTGGGCGCATAGTGAAGCCCTCCCTATGCTAGTATTTATCTACAGAGCGGGAGTCAGGCA 6159

Db 2280 CTGGGCGCAGATGGTAAGCCCTCCGATATCGTAGTTATCTACAGACGGGAGTCAGGCA 2339
Qy 6160 ACTATGGATGAACGAATAGACAGATCGCTCAGATAGTGTGCTCCTCAGTATTAAGCATTTG 6219
Db 2340 ACTATGGATGAACGAATAGACAGATCGCTCAGATAGTGTGCTCCTCAGTATTAAGCATTTG 2399
Qy 6220 TAACTGTGTCAGACCAAGTTTACTCATATATACCTTTAGATTTGATTTAAACCTTCATTTTAA 6279
Db 2400 TAACTGTGTCAGACCAAGTTTACTCATATATACCTTTAGATTTGATTTAAACCTTCATTTTAA 2459
Qy 6280 TTTAAAGGATCTAGGTGAAGATCTTTTGTGATTAATCTCATGACAAAATCCCTTAAAGT 6339
Db 2460 TTTAAAGGATCTAGGTGAAGATCTTTTGTGATTAATCTCATGACAAAATCCCTTAAAGT 2519
Qy 6340 GAGTTTTCGTTCCACTGAGCGTCAGACCCCTGAGAAAGATCAAGAGATCTTCTTGAGAT 6399
Db 2520 GAGTTTTCGTTCCACTGAGCGTCAGACCCCTGAGAAAGATCAAGAGATCTTCTTGAGAT 2579
Qy 6400 CCTTTTTCGTCGGCTAATCTGCTGCTTGCATAAACAACCAACCAACCAACCAACCAACCAAC 6459
Db 2580 CCTTTTTCGTCGGCTAATCTGCTGCTTGCATAAACAACCAACCAACCAACCAACCAACCAAC 2639
Qy 6460 GTTGTGTCGCGATCAAGAGTACCAACTCTTTTCCGAAGTAACTGGCTTCAGCAGA 6519
Db 2640 GTTGTGTCGCGATCAAGAGTACCAACTCTTTTCCGAAGTAACTGGCTTCAGCAGA 2699
Qy 6520 GCGAGATACCAACTGCTCTTCTAGTGTAGCGTAGTTAGGCCACCACTTCAAGAC 6579
Db 2700 GCGAGATACCAACTGCTCTTCTAGTGTAGCGTAGTTAGGCCACCACTTCAAGAC 2759
Qy 6580 TCTGTAGCACCCCTACATACCTCTGCTCTGCTTAATCTGTTTACAGTGGCTGCTGCCAGT 6639
Db 2760 TCTGTAGCACCCCTACATACCTCTGCTCTGCTTAATCTGTTTACAGTGGCTGCTGCCAGT 2819
Qy 6640 GCGATAAGTGTGTCTTAACGGGTGGA CTCAAGACGATAGTTACCGGATAAGCGCAG 6699
Db 2820 GCGATAAGTGTGTCTTAACGGGTGGA CTCAAGACGATAGTTACCGGATAAGCGCAG 2879
Qy 6700 CGGTGGGCTGAACGGGGGTTCTGTCACACAGCCAGCTTGGAGCGNACCACTACAC 6759
Db 2880 CGGTGGGCTGAACGGGGGTTCTGTCACACAGCCAGCTTGGAGCGNACCACTACAC 2939
Qy 6760 GAACTGAGATACCTACAGGTGAGCTATGAGAAAGCGCCAGCTTCCGAAGGAGAAAG 6819
Db 2940 GAACTGAGATACCTACAGGTGAGCTATGAGAAAGCGCCAGCTTCCGAAGGAGAAAG 2999
Qy 6820 GCGGACAGGTATCCGTAAGCGGACAGGTTCGGAACAGAGAGCGCACGAGGAGCTTCCA 6879
Db 3000 GCGGACAGGTATCCGTAAGCGGACAGGTTCGGAACAGAGAGCGCACGAGGAGCTTCCA 3059
Qy 6880 GGGGAAAGCGCTGTATCTTTATAGTCTGTCGGGTTTCGCCACCTTGATTTGAGGT 6939
Db 3060 GGGGAAAGCGCTGTATCTTTATAGTCTGTCGGGTTTCGCCACCTTGATTTGAGGT 3119
Qy 6940 CGATTTTGTGATGCTGTCAGGGGGGGAGCCCTATCGAAAAACGCCAGCAACCGCGCC 6999
Db 3120 CGATTTTGTGATGCTGTCAGGGGGGGAGCCCTATCGAAAAACGCCAGCAACCGCGCC 3179
Qy 7000 TTTTACGGTCTCTGGCCCTTTGTCGGCTTTTGTCTACATGTTCTTTCTGCGTTATCC 7059
Db 3180 TTTTACGGTCTCTGGCCCTTTGTCGGCTTTTGTCTACATGTTCTTTCTGCGTTATCC 3239
Qy 7060 CTGATTTGTGATTAACCGTATTAACCGCTTTGAGTGTAGCTGATACCGCTCGCGGACG 7119
Db 3240 CTGATTTGTGATTAACCGTATTAACCGCTTTGAGTGTAGCTGATACCGCTCGCGGACG 3299
Qy 7120 CGAACCGACCGCAGCGAGTCAGTGTAGCGAGGAGCGGAGAGCGCCCAATACGAAA 7179
Db 3300 CGAACCGACCGCAGCGAGTCAGTGTAGCGAGGAGCGGAGAGCGCCCAATACGAAA 3359
Qy 7180 CGGCTCTCTCCCGCGTGTGGCGATTCAATATGACGTGGCAGCAGAGGTTTCCGAC 7239
Db 3360 CGGCTCTCTCCCGCGTGTGGCGATTCAATATGACGTGGCAGCAGAGGTTTCCGAC 3419

Qy 7240 TGGAAAGCGGCACTGAGCGCAACGCAATTAATGTGAGTTACCTCACTTAGGCAACC 7299
Db 3420 TGGAAAGCGGCACTGAGCGCAACGCAATTAATGTGAGTTACCTCACTTAGGCAACC 3479
Qy 7300 CAGGCTTTACATTTTATGCTTCGGCTCCTATGTTGTGGAATTGTGAGCGGATAACA 7359
Db 3480 CAGGCTTTACATTTTATGCTTCGGCTCCTATGTTGTGGAATTGTGAGCGGATAACA 3539
Qy 7360 TTTTCACACAGAAACAGCTATGACCATGATTCACGCAAGCGGCAATTAACCTCACTAA 7419
Db 3540 TTTTCACACAGAAACAGCTATGACCATGATTCACGCAAGCGGCAATTAACCTCACTAA 3599
Qy 7420 AGGGAACAAAGCTGGAGCTCGTAGGAACAATTTTC 7454
Db 3600 AGGGAACAAAGCTGGAGCTCAGTTTATCATATC 3634

RESULT 13

ADC75054
ID ADC75054 standard; DNA; 6671 BP.

XX ADC75054;

XX 01-JAN-2004 (first entry)

XX T-cell receptor-related pYX112 DNA.

XX soluble T cell receptor; sTCR; TCR alpha; TCR beta chain;

KW immunosuppressive; antidiabetic; major histocompatibility complex; MHC;

KW tumour; ds; pYX122.

XX Unidentified.

XX W02003020763-A2.

XX 13-MAR-2003.

XX 30-AUG-2002; 2002WO-GB003986.

XX 31-AUG-2001; 2001GB-00021187.

PR 16-AUG-2002; 2002GB-00019146.

PR 16-AUG-2002; 2002US-0404182P.

XX (AVID-) AVIDEX LTD.

XX Jakobsen BK, Glick M;

XX WPI; 2003-313073/30.

XX Novel soluble T cell receptor comprising all or part of T cell receptor alpha or beta chain which comprise functional variable domain and part of constant domain of receptor chain, and lack transmembrane domain.

XX Example 15; Fig 107; 164pp; English.

XX The invention relates to a novel soluble T cell receptor (sTCR) which comprises all or part of a TCR alpha or TCR beta chain, except its transmembrane domain, where each chain comprises a functional variable domain and at least a part of the constant domain of the TCR chain and are linked by a disulphide bond between constant domain residues which is not present in the native TCR. The molecule of the invention demonstrates immunosuppressive and antidiabetic activities and may be useful for detecting major histocompatibility complex (MHC)-peptide complexes, for tracking or targeting cells presenting particular antigens in vitro or in vivo and as intermediates for the production of further multivalent TCR complexes having such uses. Furthermore, the molecules may be useful for delivering anti-tumour molecules specific for tumour antigens. The current sequence is that of the sTCR-related DNA of the invention.

XX Sequence 6671 BP; 1781 A; 1529 C; 1433 G; 1928 T; 0 U; 0 Other;

Query Match 43.0%; Score 3364; DB 9; Length 6671;

Best Local Similarity 80.0%; Pred. No. 0; Matches 4443; Conservative 0; Mismatches 285; Indels 828; Gaps 8;

Best Local Similarity 80.0%; Pred. No. 0; Matches 443; Conservative 0; Mismatches 285; Indels 828; Gaps 8;			
QY	1851	TCACGCGCGTCTGTTTAAACAGCTGCTGACATGGGAAAAACCTCGCGTTTACCCAACTTAAT	1910
DB	231	TCACGCGCGTCTGTTTAAACAGCTGCTGACATGGGAAAAACCTCGCGTTTACCCAACTTAAT	290
QY	1911	CGCCTTGACGACATCCCTTTTCGCGAGCTGGCGTAATAGCGAAGAGCCGCGACCGAT	1970
DB	291	CGCCTTGACGACATCCCTTTTCGCGAGCTGGCGTAATAGCGAAGAGCCGCGACCGAT	350
QY	1971	CGCCCTTCCAAACAGTTGCGCAGCTGAATGGCGAATGGCGGACGCGCCCTGTAGCGGC	2030
DB	351	CGCCCTTCCAAACAGTTGCGCAGCTGAATGGCGAATGGCGGACGCGCCCTGTAGCGGC	410
QY	2031	GCATTAAGCGCGCGGGTGTGGTGTATACGCGACGCTGACCGCTACACTTTGCCAGCGCC	2090
DB	411	GCATTAAGCGCGCGGGTGTGGTGTATACGCGACGCTGACCGCTACACTTTGCCAGCGCC	470
QY	2091	CTAGCGCCGCTCTTTTCGCTTTCTCCCTTTCGCCAAGTTTCGCGGCTTTTCCC	2150
DB	471	CTAGCGCCGCTCTTTTCGCTTTCTCCCTTTCGCCAAGTTTCGCGGCTTTTCCC	530
QY	2151	CGTCAAGCTCTAATCGGGGCTCCCTTTAGGGTTCCGATTTAGTCTTTACGGCACCTC	2210
DB	531	CGTCAAGCTCTAATCGGGGCTCCCTTTAGGGTTCCGATTTAGTCTTTACGGCACCTC	590
QY	2211	GACCCCAAAAACTTGATPAGGGTGATGGTTCAAGCTAGTGGGCCATCGCCCTGATAGACG	2270
DB	591	GACCCCAAAAACTTGATPAGGGTGATGGTTCAAGCTAGTGGGCCATCGCCCTGATAGACG	650
QY	2271	GTTTTTGCGCCCTTGACGTTGGAGTCCACGTTCTTTTAAATAGTGGACTCTTTGTTCCAAACT	2330
DB	651	GTTTTTGCGCCCTTGAGGTTGGAGTCCACGTTCTTTTAAATAGTGGACTCTTTGTTCCAAACT	710
QY	2331	GGAAACAACCTCAACCTATCTCGGTCTATCTTTTGATTTTAAAGGATTTTGC CGAAT	2390
DB	711	GGAAACAACCTCAACCTATCTCGGTCTATCTTTTGATTTTAAAGGATTTTGC CGAAT	770
QY	2391	TCGGCCTATTTGTTTAAAAAATGAGCTGATTTTAAACAAAAATTTTAAACGGAATTTTAAACAA	2450
DB	771	TCGGCCTATTTGTTTAAAAAATGAGCTGATTTTAAACAAAAATTTTAAACGGAATTTTAAACAA	830
QY	2451	ATATTAAACGTTTAAATTTCTGATCGGTAATTTTCTCTTTACGCATCTGTGCGGTATTT	2510
DB	831	ATATTAAACGTTTAAATTTCTGATCGGTAATTTTCTCTTTACGCATCTGTGCGGTATTT	890
QY	2511	CACACCGCATAGGTAATTAACATGATATAATTTAAATTTGAAGCTCTAAATTTGTGAGTTAGT	2570
DB	891	CACACCGCATAGGTAATTAACATGATATAATTTAAATTTGAAGCTCTAAATTTGTGAGTTAGT	950
QY	2571	ATACATGCTTACTTATAATACAGTTTATTTTGTGCGGCTCTTCTCAAAAT	2630
DB	951	ATACATGCTTACTTATAATACAGTTTATTTTGTGCGGCTCTTCTCAAAAT	1010
QY	2631	GCTTCCAGCGCTGCTTTTCTGTAACGTTTCAACCTCTACCTTAGCATCCCTTCCCTTTGCA	2690
DB	1011	GCTTCCAGCGCTGCTTTTCTGTAACGTTTCAACCTCTACCTTAGCATCCCTTCCCTTTGCA	1070
QY	2691	AATAGTCTCTTCCAAATAATAATGTCAGATCTCTGTAGAGACCATCATCCAGGTT	2750
DB	1071	AATAGTCTCTTCCAAATAATAATGTCAGATCTCTGTAGAGACCATCATCCAGGTT	1130
QY	2751	CTATCTGTTGACCAATGCTCTCCCTGTCTCATCTAAACCCACACCGGCTGTCAATC	2810
DB	1131	CTATCTGTTGACCAATGCTCTCCCTGTCTCATCTAAACCCACACCGGCTGTCAATC	1190
QY	2811	AACCAATCGTAACCTTCACTCTTCCACCATGCTCTTTGAGCAATAAAGCCGATAACA	2870
DB	1191	AACCAATCGTAACCTTCACTCTTCCACCATGCTCTTTGAGCAATAAAGCCGATAACA	1250
QY	2871	AAATCTTTGCTCTTTCGCAATGTCAAAGTACCTTTAGTATATTTCTCCAGTAGATAGG	2930
DB	2931	GAGCCCTTGATGACAAATTTCTGCTAAACATCAAAAGGCTCTAGGTCTCTTTGTTACTTCT	2990
DB	1311	GAGCCCTTGATGACAAATTTCTGCTAAACATCAAAAGGCTCTAGGTCTCTTTGTTACTTCT	1370
QY	2991	TCGCGCGCTGTTTCAAAACGCTTAAACAATACCTGGGCCCCACACCGTGTGCAATTCGTA	3050
DB	1371	TCGCGCGCTGTTTCAAAACGCTTAAACAATACCTGGGCCCCACACCGTGTGCAATTCGTA	1430
QY	3051	ATGCTGTCGCCATCTCTGCTATTCGTATACACCGCAGAGTACTGCAATTTGACTGTATTA	3110
DB	1431	ATGCTGTCGCCATCTCTGCTATTCGTATACACCGCAGAGTACTGCAATTTGACTGTATTA	1490
QY	3111	CCAAATGTGACGAAATTTTCTGCTTCGAAAGAGTAAAAAATTTGACTTGGCGGATAATGCC	3170
DB	1491	CCAAATGTGACGAAATTTTCTGCTTCGAAAGAGTAAAAAATTTGACTTGGCGGATAATGCC	1550
QY	3171	TTTAGCGGCTTAACTGTGCGCTCCATGGAATAATCAAGTCAAGATATCCACATGTGTTTTT	3230
DB	1551	TTTAGCGGCTTAACTGTGCGCTCCATGGAATAATCAAGTCAAGATATCCACATGTGTTTTT	1610
QY	3231	AGTAAACAAATTTTGGGACCTAATGCTTCAACTAACTCCAGTAAATTTCTTGGTGGTACGA	3290
DB	1611	AGTAAACAAATTTTGGGACCTAATGCTTCAACTAACTCCAGTAAATTTCTTGGTGGTACGA	1670
QY	3291	ACATCAATGAAGCACACAAGTTTGTGCTTTCTGTCATGATATTAATAAGCTTGGCA	3350
DB	1671	ACATCAATGAAGCACACAAGTTTGTGCTTTCTGTCATGATATTAATAAGCTTGGCA	1730
QY	3351	GCAACAGGACTAGGATGAGTAGCAGCACGTTTCTTATATGTAGCTTTCGACATGATTTAT	3410
DB	1731	GCAACAGGACTAGGATGAGTAGCAGCACGTTTCTTATATGTAGCTTTCGACATGATTTAT	1790
QY	3411	CTTCTGCTTCTGACGCTTTTGTCTGTCAGTTGGGTTAAGATACTGGGCAATTTTCT	3470
DB	1791	CTTCTGCTTCTGACGCTTTTGTCTGTCAGTTGGGTTAAGATACTGGGCAATTTTCT	1850
QY	3471	GTTCCTTCAACACTACATATGCTATATATACCAATCTAAGTCTGTGCTCTTCTCTTCGT	3530
DB	1851	GTTCCTTCAACACTACATATGCTATATATACCAATCTAAGTCTGTGCTCTTCTCTTCGT	1910
QY	3531	TCCTCTCTGTTTGGAGATTAACGAAATCAAAAAATTTTCAAGAAACCGAAATCAAAAA	3590
DB	1911	TCCTCTCTGTTTGGAGATTAACGAAATCAAAAAATTTTCAAGAAACCGAAATCAAAAA	1970
QY	3591	AAAGATAAAATAATGATGAAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGAAT	3650
DB	1971	AAAGATAAAATAATGATGAAATTTGAATTTGAATTTGAATTTGAATTTGAATTTGAAT	2030
QY	3651	ACAATCTGCTCTGATCGCGCATAGTTTAAAGCCAGCCCGCACACCCGCGTAC	3710
DB	2031	ACAATCTGCTCTGATCGCGCATAGTTTAAAGCCAGCCCGCACACCCGCGTAC	2090
QY	3711	GCGCCCTGACGCGCTTGTCTCTCCCGCATCCGCTTACAGCAAGCTGTGACCGTCTCC	3770
DB	2091	GCGCCCTGACGCGCTTGTCTCTCCCGCATCCGCTTACAGCAAGCTGTGACCGTCTCC	2150
QY	3771	GGGAGCTGCATGTCAGAGGTTTTCACCGTCTATCCCGAAACCGCGGAGACGAAAGGCG	3830
DB	2151	GGGAGCTGCATGTCAGAGGTTTTCACCGTCTATCCCGTATCCCGGAGACGAAAGGCG	2210
QY	3831	CTCGTATACGCTATTTTATAGGTTAATGTGATGATAATGTTTCTTAGTATGAT	3890
DB	2211	CTCGTATACGCTATTTTATAGGTTAATGTGATGATAATGTTTCTTAGTATGAT	2264
QY	3891	CCAATATCAAGGAAATGATGCAITTTGAAGGATGAGACTAATCCAATTTGAGGATGGCAG	3950
DB	2265	-----	2264
QY	3951	CATATAGAACGCTAAAGGGTAGTCTGTAAGGAGCATACGATACCCCGCATGGAATGGG	4010
DB	2265	-----	2264

QY 4011 ATAATATCACAGGAGTACTAGACTACCTTTTCATCTACATAAATAGACGCATATAAGTA 4070
Db 2265 ----- 2264
QY 4071 CGCATTTAAGCATAAACAGCAGCTATGCGGTTCTCTCATGTATATATATATACAGGCAA 4130
Db 2265 ----- 2264
QY 4131 CAGCGAGATATAGGTGCGACGTAACAGCTGATGTATGTGGGAGCTCGGTTGCATTTT 4190
Db 2265 -----GACGGATCGCTTGGCTGTAACTTACACGCGCTCGTATCTTTT 2307
QY 4191 TCGGAAGCGCTGTTTGGGAACGCTTTGAAGTTTCTTCTCCGAAAGTTCCTATCTCTA 4250
Db 2308 AATGATGNAATATTTGGGAATTTACTCTGTGTTT----- 2342
QY 4251 GAAAGTATAGGAACCTTCAGAGCGCTTTTGAACCAAAAGCGCTCTGAAGACGCATTTTC 4310
Db 2343 ----- 2342
QY 4311 AAAAAACCAAAACGACCGGAGCTGTAAAGAGCTACTAAAAATATTCGGAATACCGCTTCC 4370
Db 2343 ----- 2342
QY 4371 ACAAACATTTGCTCAAAAGTATCTCTTTGCTATATATCTCTGTCTATATATCCCTATATAAC 4430
Db 2343 ----- 2342
QY 4431 CTACCATCCACCTTTTCGCTCTTGAACCTTGCACTCTAAACCTCGACCTCTACATTTTAT 4490
Db 2343 -----ATTATTTT 2351
QY 4491 GTTTATCTCTAGTATATCTCTTTAGACAAAAAATTTAGTAAGNACTATTCATAGAGTG 4550
Db 2352 TATGTTTGTATTTGGATTTTAGAAGTAAATAAAGAAAGGTAGAGAGTTACGGAATGAA 2411
QY 4551 AATCGAAAAAATACGAAAACTGAAACATTTCTCTATAGTAGTATATAGACAAAAATAG 4610
Db 2412 GAAAAAATAAACAAGGTTTAAAAATTTCAACA-----AAAGCG 2455
QY 4611 AAGAAACCGTTCATATTTTCTGACCAATGAAGAAATCATCAACGCTATCACTTTCTGTTTC 4670
Db 2456 TACTTTACATATATATTTATTTAGACAAGAAAGCAGATTAATAATAGATATATATTCGATTA 2515
QY 4671 ACNAGATGCGCAATCCACATCGGTATAGATATATAATCGGGGATGCCTTTATCTTGAA 4730
Db 2516 ACGA-----TAAATAAATGTAAATCAAGGATTTTCGTGTGGTCTCTCTACACA 2567
QY 4731 AAATGCACCGCAGCTCTCTAGTAAATCAGTAAACGCGGGAAGTGGAGTCAGGCTTTTTT 4790
Db 2568 GACNAGATGAACAATTCGGCTTAATACCTGAGAGCAGGAAG----- 2610
QY 4791 TATGGAAGAGAAAAATAGACACAAAAGTAGCCTTCTTCTAACCTTAAACGGACCTACAGTGC 4850
Db 2611 ----- 2610
QY 4851 AAAAGTTATCAAGAGACTGCATTTATAGCGCACAAAGGAGAAAAAAGTAATCTAAGA 4910
Db 2611 -----AGCAGATAAAA 2622
QY 4911 TGCCTTTGTAGAAAAATAGCGCTCTCGGATGCAATTTTGTAGAACAAAAAAGAGTATA 4970
Db 2623 GGTAGTATTTGTGGGATCCCGCTTAGAGTCTTTTACATCTTCGGAACAAAAACTATT 2682
QY 4971 GATTCCTTTGTGGAATAATAGCGCTCTCGCGTTGCAATTTCTGTTCTGTAAAAATGCAGCT 5030
Db 2683 TTTTCTTTA----- 2691
QY 5031 CAGATCTTTTGTGAAAAATTAGCGCTCTCGGTTGCAATTTTGTGTTTTTACAAAAATGAA 5090
Db 2692 -----ATTCTCTTTTACTTCTTATTTTAAATTTATATATATTTATATAAAAAATTTAA 2745

QY 5091 GCACAGATTTCTCGTTGGTAAAAATAGCGCTTTTCGCGTTGCATTTTCTGTCTGTAAAAATG 5150
Db 2746 ----- 2745
QY 5151 CAGCTCAGATTTCTTTGTTTGAATAAATTAGCGCTCTCGGTTTGCATTTTGTGTTCTTACAAA 5210
Db 2746 -----ATTATAATTTATTTTATAGCAG 2768
QY 5211 TGAGACACAGATGCTTCGTTTCAGGTGGCACTTTTCGGGGAATGTGCGGAAACCCCTAT 5270
Db 2769 TGATGAAAAGGAGC-----CAGGTGGCACTTTTCGGGGAATGTGCGGGAACCCCTAT 2822
QY 5271 TTGTTTATTTTCTAAATATACATTCAAATATGTATCCGCTCATGAGACAAATACCCGTGATA 5330
Db 2823 TTGTTTATTTTCTAAATATACATTCAAATATGTATCCGCTCATGAGACAAATACCCGTGATA 2882
QY 5331 AATGCTTCAATAATATTTGAAAAAGGAAGATATGAGTATTCAAATTTCCGTGTGCGCCT 5390
Db 2883 AATGCTTCAATAATATTTGAAAAAGGAAGATATGAGTATTCAAATTTCCGTGTGCGCCT 2942
QY 5391 TATTCCTCTTTTTCGGCATTTTTCGCTTTCCTGTTTTCCTCACCAGAAACGCTGCTGAA 5450
Db 2943 TATTCCTCTTTTTCGGCATTTTTCGCTTTCCTGTTTTCCTCACCAGAAACGCTGCTGAA 3002
QY 5451 AGTAAAAAGATGCTGAAGATCAGTTGGGTGCACAGTGGTTTACATCGAACTGGATCTCAA 5510
Db 3003 AGTAAAAAGATGCTGAAGATCAGTTGGGTGCACAGTGGTTTACATCGAACTGGATCTCAA 3062
QY 5511 CAGCGTAAGATCTTCGAGATTTTCGCCCGGAAAGAGTTTTCCAATGTAGAGCACTTT 5570
Db 3063 CAGCGTAAGATCTTCGAGATTTTTCGCCCGGAAAGAGTTTTCCAATGTAGAGCACTTT 3122
QY 5571 TAAAGTTCTGCTATGTCGCGGTATTTATCCGTTTATGACCGCGGGAAGCAACTCGG 5630
Db 3123 TAAAGTTCTGCTATGTCGCGGTATTTATCCGTTTATGACCGCGGGAAGCAACTCGC 3182
QY 5631 TCGCGCATACACTATTTCTCAGATGACTTGGTTTGGTGTAGTACTCACCAGTCACAGAAAAGCA 5690
Db 3183 TCGCGCATACACTATTTCTCAGATGACTTGGTTTGGTGTAGTACTCACCAGTCACAGAAAAGCA 3242
QY 5691 TCTTACCGATGGCATGACAGTAAGAGAAATTTATGACGTGCTGCCATAACCATGAGTGATA 5750
Db 3243 TCTTACCGATGGCATGACAGTAAGAGAAATTTATGACGTGCTGCCATAACCATGAGTGATA 3302
QY 5751 CACTGCGGCAACTTCTCTGCAACGATCGGAGGACCGAAGAGCTTAAACCGCTTTT 5810
Db 3303 CACTGCGGCAACTTCTCTGCAACGATCGGAGGACCGAAGAGCTTAAACCGCTTTT 3362
QY 5811 GCACAAATGGGGATCATGTAATCGCTTTGATCGTTGGAAACGGAGCTGAATGAAGC 5870
Db 3363 GGACAAATGGGGATCATGTAATCGCTTTGATCGTTGGAAACGGAGCTGAATGAAGC 3422
QY 5871 CATACAAACGACGAGGTGACACCAAGATGCTGTAGCAATGCGCAACAACTGTCGCA 5930
Db 3423 CATACAAACGACGAGGTGACACCAAGATGCTGTAGCAATGCGCAACAACTGTCGCA 3482
QY 5931 ACTATTAACTGGCGAACTACTTACTCTAGCTTCCCGCAACAAATTAATAGACTGATGA 5990
Db 3483 ACTATTAACTGGCGAACTACTTACTCTAGCTTCCCGCAACAAATTAATAGACTGATGA 3542
QY 5991 GCGGATAAAGTTGACGAGCACCTTCTCGCTCGGCGCTTCCGCTGCTGCTGTTTATGTC 6050
Db 3543 GCGGATAAAGTTGACGAGCACCTTCTCGCTCGGCGCTTCCGCTGCTGCTGTTTATGTC 3602
QY 6051 TGATAAATCTGGAGCCGCTGAGCGTCTCGCGGTATCATTTGACAGCACTGGGCGCAGA 6110
Db 3603 TGATAAATCTGGAGCCGCTGAGCGTCTCGCGGTATCATTTGACAGCACTGGGCGCAGA 3662
QY 6111 TGGTAAACCTCTCCGATCTGAGTATCTACACGACGGGAGTCAGGCAACTATCTGATGA 6170
Db 3663 TGGTAAACCTCTCCGATCTGAGTATCTACACGACGGGAGTCAGGCAACTATCTGATGA 3722
QY 6171 ACGAAATAGACAGATCGCTGAGATAGGTGCTCTCACTGATTAAGCAATGCTGCTCAGA 6230

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294 ACTGATATAAATGAAGCTCTAAATTTGTGAGTTTAGTATACATGCAATTTACTTATA 353
QY
2590 ATACAGTTTTTTAGTTTGTGCGCGCATCTCTCAAAATATGCTTCCGAGCTGCTTTTC 2649
Db
354 ATACAGTTTTTTAGTTTGTGCGCGCATCTCTCAAAATATGCTTCCGAGCTGCTTTTC 413
QY
2650 TGTAAAGTTTCAACCTCTACCTTAGCATCCCTTCCCTTTGCAAAATAGTCTCTTCCAAACA 2709
Db
414 TGTAAAGTTTCAACCTCTACCTTAGCATCCCTTCCCTTTGCAAAATAGTCTCTTCCAAACA 473
QY
2710 TAAATATGTACAGTCTCTGATAGACCAATCATCCATCCAGGTTCTATACCTGTTGACCCCAATG 2769
Db
474 TAAATATGTACAGTCTCTGATAGACCAATCATCCATCCAGGTTCTATACCTGTTGACCCCAATG 533
QY
2770 CGTCTCCCTTGTCACTTAACCCACACCGGGTGTCTAATCAACCAATCGTAACCTTCAT 2829
Db
534 CGTCTCCCTTGTCACTTAACCCACACCGGGTGTCTAATCAACCAATCGTAACCTTCAT 593
QY
2830 CTCCTCCACCCATGCTCTTTGAGCAATAAAGCCGATAAACCAATCTTTGTGCTCTTCG 2889
Db
594 CTCCTCCACCCATGCTCTTTGAGCAATAAAGCCGATAAACCAATCTTTGTGCTCTTCG 653
QY
2890 CAAATGTCAACGACCTCTTAGTATATCTCCAGTAGATAGGGAGCCCTTGCATGACAAAT 2949
Db
654 CAAATGTCAACGACCTCTTAGTATATCTCCAGTAGATAGGGAGCCCTTGCATGACAAAT 713
QY
2950 CTGCTAAACATCAAAAGGCTCTAGGTTCTTTGTTACTCTTCTGCGCGCTGCTTCAAC 3009
Db
714 CTGCTAAACATCAAAAGGCTCTAGGTTCTTTGTTACTCTTCTGCGCGCTGCTTCAAC 773
QY
3010 CGCTAACATACCTGGGCCACACACCGTGTGCAATCGTAATGCTGCCCATCTCTGCTA 3069
Db
774 CGCTAACATACCTGGGCCACACACCGTGTGCAATCGTAATGCTGCCCATCTCTGCTA 833
QY
3070 TTCTGTATACACCCGACAGTAGTCTCAATTTGACTGTATTAACCAATGTACCAAAATTTTC 3129
Db
834 TTCTGTATACACCCGACAGTAGTCTCAATTTGACTGTATTAACCAATGTACCAAAATTTTC 893
QY
3130 TGTCTTCGAGAGTAAATAATGTACTTGGCGGATATGCTTTAGCGGCTTAACGTGTC 3189
Db
894 TGTCTTCGAGAGTAAATAATGTACTTGGCGGATATGCTTTAGCGGCTTAACGTGTC 953
QY
3190 CTCCATGAAATAATCAGTCAAGATATCCACATGTGTTTTAGTAAACAAATTTTGGAC 3249
Db
954 CTCCATGAAATAATCAGTCAAGATATCCACATGTGTTTTAGTAAACAAATTTTGGAC 1013
QY
3250 CTAATGCTTCAACTCACTCCAGTAATCTCTTGGTGGTACGAACATCCCAATGAAGCACACA 3309
Db
1014 CTAATGCTTCAACTCACTCCAGTAATCTCTTGGTGGTACGAACATCCCAATGAAGCACACA 1073
QY
3310 AGTTTGTGCTTTTGTGTCATGATATTAATAGCTTGGCAGCAACAGGACTAGGNTAG 3369
Db
1074 AGTTTGTGCTTTTGTGTCATGATATTAATAGCTTGGCAGCAACAGGACTAGGNTAG 1133
QY
3370 TAGCAGCAGTTCTCTATATGATGCTTTCGACATGATTTATCTCTGTTTCTCGCAGGTTT 3429
Db
1134 TAGCAGCAGTTCTCTATATGATGCTTTCGACATGATTTATCTCTGTTTCTCGTTTC 1188
QY
3430 TTGTTCTGTGAGTTGGGTTAAGATACCTGGGCAATTTTCATGTTTCTTCAACACTACATA 3489
Db
1189 TTGTTCTGTGAGTTGGGTTAAGATACCTGGGCAATTTTCATGTTTCTTCAACACTACATA 1248
QY
3490 TCGGTATATACCAATCTAAGCTGTGCTCTTCTGCTTCTCTCTCTCTGTTGCGGAGA 3549
Db
1249 TCGGTATATACCAATCTAAGCTGTGCTCTTCTGCTTCTCTCTCTCTGTTGCGGAGA 1308
QY
3550 TTACCGAATCAAAAAATTTCAAGAAACCGGAATCAAAAAAGAAATAAAAAAAATG 3609
Db
1309 TTACCGAATCAAAAAATTTCAAGAAACCGGAATCAAAAAAGAAATAAAAAAAATG 1368
QY
3610 ATGAATGAATGAAGAGCTGTGGTATGTTGCTGCTCT-----CAGTACAAATCT 3657
|||||

Db
1369 ATGAATGAAGAGCTGTGGTATGCCATCATTTGAATTTTGAACATCCGAAACCTGGAGTTT 1428
QY
3658 GCTCTGATGCGCATAGTTAAGCCAGCCCGACACCCGCCAACACCCCTGAGCGCCCT 3717
Db
1429 TCCCTGAAACAGATAGTATATTTGAACTGTATATAATATATATAGTCTAGCGCTTTACGG 1488
QY
3718 GACGGGCTTGTGCTCCTCCGCGCATCCGCTTACAGACAAAGCTGTGACCCGCTCTCCGGAGCT 3777
Db
1489 AAGCAATGTATGTATTTTGGTTCTCGGAGAAATATTTGCAATGTATGCTATGCTAAATCT 1548
QY
3778 -----GATGTGTGAGAGTTTTCACCGTCAATCACC--GAAACGGCGGAGACGAAAG 3827
Db
1549 TGCAGTGTGATCCCGGTTCAATTTCTGCGTTTCCATCTTGCACCTTCAATAGCATATCT 1608
QY
3828 GGCCTCGTATACGCTATTTTATAGTTAATGTCAATGATAATAATGCTTTCTTTAGTAT 3887
Db
1609 TTGTTAAGAGCATCTGTGCTTCAATTTGTAGAACAAAATGCAACCGGAGCGCTAA 1668
QY
3888 GATCCAAATCAAGAGAAATGATAGCATTTGAAGGATGAGACTAATCCAAATTTGAGGAGTGG 3947
Db
1669 TTTTTCAAAACAAAGAACTCTGAGCTGCATTTTACAGAACAGAAATGCAACGCGAAAGCG 1728
QY
3948 CAGCATATGAAACAGCTAAAGGGTAGTGTGAGGAGACATACGATACCCCGCATGGAAT 4007
Db
1729 TATTTTACCAACGAAGAACTCTGTGCTTCAATTTTGTAAAAACAAAAATGCAACGCGAGAGC 1788
QY
4008 GGGATATATCACAGGAGGTACTAGA-CTACTTTTCACTCATGTATATATATATACAG 4066
Db
1789 GCTAATTTTCAACAAAGAACTCTGAGCTGCATTTTACAGAACAGAAATGCAACGCGAG 1848
QY
4067 AGTACGCAATTTAAGCATAAACACACACTATGCGCTTCTTCTCATGTATATATATATACAG 4126
Db
1849 AGCGCTATTTTACCAACAAAGAACTATATCTTCTTTTGTCTTCAAAAATGTCATCCCG 1908
QY
4127 GCAACAG-----CAGATATAGTGTGCGACGTGAAACAGTGTGATGTGCGCAGTGTG 4180
Db
1909 AGAGCGCTATTTTCTAAACAAAGCATCTTAGATTTACTTTTTTCTCTCTGTCGCTCTA 1968
QY
4181 CGTTGCAATTTTCGAAGCGCTCGTT-----TTCCGAAACGCTTTTGAAGTTCTCTAT 4230
Db
1969 TAATGCACTCTCTTGTAACTTTTGTGCACTAGGTCGTTTAAAGTTTAAAGAGGCTAC 2028
QY
4231 TCCGAACTTCTATTTCTCT-----AGAAAGTATAGGAACCTTCAGAGCGCTTTTGAAAC 4284
Db
2029 TTTGGTGTCTATTTTCTTCTCCATAAABAAAGCTGTACTCCTCCTCCGCTTTACTGTAT 2088
QY
4285 CAAGAGGCTCTGTGAGAGCGCTTTCAAAAACAAACGACGCGGAGCTGTAAAGAGC 4343
Db
2089 TACTAGCGAGCTGCGGGTGCAATTTTTCAGATAAAGGCAATCCCGGATTTATTTCTATA 2148
QY
4344 TACTAAATATTTGGAATACCGCTTCCACAAACATTTGCTCAAAAGTATCTCTTTGCTATA 4403
Db
2149 CCGATGTGATTTGGCACTATCTTTGTGAACAGAAAGTATAGCGTTGATTTCTTCTC 2204
QY
4404 TATCTGTGCTATATCCCTATATAAACCCTACCCATCCACCTTTTCGCTCTTGAACCTTGA 4463
Db
2205 -ATTGGTCAGAAAATATGAACGGTTCTTCTATTTTGTCTCTATATACTACTGATATAGGA 2263
QY
4464 TCTAACTCGACCTCTACATTTTATATGTTTATCTCTAGTATTTACTCTTTAGACAAAAA 4523
Db
2264 AATGTTTACATTTTGTGATTTTTCGATTTCACTCTATGAATAGTTTCTTACTACAAATTT 2323
QY
4524 ATTGTAGTAACTATTTCTATAGTGAATCGAAACAAATACGAAATGTAACAAATTTCC 4583
Db
2324 TTTGCTTAAAGAGTAAATCTAGATATAACATAAAATGTTAGAGGTGAGTTTAGATGTC 2383
QY
4584 TATACGTAGTATATAGACAAAAATAGAAAGAAACCGTTTCATAATTTTCTGACCAAT---- 4639
Db
2384 AAGTTCAAGGAGCGAAAGGTGATGGGTAGTTATATAGGGATATAGCACAGATATAT 2443
QY
4640 -GAAGAAATCAACAGCTATCCTTTCTGTTTCAAAAAGTATGCGCAATCCACATCGGTAT 4698
Db
2444 AGCAAGAGAGTACTTTTTTGAGCAATGTTTGTGAAAGCGGTATTCGCAATATTTTAGTAGCT 2503

Db 4651 TCGGAACAGGAGCGCACGAGGAGCTTCCAGGGGAAACGCCCTGTATCTTTATAGTC 4710
 Qy 6908 CTGTGGCTTTCGACACCTCTGACTTGAGCGTCGATTTTGTGATGCTGCTGAGGGGGC 6967
 Db 4711 CTGTGGCTTTCGACACCTCTGACTTGAGCGTCGATTTTGTGATGCTGCTGAGGGGGC 4770
 Qy 6968 GGAGCTATGGAAGAAACCCAGCAACGGCGCTTTTACGGTTCCTGGCCCTTTGCTGGC 7027
 Db 4771 GGAGCTATGGAAGAAACCCAGCAACGGCGCTTTTACGGTTCCTGGCCCTTTGCTGGC 4830
 Qy 7028 CTTTGTCTCACATGTTCTTCTCGCTTATCCCTGATTCCTGATTAACCGTATTACCG 7087
 Db 4831 CTTTGTCTCACATGTTCTTCTCGCTTATCCCTGATTCCTGATTAACCGTATTACCG 4890
 Qy 7088 CTTTGTAGTACTGATACCGTTCGCGCAGCGCAACGCCAGCGGAGCGAGTCACTGA 7147
 Db 4891 CTTTGTAGTACTGATACCGTTCGCGCAGCGCAACGCCAGCGGAGCGAGTCACTGA 4950
 Qy 7148 GCGAGAAAGCGAGAGCGCCCAATACGAAACCGCTCTCCCGCGCTTGGCGGATTC 7207
 Db 4951 GCGAGAAAGCGAGAGCGCCCAATACGAAACCGCTCTCCCGCGCTTGGCGGATTC 5010
 Qy 7208 ATTAATGACAGCTGGCAACGACAGGTTTCCCGACTGGAAGCGGGCAGTGAGCGCAACGCA 7267
 Db 5011 ATTAATGACAGCTGGCAACGACAGGTTTCCCGACTGGAAGCGGGCAGTGAGCGCAACGCA 5070
 Qy 7268 TTAATGTAGTTTACCTACTACTATAGGACCGCGGCTTTACACTTATGCTTCGGCTC 7327
 Db 5071 TTAATGTAGTTTACCTACTACTATAGGACCGCGGCTTTACACTTATGCTTCGGCTC 5130
 Qy 7328 CTATGTGTGGAAATGTGAGCGGATAACAATTTACACAGGAAACAGCT 7378
 Db 5131 GTATGTGTGGAAATGTGAGCGGATAACAATTTACACAGGAAACAGCT 5181

RESULT 15

AX85878
 ID AX85878 standard; DNA; 7063 BP.
 XX
 AC AX85878;
 XX
 DT 13-SEP-1999 (first entry)
 XX
 DE Synthetic operon comprising MSG sequence and funtionl in yeast.

XX Methylglyoxal synthase; MGS; ethanol production; 1,2-propanediol;
 KW unsaturated polyester resin; liquid laundry detergent; cosmetic;
 KW antifreeze; deicing formulation; carbon dioxide; alcohols; organic acid;
 KW animal feed; ss.

OS Synthetic.
 OS Escherichia coli.

XX WO9928481-Al.
 XX

PD 10-JUN-1999.

XX 30-NOV-1998; 98WO-US025318.

XX 03-DEC-1997; 97US-00984717.

XX (WISC) WISCONSIN ALUMNI RES FOUND.

XX Cameron DC, Shaw AJ, Hoffman ML;

XX wPI; 1999-418470/35.

XX Production of ethanol and 1,2-propanediol.

XX Example 21; Page 40-46; 48pp; English.

XX The present sequence represents a synthetic operon, comprising sequences

CC encoding methylglyoxal synthase (MGS), which is functional in yeast
 CC cells. It is used in the course of the invention. The specification
 CC describes a method for the production of ethanol and 1,2-propanediol (1,2
 CC -PD) comprising using a genetically modified yeast which expresses
 CC suitable enzymes, particularly an E. coli methyl glyoxal synthase (MGS).
 CC The microbial process can use as a substrate a renewable sugar such as
 CC glucose, xylose or lactose or products from corn and cane sugar and from
 CC lignocellulosic biomass. The process produces no toxic wastes and does
 CC not involve high temperatures and pressures. The products and methods can
 CC be used for the production of 1,2-PD which can be used in the production
 CC of unsaturated polyester resins, liquid laundry detergents,
 CC pharmaceuticals, cosmetics, antifreeze and deicing formulations. They can
 CC also be used to produce ethanol. The byproducts of fermentation are
 CC carbon dioxide, alcohols, and organic acids, all of which can be purified
 CC as valuable co-products or used as animal feed

SQ Sequence 7063 BP; 1948 A; 1592 C; 1541 G; 1982 T; 0 U; 0 Other;

Query Match 38.9%; Score 3045.4; DB 2; Length 7063;
 Best Local Similarity 78.2%; Pred. No. 0;
 Matches 3889; Conservative 0; Mismatches 996; Indels 86; Gaps 16;

Qy 2470 CTTGATGCGGTATTTCTCTTAGCGATCTGTGCGGTATTTTCACACCGCATAGGTAATA 2529
 Db 2117 CTTGATGCGGTATTTCTCTTAGCGATCTGTGCGGTATTTTCACACCGCATAGGTAATA 2176
 Qy 2530 ACTGATATAATTAATTAAGAGCTCTAATTTGTAGTTTAGTATACATCATCTTACTTATA 2589
 Db 2177 ACTGATATAATTAATTAAGAGCTCTAATTTGTAGTTTAGTATACATCATCTTACTTATA 2236
 Qy 2590 ATACAGTTTTTTAGTTTTGTCTGGCGCATCTTCTCAATAATATGCTTCCAGCGCTGTTTC 2649
 Db 2237 ATACAGTTTTTTAGTTTTGTCTGGCGCATCTTCTCAATAATATGCTTCCAGCGCTGTTTC 2296
 Qy 2650 TGTAAAGTTTCAACCTCTACCTTAGCATCCCTTCCCTTTGCAAAATAGTCTCTTCCAAACA 2709
 Db 2297 TGTAAAGTTTCAACCTCTACCTTAGCATCCCTTCCCTTTGCAAAATAGTCTCTTCCAAACA 2356
 Qy 2710 TAATAATGTAGATCCTGTAGAGACCATCATCCAGGTTCTATCTTGTGACCAATG 2769
 Db 2357 TAATAATGTAGATCCTGTAGAGACCATCATCCAGGTTCTATCTTGTGACCAATG 2416
 Qy 2770 CGTCTCCCTTGTCTATCTAAACCCACACCGGGTGTCTAATAATCAACCAATCGTAACCTTCAT 2829
 Db 2417 CGTCTCCCTTGTCTATCTAAACCCACACCGGGTGTCTAATAATCAACCAATCGTAACCTTCAT 2476
 Qy 2830 CTCTTCCACCGCATGCTCTTTTGTAGCAATAAAGCCGATAACAAAATCTTTGTGCGCTCTTCG 2889
 Db 2477 CTCTTCCACCGCATGCTCTTTTGTAGCAATAAAGCCGATAACAAAATCTTTGTGCGCTCTTCG 2536
 Qy 2890 CAATGTCAACAGTACCTTGTAGTATATTTCTCCAGTAGATAGGAGCCCTTGCATGACAAT 2949
 Db 2537 CAATGTCAACAGTACCTTGTAGTATATTTCTCCAGTAGATAGGAGCCCTTGCATGACAAT 2596
 Qy 2950 CTGCTAACATCAAAAGGCTCTAGGTTCTTTTGTACTTCTTCTGCGGCTGCTTCAAC 3009
 Db 2597 CTGCTAACATCAAAAGGCTCTAGGTTCTTTTGTACTTCTTCTGCGGCTGCTTCAAC 2656
 Qy 3010 CGCTAACAAATACCTGGGCCCCACACACCGGTGTGATTCGTAAATGTCTGCCCATTCGTCTA 3069
 Db 2657 CGCTAACAAATACCTGGGCCCCACACACCGGTGTGATTCGTAAATGTCTGCCCATTCGTCTA 2716
 Qy 3070 TTCTGTATACACCGCAGAGTACTGCAATTTGACTATTTACCAATGTGAGCAAAATTTTC 3129
 Db 2717 TTCTGTATACACCGCAGAGTACTGCAATTTGACTATTTACCAATGTGAGCAAAATTTTC 2776
 Qy 3130 TGTCTTCGAAGAGTAAAAAATTTGACTTTGGCGGTAATGCTTTAGCGGCTTAACTGTGC 3189
 Db 2777 TGTCTTCGAAGAGTAAAAAATTTGACTTTGGCGGTAATGCTTTAGCGGCTTAACTGTGC 2836
 Qy 3190 CTTCCATGGAAAATCATGTCAGATATCCCATGTGTTTTTAGTAAACAAATTTTGGGAC 3249
 Db 2837 CTTCCATGGAAAATCATGTCAGATATCCCATGTGTTTTTAGTAAACAAATTTTGGGAC 2896

Db 5034 GAAAAAGAGAGATATAGATATTAACATTTCCGTGTCGCCCTTATTTCCCTTTTTCGGG 5093
Qy |||||
Db 5408 CATTTTGCCTTCTCTGTTTGTCTACCCAGAAACGCTGTTGAAAGTAAAGATCTGAAG 5467
Qy |||||
Db 5094 CATTTTGCCTTCTCTGTTTGTCTACCCAGAAACGCTGTTGAAAGTAAAGATCTGAAG 5153
Qy |||||
Db 5468 ATCAGTTGGGTGCACGAGTGGGTATCATCGAACTCGATCTCAACAGCGGTAAAGATCTTGTG 5527
Qy |||||
Db 5154 ATCAGTTGGGTGCACGAGTGGGTATCATCGAACTCGATCTCAACAGCGGTAAAGATCTTGTG 5213
Qy |||||
Db 5528 AGAGTTTTCGCCCCGAAAGAACGTTTTCGAATGATGAGCACTTTTAAAGTTTCTGCTATGTG 5587
Qy |||||
Db 5214 AGAGTTTTCGCCCCGAAAGAACGTTTTCGAATGATGAGCACTTTTAAAGTTTCTGCTATGTG 5273
Qy |||||
Db 5588 GGGCGGTATTATCCCGTATTGACGGCGGGCAAGAGCACTCGGTCCGCGCATACACTATT 5647
Qy |||||
Db 5274 GGGCGGTATTATCCCGTATTGACGGCGGGCAAGAGCACTCGGTCCGCGCATACACTATT 5333
Qy |||||
Db 5648 CTCAGAACTGACTTGGTTGAGTACTCACAGTACACAGAAAGCACTTTACGGATGGCATGA 5707
Qy |||||
Db 5334 CTCAGAACTGACTTGGTTGAGTACTCACAGTACACAGAAAGCACTTTACGGATGGCATGA 5393
Qy |||||
Db 5708 CAGTAAGAGAAATATGCAAGTGTGTCATTAACCATGAGTGATAACACATGCGGCCCAACTTAC 5767
Qy |||||
Db 5394 CAGTAAGAGAAATATGCAAGTGTGTCATTAACCATGAGTGATAACACATGCGGCCCAACTTAC 5453
Qy |||||
Db 5768 TTCTGACAACTGAGTCCGAGGACCGAAGGAGCTTAACCGCTTTTTCGACAAATGCGGGATC 5827
Qy |||||
Db 5454 TTCTGACAACTGAGTCCGAGGACCGAAGGAGCTTAACCGCTTTTTCGACAAATGCGGGATC 5513
Qy |||||
Db 5828 ATGTAACCTGCTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGAGC 5887
Qy |||||
Db 5514 ATGTAACCTGCTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGAGC 5573
Qy |||||
Db 5888 GTGACACCACTGCTGTAGCAATGGCAACCAAGCTTGGCAAACTATTAACCTGGCGAAC 5947
Qy |||||
Db 5574 GTGACACCACTGCTGTAGCAATGGCAACCAAGCTTGGCGAACTATTAACCTGGCGAAC 5633
Qy |||||
Db 5948 TACTTACTGCTAGCTTCCCGGCAACAAATTAATAGACTGATGAGGCGGATAAAGTTGCAG 6007
Qy |||||
Db 5634 TACTTACTGCTAGCTTCCCGGCAACAAATTAATAGACTGATGAGGCGGATAAAGTTGCAG 5693
Qy |||||
Db 6008 GACCACTTCTGCGCTCGGCCCTTCCGGCTGGCTGTTTATTTGCTGATAAATCTGGAGCG 6067
Qy |||||
Db 5694 GACCACTTCTGCGCTCGGCCCTTCCGGCTGGCTGTTTATTTGCTGATAAATCTGGAGCGG 5753
Qy |||||
Db 6068 GTGAGCGTGGGTCTCGCGGTATCATTTGCAGCACTGGGGCCAGATGGTAAAGCCCTCCCGTA 6127
Qy |||||
Db 5754 GTGAGCGTGGGTCTCGCGGTATCATTTGCAGCACTGGGGCCAGATGGTAAAGCCCTCCCGTA 5813
Qy |||||
Db 6128 TCGTAGTTATCTACAGAGCGGGAGTCAAGCACTATGATGAAAGCAATAGACAGATCG 6187
Qy |||||
Db 5814 TCGTAGTTATCTACAGAGCGGGAGTCAAGCACTATGATGAAAGCAATAGACAGATCG 5873
Qy |||||
Db 6188 CTGAGATAGTCCCTCAGTATTAGCAATGGTAACTGTCAGACCAAGTTTACTCATATA 6247
Qy |||||
Db 5874 CTGAGATAGTCCCTCAGTATTAGCAATGGTAACTGTCAGACCAAGTTTACTCATATA 5933
Qy |||||
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Qy |||||
Db 5934 TACTTTAGATTGATTTAAACCTTCATTTTAAATTTAAAGGATCTAGGTGAAGATCTCTTT 5993
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Db 6308 TTGATTAATCTCATGACCAAAATCCCTTAAGCGTGGTTTTCGTTCCACTGAGCGTCAGACC 6367
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Qy |||||
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Qy |||||
Db 6174 CTCCTTTTTCGAAAGTAACTGGCTTTCAGCAGAGCGAGATACCAAACTACTGTCCTTCTAG 6233
Qy |||||
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Qy |||||
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Qy |||||
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Qy |||||
Db 6293 TGTAAATCTCTGTTACCAAGTGTCTGCTCCAGTGGCGATAAGTCTGTCTTACCGGTTGG 6352
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Qy |||||
Db 7208 ATTAATGAGTGGCAGCAGCAGGTTTCCCGACTGGAAGCGGCGAGTCAAGCGCAACGCAA 7267
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Qy |||||
Db 7268 TTAATGTGAGTTACTCTCACTCATTTAGGCACCCAGGCTTTTACATTTATGCTTCCGCTC 7327
Qy |||||
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Qy |||||
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Qy |||||
Db 7013 GTATGTTGTGTGGAATTTGTGAGCGGATAACATTTTCAACAGGAAACAGCT 7063
Qy |||||

Search completed: May 16, 2004, 01:31:57
Job time : 1907.33 secs

GenCore version 5.1.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 16, 2004, 00:27:52 ; Search time 12147.4 Seconds
(without alignments)
19243.679 Million cell updates/sec

Title: US-10-067-449-9

Perfect score: 7828

Sequence: 1 atcgctcggttcacaa.....tttttaatttaatacaaaaa 7828

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database :

EST:*

1: em_estba:*

2: em_esthum:*

3: em_estin:*

4: em_estmu:*

5: em_estov:*

6: em_estpl:*

7: em_estro:*

8: em_htc:*

9: gb_est1:*

10: gb_est2:*

11: gb_htc:*

12: gb_est3:*

13: gb_est4:*

14: gb_est5:*

15: em_estfun:*

16: em_estom:*

17: em_gss_hum:*

18: em_gss_inv:*

19: em_gss_pln:*

20: em_gss_vrt:*

21: em_gss_fun:*

22: em_gss_mam:*

23: em_gss_mus:*

24: em_gss_pro:*

25: em_gss_rod:*

26: em_gss_pbg:*

27: em_gss_vrl:*

28: gb_gss1:*

29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1459.2	18.6	3049	11 BC034387	BC034387 Homo sapi
2	1291.4	16.5	1497	29 AY421215	AY421215 Homo sapi
3	1288.2	16.5	1814	14 CD014068	CD014068 90134560
4	1074.4	13.7	1497	29 AY421216	AY421216 Pan trogl

C	5	1055.8	13.5	1070	9	AJ281552	AJ281552 4A3A-P6F1
C	6	1037	13.2	1497	29	AY421217	AY421217 Mus muscu
C	7	988.4	12.6	1067	9	AU081137	AU081137 AU081137
C	8	986.4	12.6	1013	12	BM438846	BM438846 Iplviro015
C	9	957	12.2	1089	9	AU081124	AU081124 AU081124
C	10	924	11.8	1004	9	AJ281480	AJ281480 4A3A-P4G8
C	11	916.8	11.7	973	14	CD458281	CD458281 FG08_08h0
C	12	900.6	11.5	1025	29	CG700598	CG700598 ZMMBB0C12
C	13	899.8	11.5	996	29	CG392995	CG392995 ZMMBB0C00
C	14	899.4	11.5	925	14	CB686151	CB686151 Bn01b_020
C	15	886.2	11.3	917	14	CD458286	CD458286 FG08_09a0
C	16	884.6	11.3	1021	29	CG392916	CG392916 ZMMBB0C00
C	17	873.6	11.2	935	12	BG838279	BG838279 CG01_10e0
C	18	866	11.1	918	14	CD459092	CD459092 FG08_08e0
C	19	865	11.1	1073	14	CF269652	CF269652 Fcylco1d8
C	20	850	10.9	1056	29	CG835880	CG835880 ZMMBB0C021
C	21	841	10.7	841	9	AL042026	AL042026 DKFZp434E
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C	24	820.2	10.5	870	14	CD458333	CD458333 FG08_09e0
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C	30	807.6	10.3	966	28	BZ570738	BZ570738 msh2_1513
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C	32	797.6	10.2	1011	28	BZ576726	BZ576726 msh2_5071
C	33	785.4	10.0	1574	28	BZ572566	BZ572566 msh2_2693
C	34	780.2	10.0	1194	28	BZ578985	BZ578985 msh2_6095
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C	37	774.4	9.9	789	14	CD280920	CD280920 G44224.42
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C	41	767.6	9.8	863	14	CF752100	CF752100 TGR9R Hum
C	42	767.4	9.8	959	28	BZ557985	BZ557985 pacsl-60
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ALIGNMENTS

RESULT 1
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LOCUS BC034387 3049 bp mRNA linear HTC 08-JUL-2002
DEFINITION Homo sapiens, Similar to solute carrier family 2 (facilitated glucose transporter), member 4, clone IMAGE:5187454, mRNA.
ACCESSION BC034387.1 GI:21706716
VERSION BC034387.1
KEYWORDS HTC.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 3049)
AUTHORS Strausberg,R.
TITLE Direct Submission
JOURNAL Submitted (02-JUL-2002) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK NIH-MGC Project URL: http://mgc.nci.nih.gov
COMMENT Contact: MGC help desk
Email: cgapbs@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Baylor College of Medicine Human Genome Sequencing Center

ORGANISM Homo sapiens
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 REFERENCE 1 (bases 1 to 1814)
 AUTHORS Jin, P., Fu, G.K., Wilson, A.D., Yang, J., Chien, D., Hawkins, P.R.,
 Au-Yang, J. and Stuve, L.L.
 TITLE PCR isolation and cloning of novel splice variant mRNAs from known
 drug target genes
 JOURNAL Unpublished (2003)
 COMMENT Contact: Jin, P.
 Incyte Corporation
 3160 Porter Drive, Palo Alto, CA 94304, USA
 Tel: 650 621 8639
 Fax: 650 621 8965
 Email: pj@incyte.com.
 FEATURES
 Location/Qualifiers
 1..1814
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 /mol_type="mRNA"
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 /note="Vector: pDrive Cloning Vector; RT-PCR was performed
 using gene-specific primers flanking the open-reading
 frame. PCR products were subcloned into pDrive Cloning
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 reverse primers. Sequencing gaps were closed by
 re-sequencing using primers flanking the gapped areas."

ORIGIN

Query Match 16.5%; Score 1288.2; DB 14; Length 1814;
 Best Local Similarity 92.2%; Pred. No. 1.7e-203;
 Matches 1416; Conservative 0; Mismatches 3; Indels 116; Gaps 1;
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 DB 128 ATGCCGTCGGGTTCCAAAGATAGGCTCCGAAGATGGGAAACCCCTCAGCAGCGAGTG 187
 QY 61 ACTGGAGCCCTCGTCTGCTGCTGCTCTGCGGTGCTTGGCTCCCTGCGAGTTTGGGTAC 120
 DB 188 ACTGGAGCCCTCGTCTGCTGCTGCTCTGCGGTGCTTGGCTCCCTGCGAGTTTGGGTAC 247
 QY 121 AACATTGGGGTTCATCAATGCCCTCAGAAAGTGATGAAACAGAGCTACAATAGACGTGG 180
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 QY 361 CTGGGGGAGGCTCATGGGCTTGCCCAACCGCTGCTGCTCTCTATGAATGCTCATCTT 420
 DB 488 CTGGGGGAGGCTCATGGGCTTGCCCAACCGCTGCTGCTCTCTATGAATGCTCATCTT 547
 QY 421 GGACGATTCCTCATTTGGGCGCTTACTCAGGGCTGACATCAGGGCTGGTCCCCATGACGTG 480
 DB 548 GGACGATTCCTCATTTGGGCGCTTACTCAGGGCTGACATCAGGGCTGGTCCCCATGACGTG 572
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 genomic survey sequence.
 AY421216
 AY421216.1 GI:39777173
 GSS.
 KEYWORDS

AY421216 1497 bp DNA linear GSS 17-DEC-2003
 Pan troglodytes SLC2A4 gene, VIRTUAL TRANSCRIPT, partial sequence,
 genomic survey sequence.
 AY421216
 AY421216.1 GI:39777173
 GSS.
 KEYWORDS

SOURCE
ORGANISM Pan troglodytes (chimpanzee)
Pan troglodytes
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
REFERENCE
AUTHORS 1 (bases 1 to 1497)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Inferring nonneutral evolution from human-chimp-mouse orthologous
gene trios
JOURNAL Science 302 (5652), 1960-1963 (2003)
PUBMED 14671302
REFERENCE
AUTHORS 2 (bases 1 to 1497)
Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civello, D.R., Lu, F., Murphy, B.,
Ferreira, S., Wang, G., Zheng, X.H., White, T.J., Shinsky, J.J.,
Adams, M.D. and Cargill, M.
TITLE Direct Submission
JOURNAL Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
COMMENT This sequence as made by sequencing genomic exons and ordering them
based on alignment.
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Best Local Similarity 71.8%; Pred. No. 4.7e-168;
Matches 1075; Conservative 0; Mismatches 422; Indels 0; Gaps 0;
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DB 361 GCTGCTCTCTATGAATGCT 420
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RESULT 5
AJ281552/c
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DEFINITION
4A3A-P6F11-F Anopheles gambiae immune competent 4A3A Anopheles
gambiae cDNA clone 4A3A-P6F11, mRNA sequence.
ACCESSION
AJ281552
VERSION
AJ281552.1
GI:6929432
KEYWORDS
EST.

QY 574 TTGGAGTCCCTCCTGGGCACTGCCAGCCTGTGGCCACTGCTCCTGGGCTCACAGTGCTA 633
DB 541 NNN 600
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DB 1021 CTCCATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1080
QY 1114 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1173
DB 1081 CTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140
QY 1174 GTGGCATTTTGTGAGATTGGCCCTGCGCCCATTCCTTGGTTCATCGTGCCGAGCTCTTC 1233
DB 1141 NNN 1200
QY 1234 AGCCAGGAGACCCCGCCGCGCAGCCATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1293
DB 1201 NNN 1260
QY 1294 TTCCATCATTTGGCATGGGTTTCCAGTATGTTGGGAGGCTATGGGCGCCCTACGCTCTTCCT 1353
DB 1261 NNN 1320
QY 1354 CTATTTGGGCTCCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1413
DB 1321 CTATTTGGGCTCCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1380
QY 1414 CGAGGCGGAGCCTTTGACCCAGATCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1473
DB 1381 CGAGGCGGAGCCTTTGACCCAGATCTCAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1440
QY 1474 CAGGAGGTGAACACCCAGCAGCAAGATTGAGTATTTAGGGCCAGATGAGAACGACTGA 1530
DB 1441 CAGGAGGTGAACACCCAGCAGCAAGATTGAGTATTTAGGGCCAGATGAGAACGACTGA 1497

FEATURES		based on alignment.	
source	Location/Qualifiers		
gene	1..1497		
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Query Match			
Best Local Similarity 13.2%; Score 1037; DB 29; Length 1497;			
Matches 1133; Conservative 0; Mismatches 364; Indels 0; Gaps 0;			
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DB	1	GATGGGAAACCCCTCGGACGAGTGAAGTGGGACCCCTGGTCTGCTGTGTTCTCTGGG	60
QY	94	GTGCTTGGCTCCCTGCGAGTTTGGTGAACAATTGGGGTCAATCAATGCCCTCAGAAAGTG	153
DB	61	GTGCTTGGCTCCCTCAGTTTGGCTAATAAATTGGGGTATCAATGCCCTCAGAAAGTG	120
QY	154	ATTGAACAGAGTACAAATGAGAGCTGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAG	213
DB	121	ATTGAACAGAGTACAAATGAGAGCTGGCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAG	180
QY	214	ATCCCTCCAGGACCCCTCAACACCCCTCGGGCCCTCTCGGTGGCCATCTTTTCCGGTGGC	273
DB	181	ATCCCAAGGACCCCTCAACAGCTCTGGGCTCTCGGTGGCCATCTTTCTGTGGGT	240
QY	274	GGCATGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	333
DB	241	GGCATGATCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT	300
QY	334	ATGCTGGTCAAAATGCTTCTTGGGCTCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAG	393
DB	301	ATGCTGGTCAAAATGCTTCTTGGGCTCTGGGAGGAGGAGGAGGAGGAGGAGGAGGAG	360
QY	394	GCTGCTCTTATGAATGCTTCTTGGAGGAGTCTTCTTGGGCTCTTCTTGGGCTCTTCT	453
DB	361	GCGGCTCTTATGAATGCTTCTTGGAGGAGTCTTCTTGGGCTCTTCTTGGGCTCTTCT	420
QY	454	ACATCAGGCTGGTGGCCATGATGAGTGGGAGGAGTGTCTCCACTCAGCTGGGAGGAGG	513
DB	421	ACATCAGGCTGGTGGCCATGATGAGTGGGAGGAGTGTCTCCACTCAGCTGGGAGGAG	480
QY	514	CTGGGAGGCTCAACCACTGGGCTATGATGAGGAGTGTCTGATGAGGAGGAGGAGGAG	573
DB	481	TTGGGAACACTCAACCACTGGGCTATGATGAGGAGTGTCTGATGAGGAGGAGGAGGAG	540
QY	574	TTGGAGTCTCTCTGGGCTGCTGAGGCTGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCT	633
DB	541	TTGGAGTCTATGCTGGGCTGCTGAGGCTGTGGGCTGCTGCTGCTGCTGCTGCTGCTGCT	600
QY	634	CTGCTCTCTCTGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	693
DB	601	CTGCTCTCTCTGAGTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT	660
QY	694	ATCATCCAGATCTCAGGAGGCTGCGAGAGAGTGTGAGGAGGAGGAGGAGGAGGAGGAG	753
DB	661	ATCATCCGAACTCGAGGAGGCTGCGAGAGAGTGTGAGGAGGAGGAGGAGGAGGAGGAG	720
QY	754	GATGTTTCTGAGTGTCTGCTGAGTGAAGGATGAAGGAGGAGGAGGAGGAGGAGGAGGAG	813
DB	721	GATGTTTCTGAGTGTCTGCTGAGTGAAGGATGAAGGAGGAGGAGGAGGAGGAGGAGGAG	780
QY	814	CCACTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	873
DB	781	CCAAATGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	840
QY	874	GTGCTGCTGAGTGAAGGAGTGTCTGCTGAGTGAAGGAGGAGGAGGAGGAGGAGGAGGAG	933
DB			

841	GTGGTGTGCTGAGCCAGCAGCTCTCAGGATCAATGCTGTTTCTACTATTCAACC	900
934	AGCATTTTCGAGACAGCAGGGGTAGCCAGCTGCTATGCCACCATAGGAGCTGGTGTG	993
901	AGCATTTTCGAGTGGCTGGGTGGGACAGCCAGCTAGCCACCATAGGAGCTGGTGTG	960
994	GTCAACACAGTCTTCACTTGGTCTGGTGTGTTGGTGGAGGGGGGGGGGGGGGGGGAG	1053
961	GTCAATACGGTCTTCACTTGGTCTGGTGTGTTGGTGGAGGGGGGGGGGGGGGGGGAG	1020
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1021	CTCCATCTCTGGGCTGCGGGCATGTGTGCTGTGCCATCTGATGACTGTGGCTCTG	1080
1114	CTCTCTGTGGAGCGAGTTCCAGCCATGAGCTAGCTCTCCATTGTGGCCATCTTTGGCTTC	1173
1081	CTGCTGCTGNN	1140
1174	GTGGCATTTTTTGAGATTGGCCCTGGCCCATTCCTTGGTTTCATGTCGCCGAGCTCTTC	1233
1141	NN	1200
1234	AGCCAGGAGACCCCGCCGCGCAGCCATGGCTGTGGCTGTTCTCCAACTGGAGCAGCAAC	1293
1201	NN	1260
1294	TTTCATCATTTGGCATGGGTTTCCAGTATGTGGGAGGCTATGGGGCCCTACGTTCTCTT	1353
1261	NN	1320
1354	CTATTGGGCTCTCTGCTGGGCTTCTTCATCTTCACCTCTTAAAGACTCTGAAACT	1413
1321	CTATTGGGCTCTCTGCTGGGCTTCTTCATCTTCACCTCTTAAAGACTCTGAAACT	1380
1414	CGAGCGCGGACCTTTGACCATCTCAGCTGCTTCCACCGGACCCCTCTCTTTTAGAG	1473
1381	AGAGCGCGGACCTTTGACCATCTCAGCTGCTTCCCGACGACACTTCCCTTTTAGAG	1440
1474	CAGGAGGTGAACCCAGCAGCAAGCTTGAATATTTAGGCGCCAGATGAGAACACTGA	1530
1441	CAGGAGGTGAACCCAGCAGCAAGCTTGAATATTTAGGCGCCAGATGAGAACACTGA	1497

RESULT 7			
AU081137/c	1067 bp	mRNA	linear
LOCUS	AU081137	Oncorhynchus mykiss	kidney infected by infectious
DEFINITION	hematopoietic necrosis virus	Oncorhynchus mykiss	cDNA clone KI2,
ACCESSION	AU081137	mRNA sequence.	
VERSION	AU081137		
KEYWORDS	AU081137.1	GI:6431485	
SOURCE	EST.		
ORGANISM	Oncorhynchus mykiss	(rainbow trout)	
	Oncorhynchus mykiss		
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
	Actinopterygii; Neopterygii; Teleostei; Euteleostei;		
	Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.		
REFERENCE	1 (bases 1 to 1067)		
AUTHORS	Kono,T., Sakai,M. and Iaputra,S.E.		
TITLE	Expressed Sequence Tag Analysis of Kidney and Gill Tissues from		
	Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious		
	Hematopoietic Necrosis Virus		
JOURNAL	Mar. Biotechnol. 2 (5), 493-498 (2001)		
COMMENT	Contact: Masahiro Sakai		
	Faculty of Agriculture		
	Miyazaki University		
	1-1 nishi gakuenkibanadai, Miyazaki, Miyazaki 889-2192, Japan		
	Email: m.sakai@cc.miyazaki-u.ac.jp.		
FEATURES	Location/Qualifiers		
source	1..1067		
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	/db_xref="taxon:8022"		

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 QY 5767 CTTCTGACAAAGATCGGAGGACCGAAGGAGCTAAACCGCTTTTTCGACAAACATGGGGAT 5826
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 QY 5827 C-ATGTAACCTCGCTTGTATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGA 5885
 DB 420 CAATGTAACCTCGCTTGTATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGA 479
 QY 5886 GGTGACACGATCGCTGTAGCAATGGCAACACAGTTGGCGAACTATTAACTTGGCGA 5945
 DB 480 GGTGACACGATCGCTGTAGCAATGGCAACACAGTTGGCGAACTATTAACTTGGCGA 539
 QY 5946 ACTACTTACTCTAGCTTCCCGCAACAATTAATAGACTGGAGCGGATGAAGTTGC 6005
 DB 540 ACTACTTACTCTAGCTTCCCGCAACAATTAATAGACTGGAGCGGATGAAGTTGC 599
 QY 6006 AGGACCACTTCTGCGCTCGCGCTTCCGCTGGCTGTTTATTTGCTGATAAAATCTGGAGC 6065
 DB 600 AGGACCACTTCTGCGCTCGCGCTTCCGCTGGCTGTTTATTTGCTGATAAAATCTGGAGC 659
 QY 6066 CGGTGAGCGTGGTCTCGCGGTATCATTCAGCACTGGGGCCAGATGGTAAAGCCCTCCG 6125
 DB 660 CGGTGAGCGTGGTCTCGCGGTATCATTCAGCACTGGGGCCAGATGGTAAAGCCCTCCG 719
 QY 6126 TATCGTAGTATCTACACGAGGGAGTCAGCACTATGGATGAACGAATAGACAGAT 6185
 DB 720 TATCGTAGTATCTACACGAGGGAGTCAGCACTATGGATGAACGAATAGACAGAT 779
 QY 6186 CGCTGAGTAGTGTCTCACTGAATTAAGCAATGGTAACTGTGACACCAAGTTTACTCAT 6245
 DB 780 CGCTGAGTAGTGTCTCACTGAATTAAGCAATGGTAACTGTGACACCAAGTTTACTCAT 839
 QY 6246 TATCTTTAGATTGATTTAAACTCATTTTAAATTTAAAGGATCTAGTGAAGATCT 6305
 DB 840 TATCTTTAGATTGATTTAAACTCATTTTAAATTTAAAGGATCTAGTGAAGATCT 899
 QY 6306 TTTTGTATCTCATGACCAAAATCCCTTAAAGTGGTGGTTCCTTCCACTGAGCGTCAGA 6365
 DB 900 TTTTGTATCTCATGACCAAAATCCCTTAAAGTGGTGGTTCCTTCCACTGAGCGTCAGA 959
 QY 6366 CCCCGTAGAAAGATCAAGAGTCTTCTTGAAGATCTTTTTCGCGGTAAAT 6419
 DB 960 CCCCGTAGAAAGATCAAGAGTCTTCTTGAAGATCTTTTTCGCGGTAAAT 1013

RESULT 9
 AU081124/c
 LOCUS
 DEFINITION
 hematopoietic necrosis virus Oncorhynchus mykiss cdna clone KG'12,
 mRNA sequence.
 AU081124
 AU081124.1 GI:6431472
 EST.
 Oncorhynchus mykiss (rainbow trout)
 Oncorhynchus mykiss
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Actinopterygii; Neopterygii; Teleostei; Euteleostei;
 Protacanthopterygii; Salmoniformes; Salmonidae; Oncorhynchus.
 1 (bases 1 to 1089)
 Kono, T., Sakai, M. and LaPatra, S.E.
 Expressed Sequence Tag Analysis of Kidney and Gill Tissues from
 Rainbow Trout (Oncorhynchus mykiss) Infected with Infectious
 Hematopoietic Necrosis Virus
 Mar. Biotechnol. 2 (5), 493-498 (2001)
 Contact: Masahiro Sakai
 Faculty of Agriculture
 Miyazaki University

1-1 nishi gakukenibandai, Miyazaki, Miyazaki 889-2192, Japan
 Email: m.sakai@cc.miyazaki-u.ac.jp.
 Location/Qualifiers
 1..1089
 /organism="Oncorhynchus mykiss"
 /mol_type="mRNA"
 /db_xref="taxon:8022"
 /clone="KG'12"
 /tissue_type="kidney"
 /clone_lib="Oncorhynchus mykiss kidney infected by
 infectious hematopoietic necrosis virus"
 /note="common name:rainbow trout ; infected by infectious
 hematopoietic necrosis virus"

FEATURES
source

ORIGIN

Query Match 12.2%; Score 957; DB 9; Length 1089;
 Best Local Similarity 97.0%; Pred. No. 1.5e-148;
 Matches 1018; Conservative 0; Mismatches 25; Indels 6; Gaps 4;

QY 6398 ATCTCTTTTCTGCGCGTAATCTGC-TGCTTGCACAAACAAAAA---AACCAACGCTTACCA 6453
 DB 1089 ATCTCTTTTCTGCGCGTAATCTGCCTTGCACAAACAAAAAAGACACCCCTTCCAG 1030
 QY 6454 GCGTGGTGTGTTTCCCGGAT-CAAGAGCTACCAACTCTTTTCCGAAGGTAACTGGCTT 6512
 DB 1029 CGTGTGTTTGTGTTCCCGATCCCACTCTTTTCCGAAGGTAACTGGCTT 970
 QY 6513 CAGCAGAGCGCAGATACCAATACCTGCTCTAGTGTAGCCGTAGTTAGGCCAC-CACT 6571
 DB 969 CAGCAGAGCGCAGATACCAATACCTGCTCTAGTGTAGCCGTAGTTAGGCCACAACT 910
 QY 6572 TCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTGCTAATCTCTGTGTACAGTGGCTG 6631
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 QY 6632 CTGCGAGTGGCGATGAAGTCTGTCTTACCGGTTGGACTCAAGACGATAGTTACCGGATA 6691
 DB 849 CTGCGAGTGGCGATGAAGTCTGTCTTACCGGTTGGACTCAAGACGATAGTTACCGGATA 790
 QY 6692 AGCGCGAGCGGTCTGACCGGGTCTGACACAGCCAGCTTGGAGCGCAACGA 6751
 DB 789 AGCGCGAGCGGTCTGACCGGGTCTGACACAGCCAGCTTGGAGCGCAACGA 730
 QY 6752 CTTACACCGAACTGAGATACCTTACAGCGTGAAGTATGAGAAACGCGCAACGCTTCCGGAAG 6811
 DB 729 CTTACACCGAACTGAGATACCTTACAGCGTGAAGTATGAGAAACGCGCAACGCTTCCGGAAG 670
 QY 6812 GGAGAAAGCGGACAGGTATCCGTTAAGCGGAGGGTGGAAACAGAGAGCGCACGAGGG 6871
 DB 669 GGAGAAAGCGGACAGGTATCCGTTAAGCGGAGGGTGGAAACAGAGAGCGCACGAGGG 610
 QY 6872 AGCTTCCAGGGGAAACGCTGCTATCTTTATAGTCTGTGCGGTTTCCCACTCTGTAC 6931
 DB 609 AGCTTCCAGGGGAAACGCTGCTATCTTTATAGTCTGTGCGGTTTCCCACTCTGTAC 550
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 DB 549 TTGAGCGTCTGATTTTGTGATGCTCTGTCAGGGGGCGGAGCCTATGGAACAGCCAGCA 490
 QY 6992 AGCGCGCTTTTACGTTCTGGCTTTTGTGCGCTTTTGTGCTACATGTTCTTTCCTG 7051
 DB 489 AGCGCGCTTTTACGTTCTGGCTTTTGTGCGCTTTTGTGCTACATGTTCTTTCCTG 430
 QY 7052 CGTTATCCCTGATTTCTGTGATACCGTATTTACCGCTTTTGTGAGTGAGCTGATACCGCTC 7111
 DB 429 CGTTATCCCTGATTTCTGTGATACCGTATTTACCGCTTTTGTGAGTGAGCTGATACCGCTC 370
 QY 7112 GCCGAGCGCAACGACCGAGCGCAGTCACTGAGCGAGGAAGCGGAAGAGCGCCAA 7171
 DB 369 GCCGAGCGCAACGACCGAGCGCAGTCACTGAGCGAGGAAGCGGAAGAGCGCCAA 310
 QY 7172 TACGCAACCGCTCTCCCGCGGTGCGGATTCATTAAATGCGCTGGCAGCAGGT 7231

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Db      309  TACGCAAAACCCCTCTCCCCCGCGTGGCGGATTCATTAAATGACGCTGCACGACAGGT 250
Qy      7232  TTCCCGACTGGAAGCGGCGAGTCAGCGCAACGCAATTAAATGTGAGTTACTCTACTCATTT 7291
Db      249  TTCCCGACTGGAAGCGGCGAGTCAGCGCAACGCAATTAAATGTGAGTTAGTCTACTCATTT 190
Qy      7292  AGGCAACCCAGGCTTTACACTTTATGCTTCGGCTCCTCTATGTTGTGGAATGTGAGCG 7351
Db      189  AGGCACCCAGGCTTTACACTTTATGCTTCGGCTCCTCTATGTTGTGGAATGTGAGCG 130
Qy      7352  GATAACAATTTACACAGGAACAGCTATGACCATGATTACGCCAAGCGCGCAATTAACC 7411
Db      129  GATAACAATTTACACAGGAACAGCTATGACCATGATTACGCCAAGCTCGAAATTAACC 70
Qy      7412  CTCACCTAAAGGGAACAAAGCTGCGAGCTC 7440
Db      69  CTCACCTAAAGGGAACAAAGCTGCGAGCTC 41

RESULT 10
AJ281480/c
LOCUS      1004 bp      mRNA      linear      EST 30-JUN-2000
DEFINITION 4A3A-P4G8-F Anopheles gambiae immune competent 4A3A Anopheles
gambiae cDNA clone 4A3A-P4G8, mRNA sequence.
ACCESSION  AJ281480
VERSION     AJ281480.1  GI:6929360
KEYWORDS   Anopheles gambiae (African malaria mosquito)
SOURCE     Anopheles gambiae
ORGANISM   Anopheles gambiae
            Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
            Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea;
            Anopheles.
REFERENCE   1 (bases 1 to 1004)
AUTHORS    Dimopoulos, G., Casavant, T.L., Chang, S., Scheetz, T., Roberts, C.,
            Donohue, M., Schultz, J., Benes, V., Bork, P., Ansoorge, W., Soares, M.B.
            and Kafatos, F.C.
TITLE      mosquito innate immunity genes from expressed sequence tags
            generated from immune-competent cell lines
JOURNAL    Proc. Natl. Acad. Sci. U.S.A. 97 (12), 6619-6624 (2000)
MEDLINE    20300950
PUBMED     10841561
COMMENT    Contact: Dimopoulos G
            Fotis C. Kafatos laboratory
            European Molecular Biology Laboratory
            Meyerhofstrasse 1, 69117 Heidelberg, Germany.
            Location/Qualifiers
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               /organism="Anopheles gambiae"
               /mol_type="mRNA"
               /strain="4A r/r"
               /db_xref="taxon:7165"
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               /cell_lines="immune competent 4A3A"
               /lab_host="E. coli DH10B"
               /clone_lib="Anopheles gambiae immune competent 4A3A"
               /note="Vector: p773D-Pac (Pharmacia) with a modified
               polylinker; Site 1: EcoRI; Site 2: NotI; sequenced from
               forward priming site which reads from the 3' end of the
               cDNA. The 4A3A is a directionally cloned and normalized
               cDNA library that was constructed from the 4A3A cell line
               oligo-T primed cDNA according to: Bonaldo, Lennon & Soares
               (1996). Normalization and Subtraction: Two approaches to
               Facilitate Gene Discovery, Genome Research 6, 791-806."

ORIGIN
Query Match      11.8%; Score 924; DB 9; Length 1004;
Best Local Similarity 99.0%; Pred. No. 4.5e-143;
Matches 1001; Conservative 1; Mismatches 2; Indels 7; Gaps 7;

Qy      6011  CACTTCTCGGCTCGGCCCTTCGGCTGGCTGGTTTATGCTGATAAATCTGGAGCCGGTG 6070
Db      1004  CACTTCTCGGCTCGG-CCTTCGGCTGGCTGGTTTATGCTGTA-AAATCTGGAGCC-GTG 948

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Qy      6071  AGCGTGGTCTCGCGGTATCATTTGCAGCACTGGGGCCAGATGGTAAGCCCTCCGATATCG 6130
Db      947  AGCGT-GGTCTCGGTATCATTTGCAGCACT-GGGCCARATGGTAAGCCCTCCGATATCG 890
Qy      6131  TAGTTATCTACAGACGGGGAGTCAGCAACTATGATGAACGAAATAGACAGATCGGTG 6190
Db      889  TAG-TATCTACAGACGGGGAGTCAGCAACTATGATGAACGAAATAGACAGATCGGTG 831
Qy      6191  AGATAGGTGCTCACTGATTTAAGCATTTGTAACCTGTCCAGACCAAGTTTACTCATATATAC 6250
Db      830  AGATA-GTGCTCACTGATTTAAGCATTTGTAACCTGTCCAGACCAAGTTTACTCATATATAC 772
Qy      6251  TTTAGATTGATTTAAAACTTTCAATTTTAAATTTAAAGGATCTAGGTGAAGATCTCTTTTG 6310
Db      771  TTTAGATTGATTTAAAACTTTCAATTTTAAATTTAAAGGATCTAGGTGAAGATCTCTTTTG 712
Qy      6311  ATAACTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCG 6370
Db      711  ATAACTCATGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACCCCG 652
Qy      6371  TAGAAAAGATCAAGGATCTTCTTGAGATCCTTTTTTCTGCGGTAAATCTGCTGCTTGC 6430
Db      651  TAGAAAAGATCAAGGATCTTCTTGAGATCCTTTTTTCTGCGGTAAATCTGCTGCTTGC 592
Qy      6431  AAAACAAAAAACCAACCGCTACCAAGCGGTGTTGTTTCCCGGATCAAGAGCTACCAACTC 6490
Db      591  AAACAAAAAACCAACCGCTACCAAGCGGTGTTGTTTCCCGGATCAAGAGCTACCAACTC 532
Qy      6491  TTTTTCGGAAGTAACTGGCTTCAGAGAGCGGAGATACCAAAATCTGCTCTTAGTGT 6550
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Qy      6551  AGCGTAGTTAGCCACCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTGC 6610
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Db      351  CAAGACGATAGTTACCGGATAAGCGCGAGCGGTGCGGCTGAACGGGGGTTCTGTCANAC 292
Qy      6731  AGCCAGCTTGGAGCGAAACGACCTACACCGAACTGAGATACCTACAGCGCTGAGCTATCAG 6790
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Db      171  GAACAGAGAGCGACAGAGGAGGCTTCAGGGGGAAAGCGCTGATCTTTATAGTCTCTG 112
Qy      6911  TCGGGTTCCCACTCTGACTTGGAGCTCGATTTTGTGATGCTCGTCAGGGGGCGGA 6970
Db      111  TCGGGTTCCCACTCTGACTTGGAGCTCGATTTTGTGATGCTCGTCAGGGGGCGGA 52
Qy      6971  GCCTATGGAAAAACGCCAGCAACGCGGCTTTTTTACGGTTCTTGGCCCTTTT 7021
Db      51  GCCTATGGAAAAACGCCAGCAACGCGGCTTTTTTACGGTTCTTGGCCCTTTT 1

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RESULT 11
CD458281
LOCUS      973 bp      mRNA      linear      EST 03-JUN-2003
DEFINITION Fg08_08r09 R Fg08 AAFc ECORC Fusarium graminearum complex_substrate
Gibberella zeae cDNA clone Fg08_08r09, mRNA sequence.
ACCESSION  CD458281
VERSION     CD458281.1  GI:31373021

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KEYWORDS EST.
SOURCE Gibberella zeae
ORGANISM Gibberella zeae
REFERENCE Hypocremycetidae; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
AUTHORS Hypocremycetidae; Hypocreales; Nectriaceae; Gibberella.
1 (bases 1 to 973)
Watson,R.J., Heys,R., Chapados,J., Couroux,P., Harris,L.J.,
Hattori,J., Lacroix,C., Ouellet,T., Robert,L.S., Singh,J.A.,
Spratt,D. and Tinker,N.A.
A cDNA library prepared from Fusarium graminearum grown on a
complex plant substrate
Unpublished (2003)
JOURNAL Contact: Watson, Robert.J.
COMMENT Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bldg. 20, Central Experimental Farm, Ottawa, Ontario, K1A 0C6,
CANADA
Tel: (613) 759-1655
Fax: (613) 759-1701
Email: watsonrj@agr.gc.ca.
FEATURES
Location/Qualifiers
1..973
/organism="Gibberella zeae"
/mol_type="mRNA"
/strain="DAOM 180378"
/db_xref="taxon:5518"
/clone="Fg08_08h09"
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/lab_host="E. coli DH10B"
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/note="Vector: pBluescript II+; Site 1: EcoRI; Site 2:
XhoI; Fusarium graminearum grown on a complex plant
substrate-- wheat leaves treated to remove most of the low
molecular weight, water-soluble components."
ORIGIN
Query Match 11.7%; Score 916.8; DB 14; Length 973;
Best Local Similarity 98.1%; Pred. No. 7e-142;
Matches 932; Conservative 5; Mismatches 12; Indels 1; Gaps 1;
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DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
25 TTAGTGGCATTTCGGGAAATGTGCGGGAACCCCTATTGTTTATTTTCTAAAT 84
QY ACATTCAATATGATCGCTCATGAGCAATAACCCCTGATAAAGCTTCAATAATATG 5348
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
85 ACATTCAATATGATCGCTCATGAGCAATAACCCCTGATAAAGCTTCAATAATATG 144
QY AAAAAAGGAGATGATGATGATTTCAACATTTCCGTGTGCGCCCTATTCCCTTTTTCGCGC 5408
DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
145 AAAAAAGGAGATGATGATGATTTCAACATTTCCGTGTGCGCCCTATTCCCTTTTTCGCGC 204
QY ATTTTGCCTTCCTTTTGTCTCACCAGAAACCGTGTGGAAGTAAAGATGCTGAAGA 5468
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205 ATTTTGCCTTCCTTTTGTCTCACCAGAGACGCTGTGGAAGTAAAGATGCTGAAGA 264
QY TCAGTGTGGTGCCAGGTGGTGTACATCGAATCGGATCTCAACAGCGGTAAAGATCCTTGA 5528
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QY GAGTTTTCGCCCGGAGAACGTTTTCATGATGAGCACTTTTAAAGTTCTCTATGTGG 5588
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325 GAGTTTTCGCCCGGAGAACGTTTTCATGATGAGCACTTTTAAAGTTCTCTATGTGG 384
QY CGCGGTATTATCCCGTATTGACCGCGGCAAGAGCAACTCGGTGCGCGCATACATTTC 5648
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385 CGCGGTATTATCCCGTATTGACCGCGGCAAGAGCAACTCGGTGCGCGCATACATTTC 444
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QY 5709 ACTAAGAGAAATTATGCAGTGTGCCATAACCATGAGTGATAACACTGCGGCCCAACTTACT 5768
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505 ACTAAGAGAAATTATGCAGTGTGCCATAACCATGAGTGATAACACTGCGGCCCAACTTACT 564
QY 5769 TCTGCAACGATCGGAGGACCGAAGAGGCTAACCGCTTTTTCGCAACAATGCGGGATCA 5828
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565 TCTGCAACGATCGGAGGACCGAAGAGGCTAACCGCTTTTTCGCAACAATGCGGGATCA 624
QY 5829 TGTAACTCGCCTTGTATCGTTGGGAAACCGGAGCTGAATGAAGCCATACCAACGACGAGCG 5888
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805 ACCACTTCTGCGCTCGGCCCTTCCGCTGGCTGGCTTTTATTCGTGATAAATCTGGAGSCGG 864
QY 6069 TGAGCGTGGCTCTCGCGGTATCATTTGCAGCACTGCGGCGCAGATGGTAAGCCCTCCCGTAT 6128
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865 TGAGCGTGGCTCTCGCGGTATCATTTGCAGCACTGCGGCGCAGATGGTAAG-CCVCCGCTAT 923
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924 CGTACTTATCTACACGAGGGGAGTCTAGGCACTATGATGAACGAAATA 973
RESULT 12
CG700598/c
LOCUS 1025 bp DNA linear GSS 15-OCT-2003
DEFINITION ZMMBBC0120G04f ZMMBBC (EcoRI) Zea mays subsp. mays genomic clone
ZMMBBC0120G04 5', genomic survey sequence.
ACCESSION CG700598
VERSION 1
KEYWORDS Zea mays subsp. mays (maize)
SOURCE Zea mays subsp. mays
ORGANISM Zea mays subsp. mays
REFERENCE 1. (bases 1 to 1025)
AUTHORS Bharti,A.K., Young,S., Kavchok,S., Keizer,G., Bronzino,A.C.,
Zohovetz,V., Fuks,G., Yu,Y., Wing,R. and Messing,J.
TITLE Sequencing of the maize genome at PGIR (2003c)
JOURNAL Unpublished (2003)
COMMENT Contact: Bharti,A.K.
Dr.Joachim Messing's lab
The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers
University
190 Frelinghuysen Road, Piscataway, NJ 08854, USA
Tel: 732 445 3801
Fax: 732 445 5735
Email: bharti@waksman.rutgers.edu
Seq primer: T7
Class: BAC ends
High quality sequence start: 24.
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/clone_lib="ZMMBBC (EcoRI)"

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ORIGIN /note="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"
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Best Local Similarity 98.2%; Pred. No. 3.3e-139;
Matches 932; Conservative 0; Mismatches 14; Indels 3; Gaps 2;

QY 6459 GGTGTTGTCGGGATCAAGAGCTACC--AACTCTTTTTCGAAAGTAAGTGGCTTCAGC 6516
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QY 6517 AGAGCGCAGATACCAATACACTGCTTCTAGTGTAGCGGTAGTGGCCACCACTTCAAG 6576
DB 965 AGAGCGCAGATACCAATACACTGCTTCTAGTGTAGCGGTAGTGGCCACCACTTCAAG 906
QY 6577 AACTCTGTAGCAGCGCTACATACCTCGCTCTGTAATCTCTGTGTACAGTGGCTGGCC 6636
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DB 845 AGTGGCGATAAGTGTGCTTTTACCGGTTGGACTCAAGACGATAGTTACCGGATAAGCG 786
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DB 785 CAGCGGTCGGGCTGAACGGGGGTTCTGTGCACACAGCCAGCTTGGAGCGAACGACCTAC 726
QY 6757 ACCGAACTGATACCTACAGCGTGAAGCGGAGCTATGAGAAAGCGCCAGCTTCCGAGGAGA 6816
DB 725 ACCGAACTGATACCTACAGCGTGAAGCGGAGCTATGAGAAAGCGCCAGCTTCCGAGGAGA 666
QY 6817 AAGCGGACAGGTATCCGGTAAGCGGAGGCTCGGAACAGAGAGCGACACGAGGAGCTT 6876
DB 665 AAGCGGACAGGTATCCGGTAAGCGGAGGCTCGGAACAGAGAGCGACACGAGGAGCTT 606
QY 6877 CCAGGGGAAA CGCTGTGTATCTTTATAGTCTCTCTCGGTTTCCCACTCTGACTTGAG 6936
DB 605 CCAGGGGAAA CGCTGTGTATCTTTATAGTCTCTCTCGGTTTCCCACTCTGACTTGAG 546
QY 6937 GTCGATTTTGTGATGCTCTGACGGGGGGGAGCTATGGAAGAAAGCGGACGACGCG 6996
DB 545 GTCGATTTTGTGATGCTCTGACGGGGGGGAGCTATGGAAGAAAGCGGACGACGCG 486
QY 6997 GCCTTTTACGGTCTCGGCTTTTGTGCTGCTTTTGTCTACATGTTCTTTCTGCGTTA 7056
DB 485 GCCTTTTACGGTCTCGGCTTTTGTGCTGCTTTTGTCTACATGTTCTTTCTGCGTTA 426
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DB 425 TCCCTGTATCTGTGATAACCGTATTACCGCTTATAAGTGAGCTGATACCGCTCGCG 366
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QY 7176 CAACCGGCTCTCCCGCGGCTTGGCGATTATTATGACGCTGGCACACAGGTTTC 7235
DB 305 CAACCGGCTCTCCCGCGGCTTGGCGATTATTATGACGCTGGCACACAGGTTTC 246
QY 7236 CGACTGGAAGCGGCGAGTACGAGCGCAACGCAATTAATGTGAGTTACCTCACTATTAGG 7295
DB 245 CGACTGGAAGCGGCGAGTACGAGCGCAACGCAATTAATGTGAGTTACCTCACTATTAGG 186
QY 7296 ACCCAGGCTTTACACTTTATGCTTCCGCTCCTATGTTGTGGAATTTGTAGCGGATA 7355
DB 185 ACCCAGGCTTTACACTTTATGCTTCCGCTCCTATGTTGTGGAATTTGTAGCGGATA 126
QY 7356 ACAATTTACACAGGAACAGCTATGACCATGATTACGCCAAGCGCGCA 7404
DB 125 ACAATTTACACAGGAACAGCTATGACCATGATTACGCCAAGCTTGCA 77
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CG392995/c

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

CG392995
ZMMBc0004E12f ZMMBc (EcoRI) Zea mays subsp. mays genomic clone
ZMMBc0004E12 5', genomic survey sequence.

CG392995
CG392995.1 GI:34336220
GSS.

Zea mays subsp. mays (maize)
Zea mays subsp. mays
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea;
1 (bases 1 to 996)

Bharti, A.K., Young, S., Kavchok, S., Keizer, G., Bronzino, A.C.,
Rouard, K., Fuks, G., Yu, Y., Wing, R., and Messing, J.

Sequencing of the maize genome at PGIR (2003b)
Contact: Bharti, A.K.

Unpublished (2003)

Dr. Joachim Messing's lab

The Plant Genome Initiative at Rutgers, Waksman Institute, Rutgers

University

190 Frelinghuysen Road, Piscataway, NJ 08854, USA

Tel: 732 445 3801

Fax: 732 445 5735

Email: bharti@waksman.rutgers.edu

Seq primer: T7

Class: BAC ends

High quality sequence start: 11.

Location/Qualifiers

1..996

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/lab_host="E. coli DH10B"

/clone_lib="ZMMBc (EcoRI)"

/notes="Vector: pTARBAC2.1; Site_1: EcoRI; Site_2: EcoRI"

Query Match 11.5%; Score 899.8; DB 29; Length 996;

Best Local Similarity 98.7%; Pred. No. 4.6e-139;

Matches 907; Conservative 0; Mismatches 12; Indels 0; Gaps 0;

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DB 996 ACCTCTTTTCCGAGGTAACTGGCTTCAGCAGAGCGCAGATACCAATACCTGCTTCT 937

QY 6546 AGTGTAGCCCTAGTATAGGCCACCACTTCAAGAACTCTGTAGCAGCCCTACATACCTCGC 6605

DB 936 AGTGTAGCCCTAGTATAGGCCACCACTTCAAGAACTCTGTAGCAGCCCTACATACCTCGC 877

QY 6606 TCTGCTAATCTGTTACCACTGGCTGTCCAGTGGCGATAAGTGTCTTACCGGGTT 6665

DB 876 TCTGCTAATCTGTTACCACTGGCTGTCCAGTGGCGATAAGTGTCTTACCGGGTT 817

QY 6666 GGACTCAAGACGATAGTTACCGGATAGCGCAGCGGTCCGGCTGAACGGGGGTTCTG 6725

DB 816 GGACTCAAGACGATAGTTACCGGATAGCGCAGCGGTCCGGCTGAACGGGGGTTCTG 757

QY 6726 CACACAGCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCT 6785

DB 756 CACACAGCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCT 697

QY 6786 ATGAGAAAGCGCCACCGTTCCTCGAAGGAGAAAGCGGACAGGATCCGGTAAGCGGAC 6845

DB 696 ATGAGAAAGCGCCACCGTTCCTCGAAGGAGAAAGCGGACAGGATCCGGTAAGCGGAC 637

QY 6846 GGTTCGGAACAGGAGAGCGCAGGAGGAGCTTCCAGGGGAAACGCTGCTATCTTTATAG 6905

DB 636 GGTTCGGAACAGGAGAGCGCAGGAGGAGCTTCCAGGGGAAACGCTGCTATCTTTATAG 577

QY 6906 TCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTTCGATTTTGTGATGCTCTCAGGGG 6965
 Db 576 TCCTGTCGGGTTTCGCCACCTCTGACTTGAGCGTTCGATTTTGTGATGCTCTCAGGGG 517
 QY 6966 GCGGAGCCTATGGAAGAACCGCAGCAACCGCGCCTTTTACGGTTCCCTGGCCTTTTGTG 7025
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 QY 7026 GCCTTTTGTCTACATGTTCTTCTGCGGTTATPCCCTGATTCTGTGGATAACCGTATTAC 7085
 Db 456 GCCTTTTGTCTACATGTTCTTCTGCGGTTATPCCCTGATTCTGTGGATAACCGTATTAC 397
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 Db 336 GAGCGAGGAGCGGAGGAGCGGCAATAGCAAAACCGCTCTCCCGCGGCTTGCGCCGAT 277
 QY 7206 TCATTAATGCACTGGCAGCAGCAGGTTTCCGACTGGAAAGCGGCGAGTGAGCGCAACGC 7265
 Db 276 TCATTAATGCACTGGCAGCAGCAGGTTTCCGACTGGAAAGCGGCGAGTGAGCGCAACGC 217
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 Db 216 AATTAATGAGTACCTACCTACCTATAGCACCCAGCGCTTTACACTTTATGCTTCCGGC 157
 QY 7326 TCCTATGTTGTGTAATGAGCGGATTAACAATTTTACACAGGAAACAGCTATGACCA 7385
 Db 156 TCGTATGTTGTGTAATGAGCGGATTAACAATTTTACACAGGAAACAGCTATGACCA 97
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 Db 96 TGATTAACGCCAAGCTTGCA 78

RESULT 14
 CB686151
 LOCUS
 DEFINITION
 Bn01b_02008 A 925 bp mRNA line8r EST 09-APR-2003
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 mRNA sequence.
 CB686151
 CB686151.1 GI:29689876
 EST
 SOURCE
 Brassica napus (rape)
 ORGANISM
 Brassica napus
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 Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
 rosids; eurosids II; Brassicales; Brassicaceae; Brassica.
 1 (bases 1 to 925)
 Singh, J., Allard, G., Tinker, N., Robert, L., Lacroix, C., De Moors, A.,
 Chagnon, J., Farah, S., Couroux, P. and Hattori, J.
 Expressed Sequence Tags from Constitutively frost tolerant
 transgenic Brassica napus overexpressing BNCBF17
 Unpublished (2002)
 Contact: Singh, J.A.
 Eastern Cereal and Oilseed Research Centre
 Agriculture and Agri-food Canada
 KW Neatby Bldg., Central Experimental Farm, Ottawa, Ontario, KIA
 OC6, Canada
 Tel: (613) 759-1662
 Fax: (613) 759-1701
 Email: singhja@em.agr.ca.
 Location/Qualifiers
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 /clone="Bn01b_02008"

FEATURES
 source

/tissue_type="fourth leaf"
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 overexpressing BNCBF17 constitutively frost tolerant"
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 Site 2: XhoI; Germinated in soil flats and seedlings grown
 for 3 weeks in a Conviron E-15 cabinet set at 20°C / 16 hr
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 collected at 9 am and immediately frozen."

ORIGIN

Query Match 11.5%; Score 899.4; DB 14; Length 925;
 Best Local Similarity 98.5%; Pred. No. 5.5e-139;
 Matches 911; Conservative 6; Mismatches 7; Indels 1; Gaps 1;

QY 6505 ACTGCTTTCAGCAGAGCGCAGATACAAATACCTGCTCTTAGTGTAGCGGTAGTTAGCG 6564
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 QY 6565 CACCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTGCTAATCTGTTACCA 6624
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 QY 6625 GTGGCTGCTGCCAGTGGCGATAAGTGTCTTACCGGGTTGGACTCAAGACGATGTTA 6684
 Db 121 GTGGCTGCTGCCAGTGGCGATAAGTGTCTTACCGGGTTGGACTCAAGACGATGTTA 180
 QY 6685 CCGGATAAGGCGCAGCGGTGGGCTGAACGGGGGTTCTGTGCACACAGCCAGCTTGGAG 6744
 Db 181 CCGGATAAGGCGCAGCGGTGGGCTGAACGGGGGTTCTGTGCACACAGCCAGCTTGGAG 240
 QY 6745 CGAAGCACTTACCGAACTGAGATACCTACAGCGTGTAGCTATGAGAAAGCGCCACGCTT 6804
 Db 241 CGAAGCACTTACCGAACTGAGATACCTACAGCGTGTAGCTATGAGAAAGCGCCACGCTT 300
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 Db 301 CCGGAGGAGAAAGGCGGACAGGTATCCGTAAAGCGCAGGTTGGAAACAGGAGAGAGCGC 360
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 Db 721 GACAGGTTTCCCGACTGGAAGCGGCGAGTGGCGCAACGCAATTAATGAGTTAGCTTC 780
 QY 7285 ACTCATTAGGCAACCCAGGCTTTTACACTTTATGCTTCCGGCTCTTATGTTGTGGAATT 7344
 Db 781 ACTCATTAGGCAACCCAGGCTTTTACACTTTATGCTTCCGGCTCTTATGTTGTGGAATT 840
 QY 7345 GTGAGCGGATTAACCAATTTTCAACAGGAAACAGCTATGATGATGATGATGATGATGAT 7404

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Db      841 GTGAGCGGATAACAATTTACACACA-GAAACAGCTATGACCATGATTACGCCAAGCGCGCA 899
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RESULT 15
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DEFINITION Fg08_09a03_R Fg08_AAPC_ECORC_Fusarium_graminearum_complex_substrate
Gibberella zeae cDNA clone Fg08_09a03, mRNA sequence.
ACCESSION CD458286
VERSION   CD458286.1 GI:31373026
KEYWORDS EST.
SOURCE   Gibberella zeae
ORGANISM Gibberella zeae
Eukaryota; Fungi; Ascomycota; Pezizomycotina; Sordariomycetes;
Hypocreomycetidae; Hypocreales; Nectriaceae; Gibberella.
REFERENCE 1 (bases 1 to 917)
AUTHORS   Watson,R.J., Heyls,R., Chapados,J., Couroux,P., Harris,L.J.,
Hattori,J., Lacroix,C., Ouellet,T., Robert,L.S., Singh,J.A.,
Sprott,D. and Tinker,N.A.
TITLE     A cDNA library prepared from Fusarium graminearum grown on a
complex plant substrate
JOURNAL   Unpublished (2003)
COMMENT   Contact: Watson, Robert.J.
Eastern Cereal and Oilseed Research Centre
Agriculture and Agri-food Canada
Bldg. 20, Central Experimental Farm, Ottawa, Ontario, K1A 0C6,
CANADA
Tel.: (613) 759-1655
Fax: (613) 759-1701
Email: watsonrj@agr.gc.ca.

FEATURES             source
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XhoI; Fusarium graminearum grown on a complex plant
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molecular weight, water-soluble components."

ORIGIN
Query Match      11.3%; Score 886.2; DB 14; Length 917;
Best Local Similarity 99.7%; Pred. No. 8.4e-137;
Matches 888; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY      5289 ACATTCAATATGTATCCGCTCATGAGACATAACCCCTGATAAATGCTTCAATAATATTG 5348
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QY      5349 AAAAGGAAGAGTAGAGTATTCACATTTCGGTGTGCCCTTATTCCTTTTTCGGCG 5408
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QY      5409 ATTTTGCCTTCCTGTTTTCCTCCAGAACCCCTGGTGAAGTAAAGATGCTGAAGA 5468
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QY      5469 TCAGTTGGGTGCACGAGTGGGTATACATCGAACTGGATCTCAACAGCGGTAAAGATCCTTGA 5528

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Db      267 TCAGTTGGGTGCACGAGTGGGTACATCGAACTGGATCTCAACAGCGGTAAAGATCCTTGA 326
QY      5529 GAGTTTTCGCCCCGAAGAAGTGTTCCTAATGATGAGCAGCTTTTAAAGTTCCTGCTATGTTG 5588
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QY      5589 CGCGGTATTATCCGCTATTGACGCCGGGCAAGAGCAACTCGGTCCGCGCATACACTATTTC 5648
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QY      5709 AGTAAGAGATTAATGACAGTCTGCCATAACCATGAGTGATAACACTGGGCGCAACTTACT 5768
Db      507 AGTAAGAGATTAATGACAGTCTGCCATAACCATGAGTGATAACACTGGGCGCAACTTACT 566
QY      5769 TCTGACAAACGATCGGAGGACCGAAGAGCTAAACCGCTTTTTCACAAACATGGGGGATCA 5828
Db      567 TCTGACAAACGATCGGAGGACCGAAGAGCTAAACCGCTTTTTCACAAACATGGGGGATCA 626
QY      5829 TGTAACCTCGCCTTGTGATCGTTGGAAACCGGAGCTGAATGAAGCCATACCAACAGCAGCG 5888
Db      627 TGTAACCTCGCCTTGTGATCGTTGGAAACCGGAGCTGAATGAAGCCATACCAACAGCAGCG 686
QY      5889 TGACACCAAGATCGCTGTAGCAATGSCAAACAGTTGCGGCAAACTATTAACTGGCGAAT 5948
Db      687 TGACACCAAGATCGCTGTAGCAATGSCAAACAGTTGCGGCAAACTATTAACTGGCGAAT 746
QY      5949 ACTTACTCTAGCTTCCCGCAACAATTAATAGACTGGATGGAGCGGATAAAGTTGCAGG 6008
Db      747 ACTTACTCTAGCTTCCCGCAACAATTAATAGACTGGATGGAGCGGATAAAGTTGCAGG 806
QY      6009 ACCACTTTCGCGTCCGCGCCCTTCGCGCTGGCTGTTTATTGCTGATAAATCTGGAGCGG 6068
Db      807 ACCACTTTCGCGTCCGCGCCCTTCGCGCTGGCTGTTTATTGCTGATAAATCTGGAGCGG 866
QY      6069 TGAGCGTGGGTCTCGCGGTATCATTCGACGACTGGGGCCAGATGTTAAGCC 6119
Db      867 TGAGCGTGGGTCTCGCGGTATCATTCGACGACTGGGGCCAGATGTTAAGCC 917

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Search completed: May 16, 2004, 13:01:06
Job time : 12155.4 secs

GenCore version 5.1.6
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OM nucleic - nucleic search, using sw model

Run on: May 16, 2004, 00:32:57 ; Search time 346.412 Seconds
(without alignments)
12540.417 Million cell updates/sec

Title: US-10-067-449-9
Perfect score: 7828
Sequence: 1 atgcgcgcgggtcccaaca.....tttttaatttaatacaaaaa 7828

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 682709 seqs, 277475446 residues

Total number of hits satisfying chosen parameters: 1365418

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents NA.*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
C 1	4492.6	57.4	10288	4	US-09-845-917A-28
C 2	4492.6	57.4	13414	4	US-09-845-917A-27
C 3	3057.4	39.1	5181	3	US-08-801-344-5
C 4	3057.4	39.1	5181	4	US-09-498-599-5
C 5	2207.2	28.2	7432	4	US-09-367-891A-6
C 6	2206.2	28.2	5534	1	US-08-452-267-3
C 7	2206.2	28.2	5534	3	US-09-123-644-3
C 8	2204.6	28.2	12479	4	US-09-318-138-13
C 9	2204.6	28.2	12494	3	US-08-355-312-13
C 10	2204.6	28.2	12494	3	US-08-848-760B-33
C 11	2204	28.2	4883	4	US-09-608-730B-21
C 12	2204	28.2	7287	2	US-08-659-206A-1
C 13	2203.8	28.2	2961	3	US-08-446-935-6
C 14	2203.8	28.2	4145	3	US-08-451-472-62
C 15	2203.8	28.2	4145	3	US-08-358-928-62
C 16	2203.8	28.2	4277	3	US-08-651-472-63
C 17	2203.8	28.2	4277	3	US-08-358-928-63
C 18	2203.8	28.2	5356	3	US-08-446-935-1
C 19	2203.8	28.2	5352	3	US-08-651-472-72
C 20	2203.8	28.2	5352	3	US-08-358-928-72
C 21	2203.8	28.2	6811	3	US-08-651-472-67
C 22	2203.8	28.2	6811	3	US-08-358-928-67
C 23	2203.8	28.2	6926	3	US-08-651-472-69
C 24	2203.8	28.2	6926	3	US-08-358-928-69
C 25	2203.6	28.2	3699	3	US-08-646-538-6
C 26	2203.6	28.2	3699	3	US-08-503-222-6
C 27	2203.6	28.2	4965	3	US-08-675-566-22

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C 29	2203.6	28.2	6045	3	US-08-675-566-18	Sequence 18, Appl
C 30	2203.6	28.2	6196	3	US-08-675-566-5	Sequence 5, Appl
C 31	2203.6	28.2	6243	3	US-08-675-566-14	Sequence 14, Appl
C 32	2203.6	28.2	6244	3	US-08-675-566-17	Sequence 17, Appl
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C 34	2203.6	28.2	6503	3	US-08-675-566-6	Sequence 6, Appl
C 35	2203.6	28.2	6612	3	US-08-675-566-15	Sequence 15, Appl
C 36	2203.6	28.2	6958	3	US-08-675-566-2	Sequence 2, Appl
C 37	2203.6	28.2	6994	3	US-08-675-566-1	Sequence 1, Appl
C 38	2203.6	28.2	7001	3	US-08-675-566-3	Sequence 3, Appl
C 39	2203.6	28.2	7379	3	US-08-675-566-13	Sequence 13, Appl
C 40	2203.6	28.2	8618	3	US-08-675-566-21	Sequence 21, Appl
C 41	2203.6	28.2	8792	3	US-08-675-566-2	Sequence 25, Appl
C 42	2203.6	28.2	10281	2	US-08-816-155B-1	Sequence 1, Appl
C 43	2203.6	28.2	10281	3	US-09-079-587-1	Sequence 1, Appl
C 44	2201.6	28.1	7228	2	US-08-850-049-128	Sequence 128, App
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ALIGNMENTS

RESULT 1
US-09-845-917A-28/c
; Sequence 28, Application US/09845917A
; Patent No. 6653529
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/845,917A
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 10288
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8456)
; OTHER INFORMATION: "N is A, C, G, or T"
; OTHER INFORMATION: Description of Artificial Sequence: artificial
; OTHER INFORMATION: plasmid
US-09-845-917A-28

Query Match	57.4%;	Score	4492.6;	DB 4;	Length	10288;			
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Db	5531	CACAGGAGGTA	CTAGACTA	CTA	CCTTTTCATCTCCTCATATAAATAGACGCATATATAAGTAGCGCATTTT	5472
Qy	4078	AAGCATATAAAC	CAGCACTAT	GCGGTTCTTCTCATGTATATATATACAGGCAACACGCGAG	4137	
Db	5471	AAGCATATAAAC	CAGCACTAT	GCGGTTCTTCTCATGTATATATATACAGGCAACACGCGAG	5412	
Qy	4138	ATATAGGTGGA	CGAGTGAA	CGTAGCTGTATGTGCGCAGCTCGCGTTTGCATTTTCGGAAG	4197	
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Qy	4198	CGCTCGTTTTC	GGGAAACGCTTTG	AAGTTCCATATTCGGAAGTTCCTATCTCTAGAAAGTA	4257	
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Qy	4438	TCCACCTTTT	CGCTCCTTTGAACTT	GCATCTAAACCTCGACCTCTACATTTTTTATGTGTTTATC	4497	
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Qy	4858	TATCAAGAGAC	TGCAATATAGAGCG	CGCAAGAGGAAAAAAGTAATCTAAGATGCTTTG	4917	
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Qy	4978	TGTTTGTAAAA	TAGCGCTCTCGCGT	TGCAATTTCTGTGTTCTGTGTAATAAATGCAGCTCAGATT	5037	
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Qy	5098	TTCTTCGTTGGTAAATAATAGCGCTTTCCGGTTGCAATTTCTGTTCTGTGTAATAAATGCAGCTCA	51515
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Db	4331	CAGATGCTTCGTTCCAGTGGCACATTTTCCGGGAAATGTGCGGAAACCCCTATTTGTTTA	4272
Qy	5278	TTTTTCTAAATACATTCAAATATGATTCGGCTCATGAGACAAATACCCCTGATAAATGCTT	5337
Db	4271	TTTTTCTAAATACATTCAAATATGATTCGGCTCATGAGACAAATACCCCTGATAAATGCTT	4212
Qy	5338	CAATAATATTGAAAAAGGAAGATGATCAGATATTCAACATTTTCGGTTCGCGCTTTATTTCCC	5397
Db	4211	CAATAATATTGAAAAAGGAAGATGATGAGTATTTCACATTTTCGGTTCGCGCTTTATTTCCC	4152
Qy	5398	TTTTTTCGGGCATTTTCCCTTTCCTGTTTTCCTCACCAGAAAAAGCTTGGTGAAGTAAAA	5457
Db	4151	TTTTTTCGGGCATTTTCCCTTTCCTGTTTTCCTCACCAGAAAAAGCTTGGTGAAGTAAAA	4092
Qy	5458	GATGCTGAAGATCAGTTGGGTGCAAGATGGGTTTACATCGAACTGGATCTCAACAGCGGT	5517
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Qy	5698	GATGGCATGACGTAAGAGAAATTATGAGTGTGCTGCCATAACCATGAGTGATACACATGCG	5757
Db	3851	GATGGCATGACGTAAGAGAAATTATGAGTGTGCTGCCATAACCATGAGTGATACACATGCG	3792
Qy	5758	GCCAACTTACTTCTGACAAACGATCGGAGGACCGAAGAGCTTAACCGCTTTTTTGCACAAC	5817
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Qy	6178	AGACAGATCCGCTGAGATAGGTGCGCTCACTGATTAAGCATTTGGTAACTGTGCAGACCAAGTT	6237

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Db 3311 TACTCATATATATCTTTAGATGATTTAAACCTCATTTTAAATTTTAAAGGATCTAGGTG 3252
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Db 3251 AAGATCCCTTTTGTAAATCTCATGACCAAAATCCCTTAACGTGAGTTTCTGTTCCACTGA 3192
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Qy 6778 CTGAGCTATAGAAAGCGCCACGCTTCCGAAAGGAGGAGGACAGGATATCCGGTA 6837
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Db 2231 CTTCCGGCTCGTATGTTGTGTGGAAATTTGTGACGGATAACAAATTTACACAGGAACAGC 2172
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Db 2171 TATGACCATGATTACGCAAGCTTGCA 2145
RESULT 2
US-09-845-917A-27/c
; Sequence 27, Application US/09845917A
; Patent No. 6653529
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/845.917A
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 13414
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (11582)
; OTHER INFORMATION: "N is A, G, C or T"
; OTHER INFORMATION: Description of Artificial Sequence: artificial
; OTHER INFORMATION: plasmid
US-09-845-917A-27
Query Match 57.4%; Score 4492.6; DB 4; Length 13414;
Best Local Similarity 87.3%; Pred. No. 0;
Matches 5104; Conservative 0; Mismatches 629; Indels 114; Gaps 12;
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Db 10654 AGCATATCCCTTTTCCGCACTGCGCTAATAGCGAGAGCGCCGACCGCTTC 10595
Qy 1979 CCAACAGTTGCGCAGCCTGAATGGCGAATGGCGGACGCGCCCTGTGTAGCGGCGCAATAG 2038

Db	10594	CCAACAGTTTCGCAGAGCTGAATGGCGAAATGGCGCGACGCGCCCTGTAGCGCGCATTAAG	10533
Qy	2039	CGCGCGGGGTGTGGTGGTTACGCGACGCGTGACCGCTACACTTGCACGCGCCCTAGCGCC	2098
Db	10534	CGCGCGGGGTGTGGTGGTTACGCGACGCGTGACCGCTACACTTGCACGCGCCCTAGCGCC	10475
Qy	2099	CGCTCCCTTTCGCGTTCCTTCTCCCTTCTCTTTCGCGACGTTTCGCGCGCTTTCGCCGTCAAAGC	2158
Db	10474	CGCTCCCTTTCGCGTTCCTTCTCCCTTCTCTTTCGCGACGTTTCGCGCGCTTTCGCCGTCAAAGC	10415
Qy	2159	TCTAAATTCGGGGGCTCCCTTTATAGGGTTTCGATTTAGTGTCTTACGGCACTTCGACCCCAA	2218
Db	10414	TCFAAATTCGGGGGCTCCCTTTATAGGGTTTCGATTTAGTGTCTTACGGCACTTCGACCCCAA	10355
Qy	2219	AAAACTTGATTAGGGGTGATGGTTACGTAGTGGGCCATCGCCCTCATAGACGGTTTTCG	2278
Db	10354	AAAACTTGATTAGGGGTGATGGTTACGTAGTGGGCCATCGCCCTCATAGACGGTTTTCG	10295
Qy	2279	CCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGAGCATCTTGTTCCAAACCTGGAAACAAC	2338
Db	10294	CCCTTTGACGTTGGAGTCCACGTTCTTTAATAGTGAGCATCTTGTTCCAAACCTGGAAACAAC	10235
Qy	2339	ACTCAACCCATCTCCGTCTATCTTCTTTGATTTATAGGGATTTTCCCGATTTTCGGCCTA	2398
Db	10234	ACTCAACCCATCTCCGTCTATCTTCTTTGATTTATAGGGATTTTTCGGCCTATTCGGCCTA	10175
Qy	2399	TTGGTTAAAAAATGAGCTGATTTTAAACAAAAATTTAACGCGAAATTTTAAACAAATATTAAAC	2458
Db	10174	TTGGTTAAAAAATGAGCTGATTTTAAACAAAAATTTAACGCGAAATTTTAAACAAATATTAAAC	10115
Qy	2459	GTTTACAAATTCCTGATCGGGTATTTTCTCTTACGCACTCTGTGGGTATTTTACACCGC	2518
Db	10114	GTTTACAAATTCCTGATCGGGTATTTTCTCTTACGCACTCTGTGGGTATTTTACACCGC	10055
Qy	2519	ATAGGGTATAACTGATATAATTAATTTGAAGCTCTAATTTGTGAGTTTGTATATACATGC	2578
Db	10054	ATAGATCGGCAAGTCACAAACAATACTTAAATAAATACTACTCAGTAAATAACCTATTTC	9995
Qy	2579	ATTTACTTATAATACAGTTTATTTAGTTTGTGGCGCATCTTCTCAATATGCTTCCCA	2638
Db	9994	TTAGCATTTTGTAGCAAAATTTGCTATTTTGTAGTCTTTTACACCATTTGTCTCCACA	9935
Qy	2639	GCCTGCTTTTCTGTAAAGTTTACCCCTCTACCTCTAGCATCCCTTCCCTTTGCAAATAGTCC	2698
Db	9934	CTCCGCTTATACATCAAC-----ACCAATAACGC	9907
Qy	2699	TCTTCCAAATAATAATGTAGATCCTGTAGAGACCATCATCGCGTTCTATATCTG	2758
Db	9906	CATTTAATCTAAGCGCATCACCACAACTTTTCTGGGTCTAGTCCACGACGATACATAAAT	9847
Qy	2759	TTGACCCCAATGCGTCTCCCTTGTTCATCTAAACCCACACGGGTGTCTAATCAACCAATC	2818
Db	9846	GTAAGCTTTTCGGGGCTCTCTTGGCTT-----CCACCCAGTCAGAAATCGAGTTTCAATC	9792
Qy	2819	GTAACCTTCATCTCTTCCACCATGTCTCTTTGAGCAATAAAGCCGATAAACAAATCTTT	2878
Db	9791	CABAAGTTTACCTGTCTCCAC-----CTGCTTCTGAATCAACAAGGGAATAACGAATG	9738
Qy	2879	GTGCTCTTCGCAATGTCAACAGTACCTTAGTATATCTCAGTAGATATAGGAGCCCTT	2938
Db	9737	AGGTTTCTGTGAAGCTGCACTGAGTAGTATGTTCAGTCTTTTGGAAATACGAGTCTTTT	9678
Qy	2939	GCATGACAAATTCGTCTAAACATCAAAAGGCCTCTAGTTCCTTTGTTACTTCTTCGCGC	2998
Db	9677	-----AATAACTGGCAACCGAGGAACTCTGTGTATTTCTTGCACGACTCATCTCCA	9626
Qy	2999	CTGCTTCAAACTCAACATACTCGGGCCACCAACGCTGTGCAATTCGTAATGTCTGCG	3058
Db	9625	TGCAGT-----TGACGATATCAATGCGGTAAATCATTTGACGAGCGCAAAACATCTC	9573
Qy	3059	CCATTCCTGCTATTCTGTATACACCGCAGAGTACTGCAATTTTGACTGTATTACCAATGTC	3118

Db	9572	CTTAGGTTGATATAGGAACAACGCCAACCAAGTATTTTCGGAGTGCTCGAACTATTTTTTATA	9513
Qy	3119	AGCAAAATTTTCTGTCTTCGAGAGAGTAAAAAATTTGTACTTCGGCGATATATGCTTTTAGCGG	3178
Db	9512	TG-----CTTTTACAAGACTTGAAATTTTCTTTGCAATACCGGGTCAATTTGT	9465
Qy	3179	CTTAACGTGCGCCCTCCATGGAAGAAAATCAGTCAAGATATCCACATGTGTTTTTAGTAAACA	3238
Db	9464	TCTCTTTCTATTTGGGCACACATATAATACCAGCAAGTCAGCATCGGAATCTAG--AGCA	9407
Qy	3239	AAATTTTGGGACCTTAATGCTTTCAACTAACTCCAGTAATTTCTTGGTGTGAC-GAACATCCA	3297
Db	9406	CAATCTCGGGCTCTGTGCTCTCGAAGCCGCAAACTTTTCAACATGGACAGAACTACCT	9347
Qy	3298	ATGAAGCACACAAGTTTGTGTTTTTTCGTGTCATGATATTAATATAGCTTGGCAGCAACAG	3357
Db	9346	GTGAATTAATAACAGACATACTCCAAGCTGCCTTTTGTGTGCTTAATCACGTATACTCAC	9287
Qy	3358	GACTAGGAATGAGTAGAGACAGCTTCCATTATATGTAGCTTTTCGACATGATTTATCTTCGTT	3417
Db	9286	GTGCTCAATAGTCACCAATGCCCTCCCTCTTGGGCCCTCTCC-----TTTTCTTTT	9238
Qy	3418	TCCTGCAGGTTTTTGTCTGTGTCAGTTGGGTAAAGATACTGGGCAATTTTCATGTTCTTT	3477
Db	9237	TTTCGACCGAAATTAATTTCTTAATCGGCAGAAAAGAAAAGCTCCGGA-----T	9190
Qy	3478	CAACACTACATATGCGTATATATACCAATCTAAAGTCTGTGCTCTCTTCTGTTCTTCCT	3537
Db	9189	CAAGTTGTACGTAAGGTGACAAGCTATTTTTCAATAAGAAATATCTTCCACTACTGCCA	9130
Qy	3538	TCTGTTCCGAGATTACCGAATCAAAAAATTTTCAAGAAAACCGAAATCAAAAAAAGAAT	3597
Db	9129	TCTGGCGCTATAACTGCAGAAAGTACACATAATATTA-----CGATGCTGTCTATTAAAT	9078
Qy	3598	AAAAAAAATGATGAATTCGAATTTGAAAGCTGTGGTATGGTGCACTCTCAGTACATCT	3657
Db	9077	GCTTCTTATATATATATATATAGTAATGTGCTGTATCTATGGTGCACTCTCAGTACAACT	9018
Qy	3658	GCTCTGATCGGATAGTTAAGCGAGCGCCCGACACCCGCCAAACCCGCTGACGCGCCCT	3717
Db	9017	GCTCTGATCGGCATAGTTAAGCGAGCCCGACACCCGCCAAACCCGCTGACGCGCCCT	8958
Qy	3718	GAGGGCTTGTCTCTCCGGCATTCGGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCT	3777
Db	8957	GACGGCTTGTCTCTCCGGCATTCGGCTTACAGACAAGCTGTGACCGTCTCCGGGAGCT	8898
Qy	3778	GCATGTGTCAAGGTTTTTACCGTCAATCCGAAAACGGCGAGACGNAAGGGCTCTGTGA	3837
Db	8897	GCATGTGTCAAGGTTTTTACCGTCAATCCCGTCAATCCCGAAAACGGCGAGACGNAAGGGCTCTGTGA	8838
Qy	3838	TACGCCATTTTTTATAGTTAAATGTCAATGATATAATATGTTTCTTATGATGATCCAAATAT	3897
Db	8837	TACGCCATTTTTTATAGTTAAATGTCAATGATATAATATGTTTCTTATATGATCCAAATAT	8778
Qy	3898	CAAAAGGAATGATAGCAATTGAAGGATGAGACTAATCCAAATTGAGGAGTGGCAGCATATAG	3957
Db	8777	CAAAAGGAATGATAGCAATTGAAGGATGAGACTAATCCAAATTGAGGAGTGGCAGCATATAG	8718
Qy	3958	AACAGCTAAAGGGTAGTGTCTGAAGGAAGCATACGATACCCCGCATGGAATGGGATATATAT	4017
Db	8717	AACAGCTAAAGGGTAGTGTCTGAAGGAAGCATACGATACCCCGCATGGAATGGGATATATAT	8658
Qy	4018	CACAGGAGGTACTAGACTCTCTTTCATCCCTACATAAAATAGACGCATATAAGTACGCATTT	4077
Db	8657	CACAGGAGGTACTAGACTCTTTCATCCCTACATAAAATAGCGCATATAAGTACGCATTT	8598
Qy	4078	AAGCATAAACACGCATATATCGCGTTCTTCTCATGTATATATATATACAGGCAACACGCAG	4137
Db	8597	AAGCATAAACACGCACATATCGCGTTCTTCTCATGTATATATATATACAGGCAACACGCAG	8538
Qy	4138	ATATAGTGTGCACTGTGAACAGTAGTGAGCTGTATGTGCGCAGCTCGCGTTTGCATTTTCGAAG	4197
Db	8537	ATATAGTGTGCACTGTGAACAGTAGTGAGCTGTATGTGCGCAGCTCGCGTTTGCATTTTCGAAG	8478

Db 6317 GCGTCAGACCCGCTAGAAAAGATCAAGAGATCTTTTGAGATCCTTTTTCGCGGTA 6258
Qy 6418 ATCTGCTGCTTGCACAAACAAACACACCGCTACACGCGGTGTTTGTTCGCGGATCAA 6477
Db 6257 ATCTGCTGCTTGCACAAACAAACACACCGCTACACGCGGTGTTTGTTCGCGGATCAA 6198
Qy 6478 GAGCTACCAACTCTTTTTCGAAAGGTAATCTGGCTTCAGCAGAGCGAGATACCAATATCT 6537
Db 6197 GAGCTACCAACTCTTTTTCGAAAGGTAATCTGGCTTCAGCAGAGCGAGATACCAATATCT 6138
Qy 6538 GTCTTCTAGTGTAGCGGTAGTGTAGCCACCACTTCAAGAACTCTCTAGCAGCGCTACA 6597
Db 6137 GTCTTCTAGTGTAGCGGTAGTGTAGCCACCACTTCAAGAACTCTCTAGCAGCGCTACA 6078
Qy 6598 TACTCTGCTCTGTCTTAATCTCTGTACAGTGGCTGCTGCCAGTGGCGGATAGTGTCTT 6657
Db 6077 TACTCTGCTCTGTCTTAATCTCTGTACAGTGGCTGCTGCCAGTGGCGGATAGTGTCTT 6018
Qy 6658 ACCGGGTGGACTCAAGACGATAGTTACCGGATAAGCGCGAGCGGTGCGGCTGAACGGGG 6717
Db 6017 ACCGGGTGGACTCAAGACGATAGTTACCGGATAAGCGCGAGCGGTGCGGCTGAACGGGG 5958
Qy 6718 GGTTCGTGCACACAGCCAGCTTGGAGCGGAACGACCTACACCGAACTGAGATACCTACAG 6777
Db 5957 GGTTCGTGCACACAGCCAGCTTGGAGCGGAACGACCTACACCGAACTGAGATACCTACAG 5898
Qy 6778 CGTGAGCTATGAGAAAGCGCCAGCTTCCGAAAGGAGAAAGCGGACAGGTATCCGGTA 6837
Db 5897 CGTGAGCTATGAGAAAGCGCCAGCTTCCGAAAGGAGAAAGCGGACAGGTATCCGGTA 5838
Qy 6838 AGCGGAGGGTTCGAAACAGAGAGCGCACGAGGAGCTTCCAGGGGGAAACGCGCTGGTAT 6897
Db 5837 AGCGGAGGGTTCGAAACAGAGAGCGCACGAGGAGCTTCCAGGGGGAAACGCGCTGGTAT 5778
Qy 6898 CTTTATAGTCTGTGCGGTTTTCGACCTCTGACTTGGAGGTGATTTTGTGATGCTCG 6957
Db 5777 CTTTATAGTCTGTGCGGTTTTCGACCTCTGACTTGGAGGTGATTTTGTGATGCTCG 5718
Qy 6958 TCAGGGGGGGAGCCCTATGAAACAGCCAGCAACCGGCGCTTTTACGGTTTCTTGCGCC 7017
Db 5717 TCAGGGGGGGAGCCCTATGAAACAGCCAGCAACCGGCGCTTTTACGGTTTCTTGCGCC 5658
Qy 7018 TTTTGTGCGCTTTTGTCTACATGTTCTTTCTGCGTTATCCCTGATCTCTGTGATAAC 7077
Db 5657 TTTTGTGCGCTTTTGTCTACATGTTCTTTCTGCGTTATCCCTGATCTCTGTGATAAC 5598
Qy 7078 CGTATTACCGCTTTTGTAGTGTGATATACCGCTCGCGCGAGCGCAACCGAGCGGAGC 7137
Db 5597 CGTATTACCGCTTTTGTAGTGTGATATACCGCTCGCGCGAGCGCAACCGAGCGGAGC 5538
Qy 7138 GAGTCAGTGTAGCGGAGGAGGAGCGGCCCAATAGCAAAACCGCTCTCCCGCGCGCT 7197
Db 5537 GAGTCAGTGTAGCGGAGGAGGAGCGGCCCAATAGCAAAACCGCTCTCCCGCGCGCT 5478
Qy 7198 TGCGCGATTCATTAATGTCAGTGTGACGACGACAGGTTTCCGACTGGAAGCGGCGAGTGAG 7257
Db 5477 TGCGCGATTCATTAATGTCAGTGTGACGACGACAGGTTTCCGACTGGAAGCGGCGAGTGAG 5418
Qy 7258 CGCAACGCAATTAATGTGATGTACTCACTCAATTAGGCAACCGAGGTTTACATTTATG 7317
Db 5417 CGCAACGCAATTAATGTGATGTACTCACTCAATTAGGCAACCGAGGTTTACATTTATG 5358
Qy 7318 CTTCCGCTCCTATGTTGTGGAATTTGTGAGCGGATACCAATTTACACAGGAAACAGC 7377
Db 5357 CTTCCGCTCCTATGTTGTGGAATTTGTGAGCGGATACCAATTTACACAGGAAACAGC 5298
Qy 7378 TATGACCATGATTACGCCAAGCGGCA 7404
Db 5297 TATGACCATGATTACGCCAAGCTTGA 5271

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; Sequence 5, Application US/08801344
; Patent No. 6087140
; GENERAL INFORMATION:
; APPLICANT: Cameron, Douglas C.
; APPLICANT: Shaw, Anita J.
; APPLICANT: Altaras, Nedim E.
; TITLE OF INVENTION: MICROBIAL PRODUCTION OF 1,2-PROPANEDIOL
; TITLE OF INVENTION: FROM SUGAR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Dewitt Ross & Stevens S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: WI
; COUNTRY: U.S.A.
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/801,344
; FILING DATE:
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REFERENCE/DOCKET NUMBER: 09820.037
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-831-2100
; TELEFAX: 608-831-2106
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5181 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHEetical: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Yeast shuttle vector YEp352
; US-08-801-344-5

Query Match 39.1%; Score 3057.4; DB 3; Length 5181;
Best Local Similarity 78.3%; Pred. No. 0;
Matches 3890; Conservative 0; Mismatches 996; Indels 85; Gaps 15;

Qy 2470 CCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATTTTCACCGCATAGGTAATA 2529
Db 234 CCTGATGCGGTATTTTCTCCTTACGCATCTGTGCGGTATTTTCACCGCATAGGTAATA 293
Qy 2530 ACTGATATAATTAATAATGAAGCTCTAATTTGTGAGTTAGTATACATGCTTTACTTATA 2589
Db 294 ACTGATATAATTAATAATGAAGCTCTAATTTGTGAGTTAGTATACATGCTTTACTTATA 353
Qy 2590 ATACAGTTTTTGTAGTTTGTCTGCGCGCATCTTCTCAAAATATGCTTCCACGCTGCTTTTC 2649
Db 354 ATACAGTTTTTGTAGTTTGTCTGCGCGCATCTTCTCAAAATATGCTTCCACGCTGCTTTTC 413
Qy 2650 TGTAAAGTTTCAACCTCTACCTTAGCATCCCTTCCCTTTGCAAAATAGTCTCTTTCCAA 2709
Db 414 TGTAAAGTTTCAACCTCTACCTTAGCATCCCTTCCCTTTGCAAAATAGTCTCTTTCCAA 473
Qy 2710 TAATAATGTGATGCTGTAGACACATCATCCAGGTTCTATCTACTGTGACCGAATG 2769
Db 474 TAATAATGTGATGCTGTAGACACATCATCCAGGTTCTATCTACTGTGACCGAATG 533
Qy 2770 GGTCTCCCTTGTCTATCTAACCACACCGGCTGTCAATCAACCAATCGTAACCTTCAT 2829
Db 534 GGTCTCCCTTGTCTATCTAACCACACCGGCTGTCAATCAACCAATCGTAACCTTCAT 593

QY	2830	CTCTTCCACCCATGCTCTTTGAGCAATTAAGCCGATTAACAAAATCTTTGTGCTCTTCG	2889	Db	1669	TTTTTCAAAACAAAGATCTGAGCTGCATTTTTTACAGAACAGAAATGCAACGCAAGGCG	1728
Db	594	CTCTTCCACCCATGCTCTTTGAGCAATTAAGCCGATTAACAAAATCTTTGTGCTCTTCG	653	QY	3948	CAGCATATGACAGCTTAAGGGTAGTGCTCAAGGAAGCATACGATACCCCGCATGGGAT	4007
QY	2890	CAATGTCAACAGTACCCCTTAGTATATCTCCAGTAGATAGGAGCCCTTGGCATGCAAT	2949	Db	1729	TATTTTACCACGAAGATCTGTGCTTCATTTTTGTAAACAAAAATGCAACGCGAGAGC	1788
Db	654	CAATGTCAACAGTACCCCTTAGTATATCTCCAGTAGATAGGAGCCCTTGGCATGCAAT	713	QY	4008	GGGATATATACACAGGAGTACTAGA-CTACTCTTTCATCTTACATATAATAGACGCATATA	4066
QY	2950	CTGCTTAACATCAAAAGGCTCTAGTCTCTTTGTTTCTTCTTCTGCGCCCTGCTTCAAC	3009	Db	1789	GCTAATTTTTCAACAAGAAATCTGAGCTGCATTTTTTACAGAACAGAAATGCAACGCGAG	1848
Db	714	CTGCTTAACATCAAAAGGCTCTAGTCTCTTTGTTTCTTCTTCTGCGCCCTGCTTCAAC	773	QY	4067	AGTACGCATTTAAGCATPAACACGACTATGCGCTTCTTCTCATGTATATATATACAG	4126
QY	3010	CGCTAACATCTCGGCGCCACACACGCTGTGCAATCGTAAATGTCTGCCCATCTGCTA	3069	Db	1849	AGCGCTATTTTCCAAACAAAGATCTATCTCTTTTTTGTCTACAAAATGCAATCCG	1908
Db	774	CGCTAACATCTCGGCGCCACACACGCTGTGCAATCGTAAATGTCTGCCCATCTGCTA	833	QY	4127	GCAACAG-----CAGATATAGTGTGCGAGTGAACAGTGTGTATGTGCGAGCTCG	4180
QY	3070	TTCTGTATACACCCGAGAGTACTGCAATTTGACTGTATTAACCAATGTACGCAAAATTTT	3129	Db	1909	AGAGCGCTATTTTTCTAACAAGCATCTTAGATTACTTTTTTCTCTCTTGTGCGCTCTA	1968
Db	834	TTCTGTATACACCCGAGAGTACTGCAATTTGACTGTATTAACCAATGTACGCAAAATTTT	893	QY	4181	CGTTGCAATTTTCGAAGCGCTCGTT-----TTCGAAACGCTTTGAAGTTCTCTAT	4230
QY	3130	TCGTCTTCAAGAGTAAAAATTTGACTTTGGCGGATTAATGCCCTTTAGCGGCTTAACTGTC	3189	Db	1969	TAAATGCACTCTCTTGATACTTTTTTGGCAGCTGTAGTCTGTTAAGTTAGAGAGGCTTAC	2028
Db	894	TGCTCTTCAAGAGTAAAAATTTGACTTTGGCGGATTAATGCCCTTTAGCGGCTTAACTGTC	953	QY	4231	TCGGAAGTTCTATTTCT-----AGAAAGTATAGGAATCTTCAGAGCGCTTTGAAAC	4284
QY	3190	CCTCCATGGAAAAATCAGTCAAGATATCCACATGTGTTTTTTAGTAAACAAATTTTGGAC	3249	Db	2029	TTTGGTGTCTATTTCTCTTCCATAAAAGCGCTGACTCCACTTCCGCGCTTACTGAT	2088
Db	954	CCTCCATGGAAAAATCAGTCAAGATATCCACATGTGTTTTTTAGTAAACAAATTTTGGAC	1013	QY	4285	CAAAAGCGC-TCTGAAGACGCACTTTCAAAAACCAAAACGCAACGCGACTGTACGAGC	4343
QY	3250	CTAATGCTTCAACTCACTCCAGTAAATCTCTTGGTGGTAGGAACATCCAAATGAAGCACACA	3309	Db	2089	TACTAGCGAGCTGCGGGTGCAATTTTTTCAAGATAAAGGCAATCCCGAATTAATTTCTATA	2148
Db	1014	CTAATGCTTCAACTCACTCCAGTAAATCTCTTGGTGGTAGGAACATCCAAATGAAGCACACA	1073	QY	4344	TACTAAATATTTGCAATACCGCTTCCACAAACATTTGCTCAAAAGTATCTCTTTCTCTATA	4403
QY	3310	AGTTTGTGCTTTTCTGTCATGATATTAATAATAGCTTGGCAGCAACAGGACTAGGATGAG	3369	Db	2149	CCGATGTGATTTGGCATACTTTGTGAACAGAAAGTGTAGCGTTGATGATCTTC-----	2204
Db	1074	AGTTTGTGCTTTTCTGTCATGATATTAATAATAGCTTGGCAGCAACAGGACTAGGATGAG	1133	QY	4404	TATCTCTGTCTATATCCCTATATAACCTTACCCTCCACCTTTTCGCTCCTTGAACCTTGA	4463
QY	3370	TAGCAGCAGCTTCTCTTATATGTAGCTTTTCGACATGATTTATCTTCGTTTCTCGCAGGTTT	3429	Db	2205	-ATTGGTCAGAAAAATATGAACGGTTTCTTCTATTTTGTCTCTATATACGATATAGGA	2263
Db	1134	TAGCAGCAGCTTCTCTTATATGTAGCTTTTCGACATGATTTATCTTCGTTTTC-----	1188	QY	4464	TCCTAACTCCACCTCTACATTTTTTATGTTTATCTCTAGTATTACTCTTTAGACAAAAA	4523
QY	3430	TTGTTCTGTGCGATTTGGTTTAAAGATATCTGGGCAATTTTCATGTTTCTTCAACACTACATA	3489	Db	2264	AATGTTTACATTTTCGTTATTTGTTTTCGATTCACCTCTATGAATAGTCTTCTTACTACA	2323
Db	1189	TTGTTCTGTGCGATTTGGTTTAAAGATATCTGGGCAATTTTCATGTTTCTTCAACACTACATA	1248	QY	4524	ATTGTAGTAAAGAACTATTCTATAGTGAATCGAAAAACAATACGAAAAATGTAACAAATTC	4583
QY	3490	TCGCTATATATACCAATCTAAGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	3549	Db	2324	TTTGTCTAAAGAGTAACTACTAGAGATAACAATAAAATGTAGAGTGTAGTTAGATGC	2383
Db	1249	TCGCTATATATACCAATCTAAGTCTGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT	1308	QY	4584	TATACGTAGTATATAGAGACAAATAGAGAAACCGTTTCTATAATTTTCTGACCAAT----	4639
QY	3550	TTACCGAATCAAAAAATTTTCAAGAAACCGAAATCAAAAAAGAAATAAAAAAAATG	3609	Db	2384	AAGTTCAAGGAGCGAAAGTGGATGGTATATAGGATATAGCACAGAGATATAT	2443
Db	1309	TTACCGAATCAAAAAATTTTCAAGAAACCGAAATCAAAAAAGAAATAAAAAAAATG	1368	QY	4640	-GAGATCATCAACGCTATCACTTTCTGTTCAAAAGTATGCGCAATCCACATCGGTAT	4698
QY	3610	ATGAATGAATTTGAAGCTGTGTATGGTGCATCT-----CAGTCAATCT	3657	Db	2444	AGCAAGAGATATCTTTTGAAGAGCGGTATTTGGAAGCGGTATTTAGTAGCT	2503
Db	1369	ATGAATGAATTTGAAGCTGTGTATGGTGCATCT-----CAGTCAATCT	1428	QY	4699	AGAATAAATCGGGGATCGCTTTTATCTTGAATAATGCACCGCGCTTCGCTAGTAATC	4758
QY	3658	GCTCTGATGCGCATAGTTTAAAGCAGCCCGACACCCGCAACCGCTGACGCGCT	3717	Db	2504	CGTTACAGTCCGGTGGCTTTTGGTTTTTGAAGTGGTCTTCAG---AGGCTTTTGG	2560
Db	1429	TCCCTGAAACAGATAGTATATTTGAACTGTATTAATAATATAGTCTAGCGCTTTACGG	1488	QY	4759	AGTAAACGCGGAGTGGAGTCAAGCTTTTTTTTATGGAAGAGAAATAGACACCAAGTA	4818
QY	3718	GACGGGCTTGTCTGCCCGCATCCGCTTACAGCAAGCTGTGACCGCTCTCCGGGAGCT	3777	Db	2561	TTTTTCAAAAGCGCTCTGAAGTCCCTATCTTCTAGCTAGAGAAATAGGAACTTCGGAATA	2620
Db	1489	AAGACAATGTATGTTATTTCCGGTTCTCGAGAAACTTATGCAATCTATTGCAATGTAATCT	1548	QY	4819	GCCTTCTCTTAACTTAAACGCACTACAGTGTCAAAAGTATCAAGAGACTGCAATATAG	4878
QY	3778	-----GCATGTGTAGAGTTTTCACGTCATCACC--GAAACGGGCGAGACGAAG	3827	Db	2621	GGAACTTCAAGCGTTTCCGAA-----AACGAGCGCTTCGAAAAATGCAACGCGA	2670
Db	1549	TGCAGCTGCACTCCCGGTTCAATTTCTCGCTTTCCATCTTTCGACTTCAATAGCATATCT	1608	QY	4879	AGCGCAAAAGGAGAAAAAAGTAATCTAAGATCGCTTTTGTAGAAAAATAGCGCTCTCGG	4938
QY	3828	GGCCTCGTGTATAGGCTATTTTTTATAGGTAAATGTCAATGATAAATAGTTTCTTAGTAT	3887	Db	2671	GCTGGGCACATACAGCTCACTGTTTCACTGCGACCTATATCTGCGTGTGCTGTATATA	2730
Db	1609	TTGTTAAGCAAGCATCTGTGCTTCAATTTTGTAGAACAAATGCAACGCGAGCGCTAA	1668	QY	4939	GATGCAATTTTGTAGAACAAAAAGAGTATAGATTTCTTTGTTGGTAAAAATAGCGCTCTC	4998
QY	3888	GATCAATATCAAGGAATGATAGCATTTGAAGGATGAGACTAATCCAATTTAGGAGTGG	3947				

Db 2731 TATATACATGAGAAAGCGCATAGTCGGTGTATTATGCTTTAAATGCGTTATGCTGCACTC 2790
Qy 4999 GCGTTCGATT-----TCGTGTTCTGTAAATAATGCACTCAGATTCTTTGTTTGAATAATAG 5054
Db 2791 TCAGTACAACTGCTCTGTCGCGCATAGTTAAGCCAGCCCGACACCCCG 2850
Qy 5055 CGCTCTCGCGTTGCAATTTTGTGTTTACAAAATGAAGCACAGATTCTTGGTTGGTAAAT 5114
Db 2851 CTGACGCGCCCTGACGCGCTGTGCTGCCCGCATCCGCTTACAGACAAGCTGTGACCG 2910
Qy 5115 AGCGCTTTCGCGTTGCAATTTCTGTCTGTAAAAATGCAGCTCAGATTCTTTGTTGAAAA 5174
Db 2911 TCTCCGGAGCTGCAATGTGCAGAGTTTTCACCGTCATCACCGAAAGCGCGAGAGAA 2970
Qy 5175 ATTAGCGCTCTCGGTTGCAATTTTGTGTTCTACAAAATGAAGCACAGATGCTT-----C 5227
Db 2971 AGGCGCTCGTGATAGCGCTATTTTATAGTTAATGTGATGATAAATGCTTCTTAGA 3030
Qy 5228 GTTCAGGTGCACTTTTCGGGGAATGTGCGGGAACCCCTATTTGTTTATTTTCTTAA 5287
Db 3031 CGTCAGGTGCACTTTTCGGGGAATGTGCGGGAACCCCTATTTGTTTATTTTCTTAA 3090
Qy 5288 TACAATCAAAATATGATTCGCTCATAGACATAAACCCTGATAAATGCTTCAATAATATT 5347
Db 3091 TACAATCAAAATATGATTCGCTCATAGACATAAACCCTGATAAATGCTTCAATAATATT 3150
Qy 5348 GAAAAAGGAAGATGATGAGTATTCAACATTTCCGTTGCGCCCTATTCCCTTTTTCGGG 5407
Db 3151 GAAAAAGGAAGATGATGAGTATTCAACATTTCCGTTGCGCCCTATTCCCTTTTTCGGG 3210
Qy 5408 CATTTGCTTCTGTTTTCGCTACCCAGAAACGCTGTGTGAAGTAAAGATGCTGAAG 5467
Db 3211 CATTTGCTTCTGTTTTCGCTACCCAGAAACGCTGTGTGAAGTAAAGATGCTGAAG 3270
Qy 5468 ATCAGTTGGTGCACGAGTGGTTACATCGAATCGGATCTCAACAGCGGTAAAGATCCTTG 5527
Db 3271 ATCAGTTGGTGCACGAGTGGTTACATCGAATCGGATCTCAACAGCGGTAAAGATCCTTG 3330
Qy 5528 AGAGTTTTCGCCCCGAAAGACGTTTTCATATGATGAGCACTTTTAAAGTTCTCTATGTG 5587
Db 3331 AGAGTTTTCGCCCCGAAAGACGTTTTCATATGATGAGCACTTTTAAAGTTCTCTATGTG 3390
Qy 5588 GCGCGTATTTATCCGTTATTGACCGCGGCAAGCAATCTCGGTCCGCGCATACATTT 5647
Db 3391 GCGCGGTATTTATCCGTTATTGACCGCGGCAAGCAATCTCGGTCCGCGCATACATTT 3450
Qy 5648 CTGAGATGACTTGGTTGAGTACTCACAGTCTCAGAAAGCATCTTACGGATGGCATGA 5707
Db 3451 CTGAGATGACTTGGTTGAGTACTCACAGTCTCAGAAAGCATCTTACGGATGGCATGA 3510
Qy 5708 CAGTAAGAGAAATATGCAGTGCTGCCATAACCATGATGATACACTGCGGCCAACTTAC 5767
Db 3511 CAGTAAGAGAAATATGCAGTGCTGCCATAACCATGATGATACACTGCGGCCAACTTAC 3570
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Qy 5828 ATGTAATCGCTTGTATCGTTGGGAACCGAGCTGTAATGAAGCATACCAAGCAGGAGC 5887
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Qy 6008 GACCACTTTCGCGTCCGCTTCCGCTGGCTGGTTTATGCTGATAAATCTGGAGCGG 6067
Db 3811 GACCACTTTCGCGTCCGCTTCCGCTGGCTGGTTTATGCTGATAAATCTGGAGCGG 3870

Qy 6068 GTGAGCGTGGGTCTCCGCGTATCATTTGCAGCACTCGGGGCAGATGTAAGCCCTCCCGTA 6127
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Qy 6128 TCGTAGTTATCTACAGAGCGGGAGTCAGGCACTATGATGAACGAAATAGACAGATCG 6187
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Qy 6188 CTGAGATAGTGTCTCACTGATTAAGCAATGGTAACTGTGAGACCAAGTTTACTCATATA 6247
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Qy 6308 TTGATTAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCCTCACTGAGCGTCAGACC 6367
Db 4111 TTGATTAATCTCATGACCAAAATCCCTTAACGTGAGTTTTCCTCACTGAGCGTCAGACC 4170
Qy 6368 CCGTAGAAAAGATCAAAAGGATCTTCTTGAGATCCTTTTCTGCGCTAAATCTGTGCT 6427
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Db 4291 CTCCTTTTCGAAAGTAACTGCGCTTACAGAGCGGAGATACCAAAATCTGCTCTCTAG 4350
Qy 6548 TGTAGCGGTAGTTAGCGCAACCACTTCAAGAACTCTGTAGCAGCGCTTACACTCTGCTC 6607
Db 4351 TGTAGCGGTAGTTAGCGCAACCACTTCAAGAACTCTGTAGCAGCGCTTACACTCTGCTC 4410
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Db 4411 TGTAAATCTGTTTACAGTGGCTGTGCTGCGAGTGGCGATAGTCTGTTTACCGGTTGG 4470
Qy 6668 ACTCAAGACGATAGTTTACCGGATAGCGGATAGCGGCTGCGGCTGAAACGGGGGTTCTGCA 6727
Db 4471 ACTCAAGACGATAGTTTACCGGATAGCGGATAGCGGCTGCGGCTGAAACGGGGGTTCTGCA 4530
Qy 6728 CACAGCCAGCTTGGAGCGAAACGACCTTACACCGAACTGAGATACCTTACAGCGTGAGCTAT 6787
Db 4531 CACAGCCAGCTTGGAGCGAAACGACCTTACACCGAACTGAGATACCTTACAGCGTGAGCTAT 4590
Qy 6788 GAGAAAGCCCAACGCTTCCGAAAGGAGAAAGCGGACAGGTTATCCGTTAAGCGGAGGG 6847
Db 4591 GAGAAAGCCCAACGCTTCCGAAAGGAGAAAGCGGACAGGTTATCCGTTAAGCGGAGGG 4650
Qy 6848 TCGGAAACAGAGAGCGGACAGGAGCTTCCAGGGGAAACGCGCTGTTATCTTTTATGTC 6907
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Qy 6968 GGAGCCTATGGAAAAACGCGCAGCAACCGCGCTTTTACGGTTCTTGGCCTTTTGTGTCG 7027
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Qy 7028 CTTTTCCTCAGATGTTTCTTTCCTGCGTTATCCCTGATTTCTGTGGATTAACCGTATTACCG 7087
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Qy 7088 CTTTTCAGTGTAGTATACCGCTCGCGCAGCGCAACGAGCCGAGCGAGGTCAGTGA 7147
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QY 7148 GCGAGGAGCGGAGCGCCCAATACGAAACCGCTCTCCCGCGGTTGGCGGATTC 7207
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QY 7208 ATTAATGAGCTGGCAGCAGAGTTTCCGACTGGAAGCGGCGAGTGAGCGCAACGCA 7267
Db 5011 ATTAATCCAGCTGGCAGCAGAGTTTCCGACTGGAAGCGGCGAGTGAGCGCAACGCA 5070
QY 7268 TTAATGTGAGTTACCTCACTCATTAGGCACCCAGGCTTTTACACTTTATGTCTCCGGCTC 7327
Db 5071 TTAATGTGAGTTACCTCACTCATTAGGCACCCAGGCTTTTACACTTTATGTCTCCGGCTC 5130
QY 7328 CTATGTGTGGAAATGTGAGCGGATAACAATTTTCAACAGGAAACAGCT 7378
Db 5131 GTATGTGTGGAAATGTGAGCGGATAACAATTTTCAACAGGAAACAGCT 5181

RESULT 4

US-09-498-599-5
; Sequence 5, Application US/09498599
; Patent No. 6303352
; GENERAL INFORMATION:
; APPLICANT: Cameron, Douglas C.
; APPLICANT: Shaw, Anita J.
; APPLICANT: Altaras, Nedim E.
; TITLE OF INVENTION: MICROBIAL PRODUCTION OF
; TITLE OF INVENTION: 1,2-PROPANEDIOL FROM SUGAR
; NUMBER OF SEQUENCES: 11
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: DeWitt Ross & Stevens S.C.
; STREET: 8000 Excelsior Drive, Suite 401
; CITY: Madison
; STATE: WI
; COUNTRY: U.S.A.
; ZIP: 53717-1914
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/498,599
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Sara, Charles S.
; REFERENCE/DOCKET NUMBER: 09820.037
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 608-831-2100
; TELEFAX: 608-831-2106
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5181 base pairs
; TYPE: nucleic acid
; TOPOLOGY: circular
; STRANDEDNESS: single
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; ORIGINAL SOURCE:
; ORGANISM: Yeast shuttle vector YEp352

US-09-498-599-5
Query Match 39.1%; Score 3057.4; DB 4; Length 5181;
Best Local Similarity 78.3%; Pred. No. 0;
Matches 3890; Conservative 0; Mismatches 996; Indels 85; Gaps 15;
QY 2470 CCTGATGCGGTATTTCTCTTACGATCTGCGGTATTTTACACCGCATAGGTAATA 2529
Db 234 CCTGATGCGGTATTTCTCTTACGATCTGCGGTATTTTACACCGCATAGGTAATA 293
QY 2530 ACTGATATAATTAATTAAGCTCTPAATTTGTGAGTTTGTAGTATACATGCAATTATTA 2589

Db 294 ACTGATATAATTAATTAAGCTCTPAATTTGTGAGTTTGTAGTATACATGCAATTATTA 353
QY 2590 ATACAGTTTTTTAGTTTTGTGCGCGCATCTTCTCAAAATATGCTTCCAGCGCTGTTTC 2649
Db 354 ATACAGTTTTTTAGTTTTGTGCGCGCATCTTCTCAAAATATGCTTCCAGCGCTGTTTC 413
QY 2650 TGTAAAGCTTCAACCTCTACCTTAGCATCCCTTCCCTTTGCAAAATAGTCTCTCTTCCAA 2709
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QY 2710 TAATAATGTAGATCTCTGTAGAGCAGCATCATCCAGGTTCTATATCTGTTGACCCCAATG 2769
Db 474 TAATAATGTAGATCTCTGTAGAGCAGCATCATCCAGGTTCTATATCTGTTGACCCCAATG 533
QY 2770 CGTCTCCCTTGTCAATCTAAACCCACACCGGCTGTCAATCAACCAATCTGTACCTTCAAT 2829
Db 534 CGTCTCCCTTGTCAATCTAAACCCACACCGGCTGTCAATCAACCAATCTGTACCTTCAAT 593
QY 2830 CTCTTCCACCCATGTCTCTTTTGAGCAATAAAGCCGATAACAAAATCTTTTGTGCTCTTCG 2889
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QY 3010 CGCTAAACAATACCTTGGGCCCCACACACCGTGTGCAATTCGTAAATGTCTGCCCATTTCTGCTA 3069
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Qy 5828 ATGTAACCTCGCTTATCGTTGGGAAACCGGAGCTGAATGAAGCCATACCAACACGAGC 5887
Db 3631 ATGTAACCTCGCTTATCGTTGGGAAACCGGAGCTGAATGAAGCCATACCAACACGAGC 3690
Qy 5888 GTGACACCAAGTCTGTAGCAATGGCAACACAGTTTGGCAAACTATTAACTGGCGAAC 5947
Db 3691 GTGACACCAAGTCTGTAGCAATGGCAACACAGTTTGGCGCAAACTATTAACTGGCGAAC 3750
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Db 3811 GACCACTTCTGGCTCGGCTTCCGGCTGCTGCTGTTTATTGCTGATAAATCTGAGCGG 3870
Qy 6068 GTGAGCGTGGGTCTCGCGGTATCATTTGACGACCTGGGCGCAGATGGTAAGCCCTCCGTA 6127
Db 3871 GTGAGCGTGGGTCTCGCGGTATCATTTGACGACCTGGGCGCAGATGGTAAGCCCTCCGTA 3930
Qy 6128 TCGTAGTTATCTACAGAGCGGAGTCAGGCAACTATGAGATGAACGAAATAGACAGATCG 6187
Db 3931 TCGTAGTTATCTACAGAGCGGAGTCAGGCAACTATGAGATGAACGAAATAGACAGATCG 3990
Qy 6188 CTGAGATAGTGCCTCACTGATTAGCAATGCTAGTCAAGCAAGTTTACTCATATA 6247
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Qy 6308 TTGATAATCTCANGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACC 6367
Db 4111 TTGATAATCTCANGACCAAAATCCCTTAACGTGAGTTTTCGTTCCACTGAGCGTCAGACC 4170
Qy 6368 CGGTAGAAAGATCAAGGATCTCTTCAGATCCCTTTTCTCGGCTAATCTGCTGCT 6427
Db 4171 CGGTAGAAAGATCAAGGATCTCTTCAGATCCCTTTTCTCGGCTAATCTGCTGCT 4230
Qy 6428 TCGAAACAAAAAACACCGCTTACCAGCGGTGTTGTTGTTCCCGGATCAAGAGCTACCAA 6487
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Db 4291 CTCCTTTTCCGAAGGTAACTGCTTACAGAGCGGAGATACCAAAATCTGCTTCTAG 4350
Qy 6548 TGTAGCGGTAGTTAGGCGACCACTTCAGAACTCTGTAGCACCGCTTACATACCTCGCTC 6607
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Qy 6608 TCGTAATCTGTTACAGTGGCTGCTGCGAGTGGCGATAAGTCTTACCGGGTTGG 6667
Db 4411 TCGTAATCTGTTACAGTGGCTGCTGCGAGTGGCGATAAGTCTTACCGGGTTGG 4470
Qy 6668 ACTCAAGCAGATAGTTACCGGATAAGCGAGCGGTGCGGCTGAAACCGGGGGTTGTCGA 6727
Db 4471 ACTCAAGCAGATAGTTACCGGATAAGCGAGCGGTGCGGCTGAAACCGGGGGTTGTCGA 4530
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Db 4531 CACAGCCAGCTTGAGGCGAGCTTACCGAGCTGAGATACCTACAGCGTGGCTAT 4590
Qy 6788 GAGAAAGCGCCAGCTTCCGAAAGGAGAAAGCGGACAGGTATCCGTTAAGCGCGAGG 6847
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Qy 6848 TCGGAACAGGAGCGCAGAGGAGCTTCCAGGGGAAAACCGCTTGGTATCTTTATAGTC 6907

Db 4651 TCGGAACAGGAGCGCAGAGGAGCTTCCAGGGGAAACCGCTGGTATCTTTATAGTC 4710
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Db 4771 GGAGCCTATGGAATAAGCGCAGCAACCGCGCTTTTACGTTTCTGCGCTTTTCTGCTGC 4830
Qy 7028 CTTTGTCTACATGTTCTTTCTGCTGCTATCCCTGATTTCTGTGATAACCGTATTACCG 7087
Db 4831 CTTTGTCTACATGTTCTTTCTGCTGCTATCCCTGATTTCTGTGATAACCGTATTACCG 4890
Qy 7088 CTTTGTGAGTGTATACCGCTCGCGCAGCCGAAACCGAGCGCAGCGAGTCAAGTGA 7147
Db 4891 CTTTGTGAGTGTATACCGCTCGCGCAGCCGAAACCGAGCGCAGCGAGTCAAGTGA 4950
Qy 7148 GCGAGGAAGCGGAAGAGCGCCCAATACGAAACCGCTCTCCCGCGGCTTGGCCGATTC 7207
Db 4951 GCGAGGAAGCGGAAGAGCGCCCAATACGAAACCGCTCTCCCGCGGCTTGGCCGATTC 5010
Qy 7208 ATTAATGACGCTGCGCAGCAGGTTTCCCGACTCGMAAGCGGCGAGTCAAGCGCAA 7267
Db 5011 ATTAATGACGCTGCGCAGCAGGTTTCCCGACTCGMAAGCGGCGAGTCAAGCGCAA 5070
Qy 7268 TTAATGTGAGTTACTCACTCACTTAGGCAACCGGAGCTTTTACATTTATGCTTCCGGCTC 7327
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Qy 7328 CTATGTTGTGGAATTTGTAGCGGATAACAATTTTACAGGAAACAGCT 7378
Db 5131 GTATGTTGTGGAATTTGTAGCGGATAACAATTTTACAGGAAACAGCT 5181

RESULT 5
US-09-367-891A-6/c
; Sequence 6, Application US/09367891A
; Patent No. 6524816
; GENERAL INFORMATION:
; APPLICANT: RASMUSSEN, PREBEN
; TITLE OF INVENTION: EXPRESSION ELEMENT
; FILE REFERENCE: 078883/0111
; CURRENT APPLICATION NUMBER: US/09/367,891A
; CURRENT FILING DATE: 1999-12-03
; PRIOR APPLICATION NUMBER: PCT/IB98/00312
; PRIOR FILING DATE: 1998-03-02
; NUMBER OF SEQ ID NOS: 23
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 6
; LENGTH: 7432
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic
; OTHER INFORMATION: pPR70 plasmid
US-09-367-891A-6

Query Match 28.2%; Score 2207.2; DB 4; Length 7432;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2209; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

Qy 5229 TTCAAGTGGCACTTTTCGGGAAATGTGCGGAAACCGCTATTTGTTTATTTTCTAAAT 5288
Db 2247 TTAGGTGGCACTTTTCGGGAAATGTGCGGAAACCGCTATTTGTTTATTTCTAAAT 2188
Qy 5289 ACATTCAATATGATCGCTCATGAGCAATAACCTGATAAATGCTTCAATATATTG 5348
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Db 2127 AAAAAGAGATGATGATTTCAACATTTCCGTTGCGCCCTTATCCCTTTTTCGCGC 2068

QY 5409 ATTTTGGCTTCTGTTTCTGCTCACCAGAAACGCTGGTGAAAGTAAAGATGCTGGAAGA 5468
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QY 5469 TCAGTTGGGTGACAGAGTGGTTTACATCGAATCGGATCTCAACAGCGGTAAAGATCTCTGA 5528
DB 2007 TCAGTTGGGTGACAGAGTGGTTTACATCGAATCGGATCTCAACAGCGGTAAAGATCTCTGA 1948
QY 5529 GAGTTTTCGCCCCGAAAGAGTGGTTTCCAAATGATGAGCAGCTTTTAAAGTGTCTGCTATGTGG 5588
DB 1947 GAGTTTTCGCCCCGAAAGAGTGGTTTCCAAATGATGAGCAGCTTTTAAAGTGTCTGCTATGTGG 1888
QY 5589 CGCGGTATTTATCCCGTATTGAACGCGGGGCAAGAGCAACTCGGTGCGGCAATACACTATTTC 5648
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QY 5709 AGTAAGAGAAATATGCAAGTCTGCCATTAACCATGAGTGATAACACTGCGGCCAACTTACT 5768
DB 1767 AGTAAGAGAAATATGCAAGTCTGCCATTAACCATGAGTGATAACACTGCGGCCAACTTACT 1708
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DB 1527 ACTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGGATGGAGCGGATAAAGTTTCAGG 1468
QY 6009 ACCACTTCTCGCTCGGCTCCGCTCGCTGCTGTTTATGCTGATTAATCTGAGCCGG 6068
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QY 6069 TGAGCGTGGTCTCGCGGTATCAATGAGCACTGGGCGCAGATGGTAAAGCCCTCCCGTAT 6128
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QY 6129 CGTAGTTATCTACACGCGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCGC 6188
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QY 6249 ACTTTAGATTGATTAAACCTTCAATTTTAAAGATCTAGTGAAGATCTCTTTT 6308
DB 1227 ACTTTAGATTGATTAAACCTTCAATTTTAAAGATCTAGTGAAGATCTCTTTT 1168
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QY 6369 CGTAGAAGATCAAGAGTATCTTCTGAGATCTTTTCTGCGGTATCTGCTGCTT 6428
DB 1107 CGTAGAAGATCAAGAGTATCTTCTGAGATCTTTTCTGCGGTATCTGCTGCTT 1048
QY 6429 GCAACAAAAACCAACCGCTACAGCGGTGGTTGGTTGGCGGATCAAGAGCTACCAAC 6488
DB 1047 GCAACAAAAACCAACCGCTACAGCGGTGGTTGGTTGGCGGATCAAGAGCTACCAAC 988

QY 6489 TCTTTTTCGAAAGTAACTGGCTTCAGCAGAGCGGAGATACCAAACTACTGTCTCTTAGT 6548
DB 987 TCTTTTTCGAAAGTAACTGGCTTCAGCAGAGCGGAGATACCAAACTACTGTCTCTTAGT 928
QY 6549 GTAGCGGTAGTTAGGCGCACCACTTCAAGAACTCTGTAGCACCGCTTACATACCTCGCTCT 6608
DB 927 GTAGCGGTAGTTAGGCGCACCACTTCAAGAACTCTGTAGCACCGCTTACATACCTCGCTCT 868
QY 6609 GCTAATCTCTGTTTACCAAGTGGCTGCTGCCAGTGGCGATAAGTCTGTCTTACCGGGTTGA 6668
DB 867 GCTAATCTCTGTTTACCAAGTGGCTGCTGCCAGTGGCGATAAGTCTGTCTTACCGGGTTGA 808
QY 6669 CTCAGACAGATAGTTTACCGGATAAGCGCGAGCGGTGGGCTGAAACCGGGGGTTGCTGCAC 6728
DB 807 CTCAGACAGATAGTTTACCGGATAAGCGCGAGCGGTGGGCTGAAACCGGGGGTTGCTGCAC 748
QY 6729 ACAGCCAGCTTGGAGCGAAGCAGCTTACACCGAACTGAGATACCTACAGCGTCAAGTATG 6788
DB 747 ACAGCCAGCTTGGAGCGAAGCAGCTTACACCGAACTGAGATACCTACAGCGTCAAGTATG 688
QY 6789 AGAAAGCGCCACGCTTCCGAAAGGAGGAGGCGGACAGGTATCCCGGTAAAGCGGCGAGGT 6848
DB 687 AGAAAGCGCCACGCTTCCGAAAGGAGGAGGAGGCGGACAGGTATCCCGGTAAAGCGGCGAGGT 628
QY 6849 CGAAACAGAGAGCGGACAGGAGGCTTCCAGGGGAAACCGCTGCTGATCTTTTATAGTCC 6908
DB 627 CGAAACAGAGAGCGGACAGGAGGCTTCCAGGGGAAACCGCTGCTGATCTTTTATAGTCC 568
QY 6909 TGTGCGGTTTCCGCACTCTGACTTTCAGCGTTCGATTTTGTGATGCTCTGTCAGGGGGCG 6968
DB 567 TGTGCGGTTTCCGCACTCTGACTTTCAGCGTTCGATTTTGTGATGCTCTGTCAGGGGGCG 508
QY 6969 GAGCTTATGGAAGAAACCGCGGCTTTTTCAGGTTTCTGCGCTTTTTCGCTGGCC 7028
DB 507 GAGCTTATGGAAGAAACCGCGGCTTTTTCAGGTTTCTGCGCTTTTTCGCTGGCC 448
QY 7029 TTTTGTCTCATGTTCTTCTGCTGCTTATCCCGTATCTGCTGATTAACCGTATTAACGC 7088
DB 447 TTTTGTCTCATGTTCTTCTGCTGCTTATCCCGTATCTGCTGATTAACCGTATTAACGC 388
QY 7089 CTTTGTAGTCACTGATACCGCTCGCGCAGCGAGCGAGCGGAGTCAAGTGA 7148
DB 387 CTTTGTAGTCACTGATACCGCTCGCGCAGCGAGCGAGCGGAGTCAAGTGA 328
QY 7149 CGAGGAAGCGGAGAGCGCCCAATACGCAAAACCGCTCTCCCGCGCTTTGGCGGATTA 7208
DB 327 CGAGGAAGCGGAGAGCGCCCAATACGCAAAACCGCTCTCCCGCGCTTTGGCGGATTA 268
QY 7209 TTAATGCACTGGCAGCAGAGGTTTCCGACTGGAAAGCGGGGAGTGAAGCGCAACGCAAT 7268
DB 267 TTAATGCACTGGCAGCAGAGGTTTCCGACTGGAAAGCGGGGAGTGAAGCGCAACGCAAT 208
QY 7269 TAAATGAGTACCTCACTTATGAGCGCCAGCGCTTTTACACTTTATGCTTCCGGCTCC 7328
DB 207 TAAATGAGTACCTCACTTATGAGCGCCAGCGCTTTTACACTTTATGCTTCCGGCTCC 148
QY 7329 TATGTTGTGTGAATTTGTGAGCGGATAACAAATTTTACAGGAAACAGCTATGACCATGA 7388
DB 147 TATGTTGTGTGAATTTGTGAGCGGATAACAAATTTTACAGGAAACAGCTATGACCATGA 88
QY 7389 TTACGCAAGCGCGCAATTAACCTTCACTAAAGGAAACAAAGCTGGAGCTC 7440
DB 87 TTACGCAAGCGCGCAATTAACCTTCACTAAAGGAAACAAAGCTGGAGCTC 36

RESULT 6

US-08-452-267-3
; Sequence 3, Application US/08452267
; Patent No. 5801027
; GENERAL INFORMATION:
; APPLICANT: Bennett, Malcolm
; APPLICANT: May, Sean
; APPLICANT: Ramsay, Nichola

TITLE OF INVENTION: Control of Genes in Transgenic Plants

NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Barnes & Thornburg
STREET: 11 South Meridian
CITY: Indianapolis
STATE: IN
COUNTRY: USA
ZIP: 46204
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/98/452,267
FILING DATE: 26-MAY-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Breen, John P.
REGISTRATION NUMBER: 38,833
REFERENCE/DOCKET NUMBER: 6653-25744
TELECOMMUNICATION INFORMATION:
TELEPHONE: (317) 231-7745
TELEFAX: (317) 231-7433
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 5534 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: circular
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
IMMEDIATE SOURCE:
CLONE: pUMIGIT
US-08-452-267-3

Query Match 28.2%; Score 2206.2; DB 1; Length 5534;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2208; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY	5229	TTTCAAGTGGTCACTTTTCGGGGAATGTGCGGGAACCTTATTTGTTTATTTTCTAAAT	5288
DB	3324	TTTAGTGGCACTTTTCGGGGAATGTGCGGGAACCTTATTTGTTTATTTTCTAAAT	3383
QY	5289	ACATTCAAATATGATATCCGCTCATGAGCAATTAACCCCTGATTAATGCTTCAATATATG	5348
DB	3384	ACATTCAAATATGATATCCGCTCATGAGCAATTAACCCCTGATTAATGCTTCAATATATG	3443
QY	5349	AAAAAGGAGATATGATATTAACATTTCCGTTGCGCCCTTATCCCTTTTTCGGGC	5408
DB	3444	AAAAAGGAGATATGATATTAACATTTCCGTTGCGCCCTTATCCCTTTTTCGGGC	3503
QY	5409	ATTTTGCTTCTGTTTGTCTACCCAGAAACGCTGTTGAAAGTAAAGATGCTGAAGA	5468
DB	3504	ATTTTGCTTCTGTTTGTCTACCCAGAAACGCTGTTGAAAGTAAAGATGCTGAAGA	3563
QY	5469	TCAGTTGGGTGACAGATGGGTATCATCGAACTGATCTCAACAGCGGTAAAGATCTTTGA	5528
DB	3564	TCAGTTGGGTGACAGATGGGTATCATCGAACTGATCTCAACAGCGGTAAAGATCTTTGA	3623
QY	5529	GAGTTTTCGCCCGGAAGACGTTTTCGAATGATGAGCACTTTTAAAGTTCGCTATGCG	5588
DB	3624	GAGTTTTCGCCCGGAAGACGTTTTCGAATGATGAGCACTTTTAAAGTTCGCTATGCG	3683
QY	5589	CGCGGTATTTATCCCGTATTTAGCCGCGCAAGAGCACTCCGTCGCCCATACACTATTC	5648
DB	3684	CGCGGTATTTATCCCGTATTTAGCCGCGCAAGAGCACTCCGTCGCCCATACACTATTC	3743
QY	5649	TCAGAAATGACTGGTTGAGTACTCAACAGTCAAGAAAGCATCTTACGGATGCGATGAC	5708
DB	3744	TCAGAAATGACTGGTTGAGTACTCAACAGTCAAGAAAGCATCTTACGGATGCGATGAC	3803

QY	5709	AGTAAGAGAATATTGAGTGTGCTGCCATAACCATGAGTGATAAACAATGCGGCAACTTACT	5768
DB	3804	AGTAAGAGAATATTGAGTGTGCTGCCATAACCATGAGTGATAAACAATGCGGCAACTTACT	3863
QY	5769	TCTGACAAACGATCGGAGGACCGAAGGAGCTAAACCGCTTTTGTGCAACAACATGGGGGATCA	5828
DB	3864	TCTGACAAACGATCGGAGGACCGAAGGAGCTAAACCGCTTTTGTGCAACAACATGGGGGATCA	3923
QY	5829	TGTAACCTCGCTTGTATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGAGGCGG	5888
DB	3924	TGTAACCTCGCTTGTATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGAGGCGG	3983
QY	5889	TGACACCAACGATGCTCTAGCAATGGCAACAAACCTTGGCAAACTATTAACTTGGCGAATC	5948
DB	3984	TGACACCAACGATGCTCTAGCAATGGCAACAAACCTTGGCAAACTATTAACTTGGCGAATC	4043
QY	5949	ACTTACTCTAGCTTTCCCGGCAACAAATTAATAGACTGGATGGAGCGGATAAAGTTGCAGG	6008
DB	4044	ACTTACTCTAGCTTTCCCGGCAACAAATTAATAGACTGGATGGAGCGGATAAAGTTGCAGG	4103
QY	6009	ACCACTTCTGGCTCGGCCCTTCCGGCTGGCTGGTTTATTCCTGATTAATCTGAGCGCGG	6068
DB	4104	ACCACTTCTGGCTCGGCCCTTCCGGCTGGCTGGTTTATTCCTGATTAATCTGAGCGCGG	4163
QY	6069	TGAGCGTGGGTCTCGCGGTATCATTTGACGACCTGCGGCGCAGATGGTAAGCCCTCCGTAT	6128
DB	4164	TGAGCGTGGGTCTCGCGGTATCATTTGACGACCTGCGGCGCAGATGGTAAGCCCTCCGTAT	4223
QY	6129	CGTAGTTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCGC	6188
DB	4224	CGTAGTTTATCTACACGACGGGGAGTCAGGCAACTATGGATGAACGAAATAGACAGATCGC	4283
QY	6189	TGAGATAGGTGCTCACTGATTAAGCAATGGTAATCTGTCAGACCAAGTTTACTATATAT	6248
DB	4284	TGAGATAGGTGCTCACTGATTAAGCAATGGTAATCTGTCAGACCAAGTTTACTATATAT	4343
QY	6249	ACTTTAGATTGATTTAAACCTTCAATTTTAAAGGATCTAGTGAAGATCCTTTT	6308
DB	4344	ACTTTAGATTGATTTAAACCTTCAATTTTAAAGGATCTAGTGAAGATCCTTTT	4403
QY	6309	TGATAATCTCATGACCAAAATCCCTTAAACGAGTTCGTTTCCACTGAGCGTCAGACCC	6368
DB	4404	TGATAATCTCATGACCAAAATCCCTTAAACGAGTTCGTTTCCACTGAGCGTCAGACCC	4463
QY	6369	CGTAGAAAAGATCAAGGATCTTCTGAGATCCCTTTTCTGCGCGTAATCTGCTGCTT	6428
DB	4464	CGTAGAAAAGATCAAGGATCTTCTGAGATCCCTTTTCTGCGCGTAATCTGCTGCTT	4523
QY	6429	GCAACAAAAAACCACCGCTTACCGCGGTGTTTGTGCGGATCAAGAGCTAACCAAC	6488
DB	4524	GCAACAAAAAACCACCGCTTACCGCGGTGTTTGTGCGGATCAAGAGCTAACCAAC	4583
QY	6489	TCTTTTCCGAAGGTAATCGCTTTCAGCAGCGCAGATACCAATACTGTCTCTTCTAGT	6548
DB	4584	TCTTTTCCGAAGGTAATCGCTTTCAGCAGCGCAGATACCAATACTGTCTCTTCTAGT	4643
QY	6549	GTAGCCGTATGTAGGCAACCACTTCAAGAACTCTGTAGCAGCGCCTACATACCTGCTCT	6608
DB	4644	GTAGCCGTATGTAGGCAACCACTTCAAGAACTCTGTAGCAGCGCCTACATACCTGCTCT	4703
QY	6609	GCTAATCTGTTTACAGTGGCTGCTGCGAGTGGCGATAAGTCTGTTTACCGGGTGA	6668
DB	4704	GCTAATCTGTTTACAGTGGCTGCTGCGAGTGGCGATAAGTCTGTTTACCGGGTGA	4763
QY	6669	CTCAAGACGATAGTTTACCGGATAGGCGCAGCGGTGCGGCTGAACCGGGGTTCTGTCAC	6728
DB	4764	CTCAAGACGATAGTTTACCGGATAGGCGCAGCGGTGCGGCTGAACCGGGGTTCTGTCAC	4823
QY	6729	ACAGCCGACTTGGAGCGAAGCACTACACCGAAGTGAATACCTACAGCGGTGAGCTATG	6788
DB	4824	ACAGCCGACTTGGAGCGAAGCACTACACCGAAGTGAATACCTACAGCGGTGAGCTATG	4883

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QY 6789 AGAAGCGCCACGCTTCCCGAAGGAGAAAGCGGACAGGTATCCGGTAAGCGGCAAGGT 5848
Db 4884 AGAAGCGCCACGCTTCCCGAAGGAGAAAGCGGACAGGTATCCGGTAAGCGGCAAGGT 4943
QY 6849 CGAAGCAGGAGCGCAGCAGGAGCTTCCAGGGGAAACCGCTGATCTTTATAGTCC 6908
Db 4944 CGAAGCAGGAGCGCAGCAGGAGCTTCCAGGGGAAACCGCTGATCTTTATAGTCC 5003
QY 6909 TGTGCGGTTTGGCAGCTCTGACTTGAGCGTTCGATTTTGTGATGCTCGTCAGGGGGGG 6968
Db 5004 TGTGCGGTTTGGCAGCTCTGACTTGAGCGTTCGATTTTGTGATGCTCGTCAGGGGGGG 5063
QY 6969 GAGCCTATGAAAAACCGCAGCAACCGGGCTTTTACGGTCTTCTGGCCTTTTGTGGCC 7028
Db 5064 GAGCCTATGAAAAACCGCAGCAACCGGGCTTTTACGGTCTTCTGGCCTTTTGTGGCC 5123
QY 7029 TTTTGTCTACATGCTTCTTCTCGGTATCCCGTATCTCTGATTAACCGTATTAACCG 7088
Db 5124 TTTTGTCTACATGCTTCTTCTCGGTATCTCTGATTAACCGTATTAACCG 5183
QY 7089 CTTTGAGTGAGCTGATACCGCTCGCGCAGCGAAGCGGAGCGAGTCACTGAG 7148
Db 5184 CTTTGAGTGAGCTGATACCGCTCGCGCAGCGAAGCGGAGCGAGTCACTGAG 5243
QY 7149 CGAGGAAGCGGAAGAGCGGCAATACGCAACCGCCTCTCCCGCGGTTTGGCGGATTCA 7208
Db 5244 CGAGGAAGCGGAAGAGCGGCAATACGCAACCGCCTCTCCCGCGGTTTGGCGGATTCA 5303
QY 7209 TTAATGAGCTGCGCAGCAGGTTTCCCGACTGGAAGCGGCGAGTGAAGCAACCAAT 7268
Db 5304 TTAATGAGCTGCGCAGCAGGTTTCCCGACTGGAAGCGGCGAGTGAAGCAACCAAT 5363
QY 7269 TTAATGAGTGTACTCACTCATTAGGACCCCGAGGCTTTACACTTTATGCTTCCGGCTCC 7328
Db 5364 TTAATGAGTGTACTCACTCATTAGGACCCCGAGGCTTTACACTTTATGCTTCCGGCTCC 5423
QY 7329 TATGTTGTGGAATTTGTGAGCGGATAACAATTTTCAAGGAAACAGCTATGACCATGA 7388
Db 5424 TATGTTGTGGAATTTGTGAGCGGATAACAATTTTCAAGGAAACAGCTATGACCATGA 5483
QY 7389 TTAAGCGAAGCGGCAATTAACCTCACTAAAGGAAACAAAGCTGGAGCT 7439
Db 5484 TTAAGCGAAGCGGCAATTAACCTCACTAAAGGAAACAAAGCTGGAGCT 5534

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RESULT 7

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US-09-123-644-3
; Sequence 3, Application US/09123644
; Patent No. 6127606
; GENERAL INFORMATION:
; APPLICANT: Bennett, Malcolm
; APPLICANT: May, Sean
; APPLICANT: Rangay, Nicola
; TITLE OF INVENTION: Method of Using Transactivation Proteins to
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Barnes & Thornburg
; STREET: 11 South Meridian
; CITY: Indianapolis
; STATE: IN
; COUNTRY: USA
; ZIP: 46204
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/123,644
; FILING DATE: 28-JUL-1998
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Green, John P.

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; REGISTRATION NUMBER: 38,833
; REFERENCE/DOCKET NUMBER: 6653-60788
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 231-7745
; TELEFAX: (317) 231-7433
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 5534 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; IMMEDIATE SOURCE:
; CLONE: pUMIGIT
; US-09-123-644-3

Query Match      28.2%; Score 2206.2; DB 3; Length 5534;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2208; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 5229 TTCAGGTGCGACTTTTCGGGAAATGTGCGCGAACCCTATTTGTTTATTTTCTAAAT 5288
Db 3324 TTTAGGTGCGACTTTTCGGGAAATGTGCGCGAACCCTATTTGTTTATTTTCTAAAT 3383
QY 5289 ACATTCAAAATATGTATCCGCTCATGAGACAATAAACCTGATAAATGCTTCAATAATATG 5348
Db 3384 ACATTCAAAATATGTATCCGCTCATGAGACAATAAACCTGATAAATGCTTCAATAATATG 3443
QY 5349 AAAAAAGAAAGATGAGTATTAACAATTTCGTTGCGGCTTATTTCCCTTTTTCGGGC 5408
Db 3444 AAAAAAGAAAGATGAGTATTAACAATTTCGTTGCGGCTTATTTCCCTTTTTCGGGC 3503
QY 5409 ATTTTGCCTTCTGTTTGTCTCACCCAGAAACGCTGTGAAAGTAAAGATGCTGAAGA 5468
Db 3504 ATTTTGCCTTCTGTTTGTCTCACCCAGAAACGCTGTGAAAGTAAAGATGCTGAAGA 3563
QY 5469 TCAGTTGGGTGACGAGTGGGTTTACATCGAACTGATCTCAACAGCGGTAAAGATCCTTGA 5528
Db 3564 TCAGTTGGGTGACGAGTGGGTTTACATCGAACTGATCTCAACAGCGGTAAAGATCCTTGA 3623
QY 5529 GAGTTTTCGCCCGGAAAGAGCTTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGTG 5588
Db 3624 GAGTTTTCGCCCGGAAAGAGCTTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGTG 3683
QY 5589 CGCGGTATTTATCCGTTGAGCTGACGCGGCAAGCAACTCGGTGCGCGCATACACTATTC 5648
Db 3684 CGCGGTATTTATCCGTTGAGCTGACGCGGCAAGCAACTCGGTGCGCGCATACACTATTC 3743
QY 5649 TCAGAATGACTTGGTTGAGTACTCACAGTCAAGAAAAGCATCTTACGGATGGCATGAC 5708
Db 3744 TCAGAATGACTTGGTTGAGTACTCACAGTCAAGAAAAGCATCTTACGGATGGCATGAC 3803
QY 5709 AGTAAGAGAATTTATGAGTGTGCTGATTAACCATAGTATTAACCTGCGGCAACTTACT 5768
Db 3804 AGTAAGAGAATTTATGAGTGTGCTGATTAACCATAGTATTAACCTGCGGCAACTTACT 3863
QY 5769 TCTGCAACGATCGGAGGACCGAAGAGCTTAACCGCTTTTTCGCAACAATGCGGGATCA 5828
Db 3864 TCTGCAACGATCGGAGGACCGAAGAGCTTAACCGCTTTTTCGCAACAATGCGGGATCA 3923
QY 5829 TGTAACTCGCCTTGATGCTTGGGAAACCGGAGCTGAATGAAGCCATACCAACGAGCG 5888
Db 3924 TGTAACTCGCCTTGATGCTTGGGAAACCGGAGCTGAATGAAGCCATACCAACGAGCG 3983
QY 5889 TGACACCAAGTGTGATAGCAATGCAACAAAGTTGCGCAACTATTAATCTGCGCAACT 5948
Db 3984 TGACACCAAGTGTGATAGCAATGCAACAAAGTTGCGCAACTATTAATCTGCGCAACT 4043
QY 5949 ACTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGGAGCGGATTAAGTTTCAGG 6008
Db 4044 ACTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGGAGCGGATTAAGTTTCAGG 4103

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Matches 2207; Conservative 0; Mismatches 4; Indels 0; Gaps 0;			
QY	5230	TCAGGTGGCACTTTTCGGGAAATGTGCGGAAACCCCTATTGTTTATTTTCTAAATA	5289
DB	10160	TCAGGTGGCACTTTTCGGGAAATGTGCGGAAACCCCTATTGTTTATTTTCTAAATA	10219
QY	5290	CATTCAATATGTATCGCTCATGAGACATTAACCTCTGATAAATGCTTCAATAATTGA	5349
DB	10220	CATTCAATATGTATCGCTCATGAGACATTAACCTCTGATAAATGCTTCAATAATTGA	10279
QY	5350	AAAAGGAAGATATGAGTATTCACCATTTCCGTGTGCGCCCTATTCCCTTTTTCGGGCA	5409
DB	10280	AAAAGGAAGATATGAGTATTCACCATTTCCGTGTGCGCCCTATTCCCTTTTTCGGGCA	10339
QY	5410	TTTTGCCCTCCTGTTTTCCTCCACCCAGAAACGCTGCTGAAAGTAAAGATGCTGAAGAT	5469
DB	10340	TTTTGCCCTCCTGTTTTCCTCCACCCAGAAACGCTGCTGAAAGTAAAGATGCTGAAGAT	10399
QY	5470	CAGTTGGGTGACAGAGTGGGTATCATCGAACTGGAATCTCAACAGCGGTAAAGTCTTGAG	5529
DB	10400	CAGTTGGGTGACAGAGTGGGTATCATCGAACTGGAATCTCAACAGCGGTAAAGTCTTGAG	10459
QY	5530	AGTTTTCGCCCGGAAGACGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGC	5589
DB	10460	AGTTTTCGCCCGGAAGACGTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGC	10519
QY	5590	GCGGTATTATCCGGTATTGACCGCGGCAAGAGCAACTCGGTGCGCGCATACATATTCT	5649
DB	10520	GCGGTATTATCCGGTATTGACCGCGGCAAGAGCAACTCGGTGCGCGCATACATATTCT	10579
QY	5650	CAGATGACTTGGTTGAGTACTCAACAGTCAAGAAAGCATCTTACGGATGGCGATGACA	5709
DB	10580	CAGATGACTTGGTTGAGTACTCAACAGTCAAGAAAGCATCTTACGGATGGCGATGACA	10639
QY	5710	GTAAGAGAAATATGCACTGCTGCTGATTAACCACTGAGTGATTAACCTGCGGCAACTTCT	5769
DB	10640	GTAAGAGAAATATGCACTGCTGCTGATTAACCACTGAGTGATTAACCTGCGGCAACTTCT	10699
QY	5770	CTGACAAACGATCGGAGACCGAAGGAGCTAACCGCTTTTTCGACAAACATGGGGGATCAT	5829
DB	10700	CTGACAAACGATCGGAGACCGAAGGAGCTAACCGCTTTTTCGACAAACATGGGGGATCAT	10759
QY	5830	GTAATCTGCGCTTGATCTGTTGGAAACCGGAGCTGAATGAAGCCATACCAACGACGAGCGT	5889
DB	10760	GTAATCTGCGCTTGATCTGTTGGAAACCGGAGCTGAATGAAGCCATACCAACGACGAGCGT	10819
QY	5890	GACACACGATGCTGTAGCAATGGCAACCACTGCGCAAACTATTAACTGCGGAACTA	5949
DB	10820	GACACACGATGCTGTAGCAATGGCAACCACTGCGCAAACTATTAACTGCGGAACTA	10879
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DB	10880	CTTATCTAGCTTCCCGGCAACAAATTAATAGACTGGATGGAGCGGATAAAGTTGCAGGA	10939
QY	6010	CCACTTCTGCGCTCGGCGCTTTCGGGTGCTGCTGTTTATCTGATTAATCTGAGCGGCT	6069
DB	10940	CCACTTCTGCGCTCGGCGCTTTCGGGTGCTGCTGTTTATCTGATTAATCTGAGCGGCT	10999
QY	6070	GAGGTGGGTCTGCGGTATCATGACGACTGGGCGGAGATGGTAAGCCCTCCCGTATC	6129
DB	11000	GAGGTGGGTCTGCGGTATCATGACGACTGGGCGGAGATGGTAAGCCCTCCCGTATC	11059
QY	6130	GTAAGTTATCTACAGACGGGAGTCAGGCAACTATGATGAACGAAATAGACAGATCGCT	6189
DB	11060	GTAAGTTATCTACAGACGGGAGTCAGGCAACTATGATGAACGAAATAGACAGATCGCT	11119
QY	6190	GAGATAGGTCCCTCACTGATTAAGCAATGTGTAACCTGTGACCAAGTTTACTCATATATA	6249
DB	11120	GAGATAGGTCCCTCACTGATTAAGCAATGTGTAACCTGTGACCAAGTTTACTCATATATA	11179
QY	6250	CTTTAGATTGATTTAAACCTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCCTTTT	6309
DB	11180	CTTTAGATTGATTTAAACCTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCCTTTT	11239

QY	6310	GATAATCTCATGACCAAAATCCCTTAAACGTGAGTTTTTGTTCACCTGAGCGTCAGACCCC	6369
DB	11240	GATAATCTCATGACCAAAATCCCTTAAACGTGAGTTTTTGTTCACCTGAGCGTCAGACCCC	11299
QY	6370	GTAGAAAAGATCAAAAGGATCTTCTTCAGATCCCTTTTCTGCGCGTAAATCTGCTGCTTG	6429
DB	11300	GTAGAAAAGATCAAAAGGATCTTCTTCAGATCCCTTTTCTGCGCGTAAATCTGCTGCTTG	11359
QY	6430	CRAACAAAAAACAACCGCTTACAGCGGTGTTTTGTTGCGGATCAAGAGCTACCAACT	6489
DB	11360	CRAACAAAAAACAACCGCTTACAGCGGTGTTTTGTTGCGGATCAAGAGCTACCAACT	11419
QY	6490	CTTTTTCGGAAGTAACTGCTTTCAGAGAGCGCAGATACCAAAATCTGTCTTCTAGTG	6549
DB	11420	CTTTTTCGGAAGTAACTGCTTTCAGAGAGCGCAGATACCAAAATCTGTCTTCTAGTG	11479
QY	6550	TAGCCCTAGTTAGGCCACCACTTCAAGAACTCTGTAGACCGCCTACATACCTCGCTCTG	6609
DB	11480	TAGCCCTAGTTAGGCCACCACTTCAAGAACTCTGTAGACCGCCTACATACCTCGCTCTG	11539
QY	6610	CTAATCTGTACAGTGGCTGCTGCGAGTGGCGATAAGTCTGTCTTACCGGTTGGAC	6669
DB	11540	CTAATCTGTACAGTGGCTGCTGCGAGTGGCGATAAGTCTGTCTTACCGGTTGGAC	11599
QY	6670	TCAAGACGATAGTTACCGGATAAGCGCAGCGTCCGGCTGAAACGGGGGTTCTGTCACA	6729
DB	11600	TCAAGACGATAGTTACCGGATAAGCGCAGCGTCCGGCTGAAACGGGGGTTCTGTCACA	11659
QY	6730	CAGCCAGCTTGGAGCGAAGCACTTACCGAACTGAGATACCTACAGCGTGAGCTATGA	6789
DB	11660	CAGCCAGCTTGGAGCGAAGCACTTACCGAACTGAGATACCTACAGCGTGAGCTATGA	11719
QY	6790	GAAAGCGCACAACCGTCCCGAAGGGAGAAAGCGGACAGGTATCCGGTAAGCGGCGGTC	6849
DB	11720	GAAAGCGCACAACCGTCCCGAAGGGAGAAAGCGGACAGGTATCCGGTAAGCGGCGGTC	11779
QY	6850	GGAAAGGAGAGCGCAAGGGAGCTTCCAGGGGAAACCGCTGGTATCTTTTATGTCCT	6909
DB	11780	GGAAAGGAGAGCGCAAGGGAGCTTCCAGGGGAAACCGCTGGTATCTTTTATGTCCT	11839
QY	6910	GTGCGGTTCGCCACCTCTGACTTGAGCGTGCATTTTGTGATGCTGTCAGGGGGCGG	6969
DB	11840	GTGCGGTTCGCCACCTCTGACTTGAGCGTGCATTTTGTGATGCTGTCAGGGGGCGG	11899
QY	6970	AGCTATGAAAACCGCCAGCAACCGCGCTTTTTCAGGTTCTGCGCTTTTGTGCGCT	7029
DB	11900	AGCTATGAAAACCGCCAGCAACCGCGCTTTTTCAGGTTCTGCGCTTTTGTGCGCT	11959
QY	7030	TTTGTCTCACATGTTCTTCTGCTTATCCCTGATTTCTGTGATTAACCGTATTTACCGCC	7089
DB	11960	TTTGTCTCACATGTTCTTCTGCTTATCCCTGATTTCTGTGATTAACCGTATTTACCGCC	12019
QY	7090	TTTGTGTAGCTGATACCGCTCCCGCAGCGCAAGACCGAGCGCAGCGAGTCAGTGAGC	7149
DB	12020	TTTGTGTAGCTGATACCGCTCCCGCAGCGCAAGACCGAGCGCAGCGAGTCAGTGAGC	12079
QY	7150	GAGGAAGCGAAGAGCGCCCAATACCAACCGCTCTCCCGCGCTTCCCGGATTCAT	7209
DB	12080	GAGGAAGCGAAGAGCGCCCAATACCAACCGCTCTCCCGCGCTTCCCGGATTCAT	12139
QY	7210	TAAATGAGCTGGCAGCAGAGTTTCCCGACTGGAAGCGGCGAGTCAGCGCAACGCAATT	7269
DB	12140	TAAATGAGCTGGCAGCAGAGTTTCCCGACTGGAAGCGGCGAGTCAGCGCAACGCAATT	12199
QY	7270	AATGTGATTAACCTCACTATTAGGCAACCGCTTTACCTTTATGCTTCCGGCTCCT	7329
DB	12200	AATGTGATTAACCTCACTATTAGGCAACCGCTTTACCTTTATGCTTCCGGCTCCT	12259
QY	7330	ATGTTGTGGAATGTGAGCGGATAAATTTTACACAGAGAAACAGCTATGACCATGAT	7389
DB	12260	ATGTTGTGGAATGTGAGCGGATAAATTTTACACAGAGAAACAGCTATGACCATGAT	12319

QY 7390 TAGCCAGCGCGCAATTAACCTCACTAAAGGGAACAAAAGCTGGAGCTC 7440
Db 12320 TAGCCAGCTCGAATTAACCTCACTAAAGGGAACAAAAGCTGGAGCTC 12370

RESULT 9

US-08-935-312-13
; Sequence 13, Application US/08935312
; Patent No. 6207455
; GENERAL INFORMATION:
; APPLICANT: CHANG, Lung-Ji
; TITLE OF INVENTION: LENTIVIRAL VECTORS
; NUMBER OF SEQUENCES: 20
; CORRESPONDENCE ADDRESS:
; ADDRESSES: BROWDY AND NEIMARK, P.L.L.C.
; STREET: 624 Ninth Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: USA
; ZIP: 20001
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/935,312
; FILING DATE: 22-SEP-1997
; CLASSIFICATION: 435
; ATTORNEY/AGENT INFORMATION:
; NAME: COOPER, Iver P.
; REGISTRATION NUMBER: 28,005
; REFERENCE/DOCKET NUMBER: CHANG-112
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 202-628-5197
; TELEFAX: 202-737-3528
; INFORMATION FOR SEQ ID NO: 13:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 12494 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: other nucleic acid
; DESCRIPTION: /desc = "DNA"
US-08-935-312-13

Query Match 28.2%; Score 2204.6; DB 3; Length 12494;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2207; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
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Db 10165 TCAGGTGGCAGCTTTTCGGGGAAATGTGCGGAAACCCCTATTCTTTTCTTAATA 10224
QY 5290 CATTCAAATATGATCCGCTCATGAGACATAACCCCTGATAAATGCTTCAATAATATGA 5349
Db 10225 CATTCAAATATGATCCGCTCATGAGACATAACCCCTGATAAATGCTTCAATAATATGA 10284
QY 5350 AAAAGGAGATGATGAGTATTCACATTCGATTCGCTGTCGCCCTTATTCCTTTTTCGGGCA 5409
Db 10285 AAAAGGAGATGATGAGTATTCACATTCGCTGTCGCCCTTATTCCTTTTTCGGGCA 10344
QY 5410 TTTTCCCTTCCTGTTTTCCTCACCAGAACGCTGGTGAAGTAAAGATGCTGAAGAT 5469
Db 10345 TTTTCCCTTCCTGTTTTCCTCACCAGAACGCTGGTGAAGTAAAGATGCTGAAGAT 10404
QY 5470 CAGTTGGGTGACGAGTGGGTTCATCGAATCGGATCTCAACAGCGGTAAAGATCTTTGAG 5529
Db 10405 CAGTTGGGTGACGAGTGGGTTCATCGAATCGGATCTCAACAGCGGTAAAGATCTTTGAG 10464
QY 5530 AGTTTTCGCCCGAAGAACGTTTTCCTCAATGATGAGCACTTTTAAAGTTCTGCTATGTGC 5589
Db 10465 AGTTTTCGCCCGAAGAACGTTTTCCTCAATGATGAGCACTTTTAAAGTTCTGCTATGTGC 10524

QY 5590 GCGTATTATCCGTTATTGACGCGGCAAGAGCAACTCGGTGCGGCATACACTATTCT 5649
Db 10525 GCGTATTATCCGTTATTGACGCGGCAAGAGCAACTCGGTGCGGCATACACTATTCT 10584
QY 5650 CAGAAATGACCTTGGTTGAGTACTCAACAGTCAAGAAAGCATCTTACGGATGGCATGACA 5709
Db 10585 CAGAAATGACCTTGGTTGAGTACTCAACAGTCAAGAAAGCATCTTACGGATGGCATGACA 10644
QY 5710 GTAAGAGAAATATGACAGTGTGCTGCCATTAACCTAGTGTATACACTGCGGCAACTTACTT 5769
Db 10645 GTAAGAGAAATATGACAGTGTGCTGCCATTAACCTAGTGTATACACTGCGGCAACTTACTT 10704
QY 5770 CTGACAAACGATCGGAGGACCGAAGAGCTAACCCCTTTTGGCAACAATGCGGATCAT 5829
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QY 5830 GTAACTCGCCTTGATCGTTGGGAAACCGAGCTGAATGAAGCCATACCAAAACGACGAGCT 5889
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Db 10885 CTTACTCTAGCTTCCCGGCAACAATTAATAGACTGGATGGAGGCGGATAAAGTTTCAGGA 10944
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QY 6490 CTTTTCCTGAGGATTAACCTGCTTCAGCAGAGCGAGATACCAAAATCTGCTCTTCTAGTG 6549
Db 11425 CTTTTCCTGAGGATTAACCTGCTTCAGCAGAGCGAGATACCAAAATCTGCTCTTCTAGTG 11484
QY 6550 TAGCGGTAGTTAGGCCCACTTCAAGAACTCTGTAGCACCGCTTACATACCTCGCTCTG 6609
Db 11485 TAGCGGTAGTTAGGCCCACTTCAAGAACTCTGTAGCACCGCTTACATACCTCGCTCTG 11544
QY 6610 CTAATCTGTATCAGGTGGCTGCTGCGGCGGATTAAGTGTCTTACCGGTTGAC 6669
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Db 10825 GACACCAAGTCTGTTAGCAATGGCAACAAACGTTGGCAAACTATTAACTGGCGAACTA 10884
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Db 10885 CTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGGATGGAGGCGGATAAAGTTGACAGGA 10944
QY 6010 CCACCTCTGCGCTGGCGCCCTTCCCGCTGGCTGCTGTTTATTGCTGATAAATCTGGAGCCGCT 6069
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QY 6730 CAGCCCGCTTGGAGCAACGCTTACACCGAATCTGAGATACCTACAGCGTGAAGTGA 6789
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QY 6850 GGAACAGGAGCGCACGAGGAGCTTCCAGGGGAAACGCTCGGTATCTTTTATAGTCT 6909
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QY 7030 TTTGCTCACATGTTCTTCTGCTGTTATCCCTCATCTCTGTTGGATAACCGATTATACCGCC 7089
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Db 12325 TAGCCAAAGCTCGAAATTAACCTCACTAAGGGAACAAAGAGCTGGAGCTC 12375

RESULT 11
US-09-608-730B-21
; Sequence 21, Application US/09608730B
; Patent No. 6423544
; GENERAL INFORMATION:
; APPLICANT: Hardy, Stephen
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR PRODUCING RECOMBINANT
; TITLE OF INVENTION: VIRIONS
; FILE REFERENCE: PP01569.101
; CURRENT APPLICATION NUMBER: US/09/608,730B
; CURRENT FILING DATE: 2000-06-30
; PRIOR APPLICATION NUMBER: 09/476,299
; PRIOR FILING DATE: 1999-12-30
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin Ver. 2.0
; SEQ ID NO 21
; LENGTH: 4883
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: pBS CP
US-09-608-730B-21

Query Match 28.2%; Score 2204; DB 4; Length 4883;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2207; Conservative 0; Mismatches 5; Indels 0; Gaps 0;

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QY 5289 ACATTCAATATGTTATCGCTCATGACATACCCCTGATAAATGCTTCAATAATATG 5348
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Db 3590 TGAGATAGGTGCCTCACTGATTAAAGCATTTGGTAATCTGTACAGACCAAGTTTACTCATATAT 3649
Qy 6249 ACTTTAGATTGATTTAAACCTCATTTTAAATTTAAAGGATCTAGTGAAGATCTCTTTT 6308
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Qy 6489 TCTTTTCCGAAGTACTGCTTCAAGAGCGGATACCAAAATCTGCTCTCTCTAGT 6548
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Qy 6549 GTAGCGGTAGTTAGGCCACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCT 6608
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Qy 6609 GCTAATCTCTGTTTACAGTGGCTGCTGCCAGTGGCGATAAGTGTGTTTACCGGGTTGGA 6668
Db 4010 GCTAATCTCTGTTTACAGTGGCTGCTGCCAGTGGCGATAAGTGTGTTTACCGGGTTGGA 4069
Qy 6669 CTCAGACGATAGTTTACCGGATAAGCGCGAGCGGTGCGGCTGAACGGGGGTTTCGTGCAC 6728
Db 4070 CTCAGACGATAGTTTACCGGATAAGCGCGAGCGGTGCGGCTGAACGGGGGTTTCGTGCAC 4129
Qy 6729 ACAGCCCGATTTGAGCGAAACGACCTACACCGAACTGAGATACCTACAGCGTGAAGTATG 6788
Db 4130 ACAGCCCGATTTGAGCGAAACGACCTACACCGAACTGAGATACCTACAGCGTGAAGTATG 4189
Qy 6789 AGAAACGCGCCACGCTTCCGAAAGGAGAAAGCGGACAGGTATCCCGTAAAGCGGCGAGGT 6848
Db 4190 AGAAACGCGCCACGCTTCCGAAAGGAGAAAGCGGACAGGTATCCCGTAAAGCGGCGAGGT 4249
Qy 6849 CGGAAACAGGAGAGCGCACGAGGAGCTTCCAGGGGAAACGCTGCTATCTTTATAGTCC 6908
Db 4250 CGGAAACAGGAGAGCGCACGAGGAGCTTCCAGGGGAAACGCTGCTATCTTTATAGTCC 4309
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Qy 6969 GAGCTTATCGMAAAACGCGCAACGCGGCTTTTACGGTTCCTGCGCTTTTGTGCGCC 7028
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Qy 7149 CGAGGAAGCGGAGAGCGGCCAATACGCAACCGCTCTCCCGCGTTCGCGCGATTCA 7208
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Qy 7209 TTAATGCAGTGGCAGCAGAGTTTCCCGACTGGAAGCGGCGAGTGAAGCAACGCAAT 7268
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Db 4670 TTAATGCAGTGGTCACTCACTTATAGGCAACCGAGCTTTTACACTTTATGCTTCGGGCTCC 4729
Qy 7329 TATGTTGCTGGAATTTGAGCGGATAACAAATTTTACAGGAAACAGCTATACCAATGA 7388
Db 4730 TATGTTGCTGGAATTTGAGCGGATAACAAATTTTACAGGAAACAGCTATACCAATGA 4789
Qy 7389 TTAACGCAAGCGCGCAATTAACCTCACTAAAGGAAACAAAGCTGGAGCTC 7440
Db 4790 TTAACGCAAGCTCAATTAACCTCACTAAAGGAAACAAAGCTGGAGCTC 4841

RESULT 12

US-08-659-206A-1
; Sequence 1, Application US/08659206A
; Patent No. 5922685
; GENERAL INFORMATION:
; APPLICANT: Rakhmievich, Alexander
; TITLE OF INVENTION: IL-12 Gene Therapy of Tumors
; NUMBER OF SEQUENCES: 6
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Charles & Brady
; STREET: 1 South Pinckney Street

QY 5489 TCTTTTCCGAGGTACTGCTTCAGCAGCGCAGATACCAATACTGTCTCTTAGT 6548
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QY 6549 GTAGCCGTAGTATAGCCACCACTTCAAGAACTCTGTAGCACCCTACATACCTCGCTCT 6608
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Db 6921 CGAGGAAGCGGAAGAGCGCCAAATACGCAACCGCTCTCCCGCGGCTTGGCGGATTC 6980
QY 7209 TTAATGAGCTGGCAGCAGAGTTTCCGACTGGAAAGCGGGGAGTGTAGCGCAACGCAAT 7268
Db 6981 TTAATGAGCTGGCAGCAGAGTTTCCGACTGGAAAGCGGGGAGTGTAGCGCAACGCAAT 7040
QY 7269 TAAATGAGTTTACTCTACTTATAGGACCCCGAGGCTTTACATTTATGTTCTCGGCTCC 7328
Db 7041 TAAATGAGTTTACTCTACTTATAGGACCCCGAGGCTTTACATTTATGTTCTCGGCTCC 7100
QY 7329 TATGTTGTGTGGAATGTGAGCGGATAACAAATTTACAGAGGAAACAGCTATGACCATGA 7388
Db 7101 TATGTTGTGTGGAATGTGAGCGGATAACAAATTTACAGAGGAAACAGCTATGACCATGA 7160
QY 7389 TTAAGCAGCGCGCAATTAACCTCTCACTAAAGGGAACAAAGCTGTGAGTCT 7440
Db 7161 TTAAGCAGCGCGCAATTAACCTCTCACTAAAGGGAACAAAGCTGTGAGTCT 7212

RESULT 13

US-08-446-935-6/c
; Sequence 6, Application US/08446935
; Patent No. 6187991
; GENERAL INFORMATION:
; APPLICANT: Soeller, Walter C.
; APPLICANT: Carty, Maynard D.
; APPLICANT: Kreutter, David K.

; TITLE OF INVENTION: TRANSGENIC ANIMAL MODELS FOR TYPE II
; TITLE OF INVENTION: DIABETES MELLITUS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Pfizer Inc.
; STREET: 235 East 42nd Street, 20th Floor
; CITY: New York
; STATE: New York
; COUNTRY: U.S.A.
; ZIP: 10017-5755
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/446,935
; FILING DATE:
; CLASSIFICATION: 800
; ATTORNEY/AGENT INFORMATION:
; NAME: Sheyka, Robert F.
; REGISTRATION NUMBER: 31,304
; REFERENCE/DOCKET NUMBER: PC8153
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (212) 573-1189
; TELEFAX: (212) 573-1939
; TELEX: N/A
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 2961 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: double
; TOPOLOGY: circular
; MOLECULE TYPE: DNA (genomic)
; US-08-446-935-6

Query Match 28.2%; Score 2203.8; DB 3; Length 2961;
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2205; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
QY 5234 GTGGCACTTTTCGGGGAATGTGCGGGAACCCCTATTTGTTTATTTTCTAATACATT 5293
Db 2961 GTGGCACTTTTCGGGGAATGTGCGGGAACCCCTATTTGTTTATTTTCTAATACATT 2902
QY 5294 CAAATATGATCGCTCATGAGACATAACCCCTGATAAATGCTTCAATAATATTGAAAA 5353
Db 2901 CAAATATGATCGCTCATGAGACATAACCCCTGATAAATGCTTCAATAATATTGAAAA 2842
QY 5354 GGAAGATGATGATATCAACATTTCCGTGCGCCCTTATTCCTTTTTCGGCATTTT 5413
Db 2841 GGAAGATGATGATATCAACATTTCCGTGCGCCCTTATTCCTTTTTCGGCATTTT 2782
QY 5414 GCCTTCCTTTTTCCTCACCAGAAACCGTGTGGAAGTAAAGATGCTGAAGATCAGT 5473
Db 2781 GCCTTCCTTTTTCCTCACCAGAAACCGTGTGGAAGTAAAGATGCTGAAGATCAGT 2722
QY 5474 TGGGTGCACGAGTGGGTTACATCGAACTCGATCTCAACAGCGGTAAGATCTTTGAGAGTT 5533
Db 2721 TGGGTGCACGAGTGGGTTACATCGAACTCGATCTCAACAGCGGTAAGATCTTTGAGAGTT 2662
QY 5534 TTGCGCCCCGAAGAACGTTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCG 5593
Db 2661 TTGCGCCCCGAAGAACGTTTTTCCAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCG 2602
QY 5594 TATTATCCGTTATGACGGCGGAGCACTCGGTCCGCGCATACACTATTCTCAGA 5653
Db 2601 TATTATCCGTTATGACGGCGGAGCACTCGGTCCGCGCATACACTATTCTCAGA 2542
QY 5654 ATGACTTGGTTGAGTACTCACCAGTCACAGAAAGCATCTTACGGATGGCATGACAGTAA 5713
Db 2541 ATGACTTGGTTGAGTACTCACCAGTCACAGAAAGCATCTTACGGATGGCATGACAGTAA 2482
QY 5714 GAGAATTATGCACTGCTGCCATAACCATGATGATGAACACTGCGGCCAACTTACTTCTGA 5773

Db 2481 GAGATTATGAGTGTCTCCATACCATGAGTATACACTGCGCCAACTTACTTCTGA 2422
QY 5774 CAACGATCGAGGAGCGAGAGCTAACCGCTTTTGTGCAACAATGGGGATCATGTAA 5833
Db 2421 CAACGATCGAGGAGCGAGAGCTAACCGCTTTTGTGCAACAATGGGGATCATGTAA 2362
QY 5834 CTCGCTTGTATGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGAGAGCGTGACA 5893
Db 2361 CTCGCTTGTATGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGAGAGCGTGACA 2302
QY 5894 CCACGATCGCTGTAGCAATGCAACAACGTTGCGCAAACTATTAACTGGGCAACTACTTA 5953
Db 2301 CCACGATCGCTGTAGCAATGCAACAACGTTGCGCAAACTATTAACTGGGCAACTACTTA 2242
QY 5954 CTCGAGTCTCCGGCAACAATTAATAGACTCGATGAGGCGGATGAAGTTGCGAGGACAC 6013
Db 2241 CTCGAGTCTCCGGCAACAATTAATAGACTCGATGAGGCGGATGAAGTTGCGAGGACAC 2182
QY 6014 TTCTGCGCTCGGCCCTCCGGCTGGCTGTTTATTTGCTGATAAATCTGGAGCGGTGAGC 6073
Db 2181 TTCTGCGCTCGGCCCTCCGGCTGGCTGTTTATTTGCTGATAAATCTGGAGCGGTGAGC 2122
QY 6074 GTGGCTCTCGGGTATCATTTGAGCACTGCGGGCCAGATGTTAGCCCTCCCGTATCGTAG 6133
Db 2121 GTGGCTCTCGGGTATCATTTGAGCACTGCGGGCCAGATGTTAGCCCTCCCGTATCGTAG 2062
QY 6134 TTATCTACAGCGGGGAGTCAGGCAACTATGATGAACGAATAGACAGATCGCTGAGA 6193
Db 2061 TTATCTACAGCGGGGAGTCAGGCAACTATGATGAACGAATAGACAGATCGCTGAGA 2002
QY 6194 TAGGTGCTCACTGANTTAAGCAATGTTAACTGTCAGACCAAGTTTACTCATATATCTTT 6253
Db 2001 TAGGTGCTCACTGANTTAAGCAATGTTAACTGTCAGACCAAGTTTACTCATATATCTTT 1942
QY 6254 AGATTGATTAAACCTTCATTTTAAATTAAGGATCTAGTGAAGATCCCTTTTGTGATA 6313
Db 1941 AGATTGATTAAACCTTCATTTTAAATTAAGGATCTAGTGAAGATCCCTTTTGTGATA 1882
QY 6314 ATCTCATGACCAAAATCCCTTAACTGATGTTTGTCCACTGAGCGTCAGACCCCGTAG 6373
Db 1881 ATCTCATGACCAAAATCCCTTAACTGATGTTTGTCCACTGAGCGTCAGACCCCGTAG 1822
QY 6374 AAAAGATCAAAAGATCTTTGAGATCTTTTCTGCGGTAACTGTCGTTGCAAA 6433
Db 1821 AAAAGATCAAAAGATCTTTGAGATCTTTTCTGCGGTAACTGTCGTTGCAAA 1762
QY 6434 CAAAAAACCAACCGCTACCGGTTGTTGTTGCGGATCAAGAGCTACCAACTCTTT 6493
Db 1761 CAAAAAACCAACCGCTACCGGTTGTTGTTGCGGATCAAGAGCTACCAACTCTTT 1702
QY 6494 TTCCGAAGTAACTGGCTTACGAGAGCGGATACCAAACTGCTGCTTCTAGTGAGC 6553
Db 1701 TTCCGAAGTAACTGGCTTACGAGAGCGGATACCAAACTGCTGCTTCTAGTGAGC 1642
QY 6554 CTTAGTGGCCACCACTTCAAGACTCTGTAGGACCGCTACATACCTCGCTCTGCTAA 6613
Db 1641 CTTAGTGGCCACCACTTCAAGACTCTGTAGGACCGCTACATACCTCGCTCTGCTAA 1582
QY 6614 TCTGTTTACCAAGTCTGCTGCGATGCGGATGAAGTCTTCTACCGGTTGAGCTCAA 6673
Db 1581 TCTGTTTACCAAGTCTGCTGCGATGCGGATGAAGTCTTCTACCGGTTGAGCTCAA 1522
QY 6674 GACGATGTTACCGGATGAAGGCGAGCGGTGCGGTGAACGGGGGTTTGTGCAACAGC 6733
Db 1521 GACGATGTTACCGGATGAAGGCGAGCGGTGCGGTGAACGGGGGTTTGTGCAACAGC 1462
QY 6734 CCAGTCTGGAGGACGACCTACACCGAATCTGAGATACCTACGCTGAGCTATGAGAA 6793
Db 1461 CCAGTCTGGAGGACGACCTACACCGAATCTGAGATACCTACGCTGAGCTATGAGAA 1402
QY 6794 GCGCCACGCTTCCCGAAGGAGAAAGCGGACAGGTATCCGGTAAAGCGGAGGTGCGAA 6853

Db 1401 GCGCCACGCTTCCGAAGGAGAAAGCGGACAGGTATCCGGTAAAGCGGAGGTGCGAA 1342
QY 6854 CAGGAGCGCAGCAGAGGAGCTTCCAGGGGAAACGCTGTATCTTTATAGTCTGTGCG 6913
Db 1341 CAGGAGCGCAGCAGAGGAGCTTCCAGGGGAAACGCTGTATCTTTATAGTCTGTGCG 1282
QY 6914 GGTTCGCCACCTCTGACTTGTAGCGTGCATTTTGTGATGCTCGTCAGGGGCGGAGCC 6973
Db 1281 GGTTCGCCACCTCTGACTTGTAGCGTGCATTTTGTGATGCTCGTCAGGGGCGGAGCC 1222
QY 6974 TATGAAAAACGCGCAGCAACGCGCCCTTTTACGTTCTCGGCTTTTGTGCGCTTTG 7033
Db 1221 TATGAAAAACGCGCAGCAACGCGCCCTTTTACGTTCTCGGCTTTTGTGCGCTTTG 1162
QY 7034 CTCACATGTTCTTCTGCGTATCCCTGATTCCTGATTAACCGTATTAACCGCTTTG 7093
Db 1161 CTCACATGTTCTTCTGCGTATTCCTGATTCCTGATTAACCGTATTAACCGCTTTG 1102
QY 7094 AGTGAGCTGATACCGCTCGCGCAGCGCAACGACCGAGCGCAGGAGTCAGTGAGCGAGG 7153
Db 1101 AGTGAGCTGATACCGCTCGCGCAGCGCAACGACCGAGCGCAGGAGTCAGTGAGCGAGG 1042
QY 7154 AAGCGAAGAGCGCCAAATACGCAAAACGCTCTCTCCCGCGGTTGGCGATTCATTAAT 7213
Db 1041 AAGCGAAGAGCGCCAAATACGCAAAACGCTCTCTCCCGCGGTTGGCGATTCATTAAT 982
QY 7214 GCAGCTGGCAGCAGAGGTTCCGACCTGGAAGCGGCGAGTGAGCGCAACCAATTAATG 7273
Db 981 GCAGCTGGCAGCAGAGGTTCCGACCTGGAAGCGGCGAGTGAGCGCAACCAATTAATG 922
QY 7274 TGAGTTACCTCACTCATTAGGACCCCGAGCTTTTACACTTTTATGCTTCCGGCTCCTATGT 7333
Db 921 TGAGTTAGCTCACTCATTAGGACCCCGAGCTTTTACACTTTTATGCTTCCGGCTCCTATGT 862
QY 7334 TGTGTGAATGTGAGCGGATACAAATTTTCAACAGGAAACAGCTATGACCATGATTAGC 7393
Db 861 TGTGTGAATGTGAGCGGATACAAATTTTCAACAGGAAACAGCTATGACCATGATTAGC 802
QY 7394 CCAAGCGCAATTAACCTCACTTAAAGGAAACAAAGCTGAGCTC 7440
Db 801 CCAAGCGCAATTAACCTCACTTAAAGGAAACAAAGCTGAGCTC 755

RESULT 14

US-08-651-472-62

; Sequence 62, Application US/08651472

; Patent No. 6103244

; GENERAL INFORMATION:

; APPLICANT: DORNER, Friedrich

; APPLICANT: SCHEIFLINGER, Friedrich

; APPLICANT: FALKNER, Palko Gunter

; APPLICANT: PFLEIDERER, Michael

; TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC

; TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1

; TITLE OF INVENTION: (HIV-1) ANTIGENS

; NUMBER OF SEQUENCES: 95

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Foley & Lardner

; STREET: 3000 K Street, N.W., Suite 500

; CITY: Washington

; STATE: D.C.

; COUNTRY: USA

; ZIP: 20007-5109

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: Patent Release #1.0, Version #1.30

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/08/651,472

; FILING DATE:

; CLASSIFICATION: 435

; PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/914,738
FILING DATE: 20-JUL-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/750,080
FILING DATE: 26-AUG-1991
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 30472/166/IMMU
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 4145 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
IMMEDIATE SOURCE:
CLONE: pS29pt-S4
US-08-651-472-62

Query Match
Best Local Similarity 99.9%; Pred. No. 0;
Matches 2205; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

QY	5234	GTGGCACTTTTCGGGAAATGTGCGGAAACCCCTATTGTTTATTTTCTTAATACATT	5293
DB	1	GTGGCACTTTTCGGGAAATGTGCGGAAACCCCTATTGTTTATTTTCTTAATACATT	60
QY	5294	CAAAATATGATCCGCTCATGAGACAATAACCTGATAAATGCTTCAATAATATTGAAAA	5353
DB	61	CAAAATATGATCCGCTCATGAGACAATAACCTGATAAATGCTTCAATAATATTGAAAA	120
QY	5354	GGAAAGATATGAGTATTCACATTTCCGTGTGCGCCCTTATTCCTTTTTTTCGGGCATTTT	5413
DB	121	GGAAAGATATGAGTATTCACATTTCCGTGTGCGCCCTTATTCCTTTTTTTCGGGCATTTT	180
QY	5414	GCCTTCTGTTTTGCTCACCAGAAACCGTGTGGAAGTAAAGATGCTGAAGATCAGT	5473
DB	181	GCCTTCTGTTTTGCTCACCAGAAACCGTGTGGAAGTAAAGATGCTGAAGATCAGT	240
QY	5474	TGGGTGCAGAGTGGGTTCATCGAACTGGATCTCAACAGCGGTAAAGATCCTTGAGAGTT	5533
DB	241	TGGGTGCAGAGTGGGTTCATCGAACTGGATCTCAACAGCGGTAAAGATCCTTGAGAGTT	300
QY	5534	TTCCGCCCCGAAGAACGTTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCG	5593
DB	301	TTCCGCCCCGAAGAACGTTTTCCAAATGATGAGCACTTTTAAAGTTCTGCTATGTGGCGCG	360
QY	5594	TATTATCCGCTATTTGACGCGGCGAGAGCACTCCGTCGCCCATACACTATTCTCAGA	5653
DB	361	TATTATCCGCTATTTGACGCGGCGAGAGCACTCCGTCGCCCATACACTATTCTCAGA	420
QY	5654	ATGACTTGGTGTAGTACTACACAGTCAAGAAAGCATCTTACGGATGGCATGACAGATAA	5713
DB	421	ATGACTTGGTGTAGTACTACACAGTCAAGAAAGCATCTTACGGATGGCATGACAGATAA	480
QY	5714	GAGAAATTATGACGTGTGCCATTAACCATGATGATAACACTCGCGCCAACTTACTTCTGA	5773
DB	481	GAGAAATTATGACGTGTGCCATTAACCATGATGATAACACTCGCGCCAACTTACTTCTGA	540
QY	5774	CAACGATCGGAGACCGAAGAGCTAACCGCTTTTTTGCAACAATGCGGGGATCATGTAA	5833
DB	541	CAACGATCGGAGACCGAAGAGCTAACCGCTTTTTTGCAACAATGCGGGGATCATGTAA	600
QY	5834	CTCGCTTGTATCTGCGGAACCGGAGCTGAATCAAGCCATACCAACACGACGCGTGACA	5893
DB	601	CTCGCTTGTATCTGCGGAACCGGAGCTGAATCAAGCCATACCAACACGACGCGTGACA	660

QY	5894	CCACGATGCTGTAGCAATGGCAACAAACGTTGCGCAAACTATTAACTGGCGAACTACTTA	5953
DB	661	CCACGATGCTGTAGCAATGGCAACAAACGTTGCGCAAACTATTAACTGGCGAACTACTTA	720
QY	5954	CTCTAGCTTCCCGGCAACAAATTAATAGACTGGATGGAGCGGATTAAGTTGCGAGCCAC	6013
DB	721	CTCTAGCTTCCCGGCAACAAATTAATAGACTGGATGGAGCGGATTAAGTTGCGAGCCAC	780
QY	6014	TTCTGCGCTCGGCGCTTCCGCGCTTCCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	6073
DB	781	TTCTGCGCTCGGCGCTTCCGCGCTTCCGCTGCGCTGCTGCTGCTGCTGCTGCTGCTGCTG	840
QY	6074	GTGGGTCTCGCGGTATCATTTGAGCACTCGGGCGCAGATGGTAAGCCCTCCCGTATCGTAG	6133
DB	841	GTGGGTCTCGCGGTATCATTTGAGCACTCGGGCGCAGATGGTAAGCCCTCCCGTATCGTAG	900
QY	6134	TTATCTACACGACGGGAGTCAAGCACTATGAGTGAACGAAATAGACAGATCGCTGAGA	6193
DB	901	TTATCTACACGACGGGAGTCAAGCACTATGAGTGAACGAAATAGACAGATCGCTGAGA	960
QY	6194	TAGGTGCTCTCACTGATTAAAGCACTTGGTAACTGTGAGCAACCAAGTTTACTCATATATCTTT	6253
DB	961	TAGGTGCTCTCACTGATTAAAGCACTTGGTAACTGTGAGCAACCAAGTTTACTCATATATCTTT	1020
QY	6254	AGATTGATTTAAAACTTCAATTTTAAATTTAAAGGATCTAGTGAAGATCCTTTTGTGATA	6313
DB	1021	AGATTGATTTAAAACTTCAATTTTAAATTTAAAGGATCTAGTGAAGATCCTTTTGTGATA	1080
QY	6314	ATCTCATGACCAAAATCCCTTAACGTCAGCTTTTGGTTCCACTGAGCGTCAGACCCGCTAG	6373
DB	1081	ATCTCATGACCAAAATCCCTTAACGTCAGCTTTTGGTTCCACTGAGCGTCAGACCCGCTAG	1140
QY	6374	AAAAATCAAAAGATCTCTTCTGAGATCTTTTCTGCGCGTAAATCTGCTGCTGCGAAA	6433
DB	1141	AAAAATCAAAAGATCTCTTCTGAGATCTTTTCTGCGCGTAAATCTGCTGCTGCGAAA	1200
QY	6434	CAAAAAACAACCGCTTCCAGCGGTGGTTTGGTGGCGATCAAGAGCTACCAACTCTTT	6493
DB	1201	CAAAAAACAACCGCTTCCAGCGGTGGTTTGGTGGCGATCAAGAGCTACCAACTCTTT	1260
QY	6494	TTCCGGAAGTAACTGGCTTCCAGAGCGCAGATACCAATCTGCTTCTAGTCTAGC	6553
DB	1261	TTCCGGAAGTAACTGGCTTCCAGAGCGCAGATACCAATCTGCTTCTAGTCTAGC	1320
QY	6554	CGTAGTTAGCCCAACCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTGCTAA	6613
DB	1321	CGTAGTTAGCCCAACCACTTCAAGAACTCTGTAGCACCGCTACATACCTCGCTCTGCTAA	1380
QY	6614	TCTGTTTACAGTGGTGTGTCAGTGGCGATAAGTCTGCTTACCGGGTTGGAATCAA	6673
DB	1381	TCTGTTTACAGTGGTGTGTCAGTGGCGATAAGTCTGCTTACCGGGTTGGAATCAA	1440
QY	6674	GACGATAGTTACCGGATAGGCGCAGCGGTGGGCTGAAACGGGGGTTCTGTCACACAGC	6733
DB	1441	GACGATAGTTACCGGATAGGCGCAGCGGTGGGCTGAAACGGGGGTTCTGTCACACAGC	1500
QY	6734	CCAGCTTGGAGCGGAACGACTACCGAACTGAGATACCTACAGCGTGAAGTATGAGAA	6793
DB	1501	CCAGCTTGGAGCGGAACGACTACCGAACTGAGATACCTACAGCGTGAAGTATGAGAA	1560
QY	6794	GGCCACGCTTCCGGAAGGGAGAAAGCGGACAGGTATCCGGTAAAGCGGCGGCTCGGAA	6853
DB	1561	GGCCACGCTTCCGGAAGGGAGAAAGCGGACAGGTATCCGGTAAAGCGGCGGCTCGGAA	1620
QY	6854	CAGGAGCGCAGGAGGAGCTTCCAGGGGAAACCGCTGCTATCTTTATAGTCTGCTGCG	6913
DB	1621	CAGGAGCGCAGGAGGAGCTTCCAGGGGAAACCGCTGCTATCTTTATAGTCTGCTGCG	1680
QY	6914	GGTTTCCGCACTCTGACTTGAAGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	6973
DB	1681	GGTTTCCGCACTCTGACTTGAAGCGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG	1740
QY	6974	TATGGAACCAACCGCAGCAACCGCGCTTTTATACGGTTCTTCTGCGCTTTTCTGCTGCTG	7033

1741 TATGAAAAAGCCAGCAACGGCGCTTTTACGGCTTCTGGCCCTTTTGGCTGGCCCTTTTGG 1800
7034 CTCACATGTTCTTCTCGGTTATCCCTGATCTCTGTGATACCGTATACCGCCCTTTG 7093
1801 CTCACATGTTCTTCTCGGTTATCCCTGATCTCTGTGATACCGTATACCGCCCTTTG 1860
7094 AGTGAGCTGATACCGCTCGCGCAGCCGAAACGACCGAGCGCAGGAGTCAGTGAGCGAGG 7153
1861 AGTGAGCTGATACCGCTCGCGCAGCCGAAACGACCGAGCGCAGGAGTCAGTGAGCGAGG 1920
7154 AAGCGGAAGAGCGCCCAATACGCAACCGCTCTCTCCCGCGCTTGGCCGATTCATTAAT 7213
1921 AAGCGGAAGAGCGCCCAATACGCAACCGCTCTCTCCCGCGCTTGGCCGATTCATTAAT 1980
7214 GCAGCTGGCAGCAGAGTTTCCGACTGGAAGCGGCGAGTCAGGCAACGCAATTAATG 7273
1981 GCAGCTGGCAGCAGAGTTTCCGACTGGAAGCGGCGAGTCAGGCAACGCAATTAATG 2040
7274 TCAGTTTACCTCACTATAGGCACCCAGGCTTTACACTTTATGCTTCCGCTCTCATGT 7333
2041 TGAGTTAGCTCACTATAGGCACCCAGGCTTTACACTTTATGCTTCCGCTCTCATGT 2100
7334 TGTGTGGAATTGTGAGCGGATAACAATTTCAACAGGAAACAGCTATGACCATGATTAACG 7393
2101 TGTGTGGAATTGTGAGCGGATAACAATTTCAACAGGAAACAGCTATGACCATGATTAACG 2160
7394 CAAGCGGCAATTAACCTCACTAAGGGAACAAAGCTGGAGCTC 7440
2161 CAAGCGGCAATTAACCTCACTAAGGGAACAAAGCTGGAGCTC 2207

RESULT 15

US-08-358-928-62

Sequence 62, Application US/08358928

Patent No. 6265183

GENERAL INFORMATION:

APPLICANT: DORNER, Friedrich

APPLICANT: SCHEIFLINGER, Friedrich

APPLICANT: FALKNER, Falko Gunter

APPLICANT: PFLEIDERER, Michael

TITLE OF INVENTION: DIRECT MOLECULAR CLONING OF CHIMERIC

TITLE OF INVENTION: VIRUSES CONTAINING HUMAN IMMUNODEFICIENCY VIRUS TYPE 1

NUMBER OF SEQUENCES: 95

CORRESPONDENCE ADDRESS:

ADDRESS: Foley & Lardner

STREET: 3000 K Street, N.W., Suite 500

CITY: Washington

STATE: D.C.

COUNTRY: USA

ZIP: 20007-5109

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

OPERATING SYSTEM: IBM PC compatible

SOFTWARE: Patent In Release #1.0, Version #1.30

APPLICATION NUMBER: US/08/358,928

FILING DATE:

CLASSIFICATION: 435

APPLICATION NUMBER: US 07/914,738

FILING DATE: 20-JUL-1992

APPLICATION NUMBER: US 07/750,080

FILING DATE: 26-AUG-1991

ATTORNEY/AGENT INFORMATION:

NAME: BENT, Stephen A.

REGISTRATION NUMBER: 29,768

REFERENCE/DOCKET NUMBER: 30472/166/IMMU

TELECOMMUNICATION INFORMATION:

TELEPHONE: (202)672-5300

TELEFAX: (202)672-5399
TELEX: 904136
INFORMATION FOR SEQ ID NO: 62:
SEQUENCE CHARACTERISTICS:
LENGTH: 4145 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: Other nucleic acid;
DESCRIPTION: Synthetic DNA oligonucleotide
IMMEDIATE SOURCE:
CLONE: pS2gpt-S4
US-08-358-928-62

Query Match 28.2%; Score 2203.8; DB 3; Length 4145;

Best Local Similarity 99.9%; Pred. No. 0;

Matches 2203; Conservative 0; Mismatches 2; Indels 0; Gaps 0;

Qy	5234	GTGGCACTTTTCGGGGAAATGTGCGCGAAACCCCTATTGTTTATTTTCTAAATACATT	5293
Db	1	GTGGCACTTTTCGGGGAAATGTGCGCGAAACCCCTATTGTTTATTTTCTAAATACATT	60
Qy	5294	CAAAATATGATCCGCTCATGAGACAATAACCTGATAAATGCTTCAATAATATTGAAAAA	5353
Db	61	CAAAATATGATCCGCTCATGAGACAATAACCTGATAAATGCTTCAATAATATTGAAAAA	120
Qy	5354	GGAAGAGTATGAGTATTTCAACATTTCCGTGTCGCCCTTATTCCTTTTTCGGGCATTTT	5413
Db	121	GGAAGAGTATGAGTATTTCAACATTTCCGTGTCGCCCTTATTCCTTTTTCGGGCATTTT	180
Qy	5414	GCCTTCCTGTTTGTCTCACCCGAAACGCTGTGTAAGTAAAGATGCTGGAAGATCAGT	5473
Db	181	GCCTTCCTGTTTGTCTCACCCGAAACGCTGTGTAAGTAAAGATGCTGGAAGATCAGT	240
Qy	5474	TGGTGCAAGTGGTGTATCATGAACTGATCTCAACAGCGGTAAAGATCCTTGAGAGTT	5533
Db	241	TGGTGCAAGTGGTGTATCATGAACTGATCTCAACAGCGGTAAAGATCCTTGAGAGTT	300
Qy	5534	TTGCGCCCGAAGACGTTTTCATGATGAGCACTTTTAAAGTTCTGCTATGTGCGCGG	5593
Db	301	TTGCGCCCGAAGACGTTTTCATGATGAGCACTTTTAAAGTTCTGCTATGTGCGCGG	360
Qy	5594	TATTATCCGTTATGACGCGCGCAAGAGCAACTCGTTCGCGCATACACTATTCTCAGA	5653
Db	361	TATTATCCGTTATGACGCGCGCAAGAGCAACTCGTTCGCGCATACACTATTCTCAGA	420
Qy	5654	ATGACTGGTTGAGTACTCACCAGTCACAGAAAGATCTTACGGATGGCATGACAGTAA	5713
Db	421	ATGACTGGTTGAGTACTCACCAGTCACAGAAAGATCTTACGGATGGCATGACAGTAA	480
Qy	5714	GAGAAATATGCGTGTCCATACCATGATTAACACTGCGGCCCACTTACTTCTGA	5773
Db	481	GAGAAATATGCGTGTCCATACCATGATTAACACTGCGGCCCACTTACTTCTGA	540
Qy	5774	CAACGATCGGAGGACCGAAGAGCTAACCGCTTTTTCACAAACATGGGGATCATGTAA	5833
Db	541	CAACGATCGGAGGACCGAAGAGCTAACCGCTTTTTCACAAACATGGGGATCATGTAA	600
Qy	5834	CTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGCGTGACA	5893
Db	601	CTCGCCTTGATCGTTGGGAACCGGAGCTGAATGAAGCCATACCAACGACGCGTGACA	660
Qy	5894	CCAGATGCGCTGTAGCAATGGCAACAGTTTTCGCAAACTATTAACTGCGCAACTACTTA	5953
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RESULT 3

US-10-067-449-15
; Sequence 15, Application US/10067449
; Publication No. US20030166258A1
; GENERAL INFORMATION:
; APPLICANT: Muller, Gunter
; APPLICANT: Koller, Klaus-Peter
; APPLICANT: Boles, Eckhard
; APPLICANT: Wieszorke, Roman
; APPLICANT: Dlugai, Silke
; TITLE OF INVENTION: Saccharomyces cerevisiae Yeast Strain With Functional Expression
; FILE OF INVENTION: GLUT Promoter
; FILE REFERENCE: DEAV2001/00002
; CURRENT APPLICATION NUMBER: US/10/067,449
; CURRENT FILING DATE: 2002-02-05
; PRIOR APPLICATION NUMBER: DE 101 06 718.6
; PRIOR FILING DATE: 2001-02-14
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 15
; LENGTH: 6360
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Vector
US-10-067-449-15

Query Match 75.5%; Score 5908; DB 15; Length 6360;

Best Local Similarity 100.0%; Pred. No. 0;
Matches 5908; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 2012 CGACGCGCTGTAGCGCGCATTAAGCGCGCGGTGTGGTGTACGGGAGCGTGAC 2071
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QY 815 AGCGGAGGGTTCGAAACAGGAGAGCGACAGGGAGCTTCCAGGGCGGAAACCGCTGCTAT 756
DB |||||
QY 6898 CTTTATAGTCTGTGCGGTTCGCCACTCTGACTTGAGCGTTCGATTTTGTGATGCTCG 6957
DB |||||
QY 755 CTTTATAGTCTGTGCGGTTCGCCACTCTGACTTGAGCGTTCGATTTTGTGATGCTCG 696
DB |||||
QY 6958 TCAGGGGGCGGAGCCCTATGGAATAACCGCAGCAACCGCGCTTTTACGTTTCTGGCC 7017
DB |||||
QY 695 TCAGGGGGCGGAGCCCTATGGAATAACCGCAGCAACCGCGCTTTTACGTTTCTGGCC 636
DB |||||
QY 7018 TTTTGTGCGCTTTTGTCTCATGTTCTTCTCGCTTATCCCTGATTTCTGTGATTAAC 7077
DB |||||
QY 635 TTTTGTGCGCTTTTGTCTCATGTTCTTCTCGGTATCCCTGATTTCCCTGATTTCTGTGATTAAC 576
DB |||||
QY 7078 CGTATTACCGCTTTTGTGATGAGCTGATACCGCTCGCGCGAACCGGAAACGACCGGCGGAT 7137
DB |||||

Db 575 CGTATTACCGCCCTTTGAGTGAGCTGATACCGCTCGCGCAGCGAAGCAGCGGCGCAGC 516
QY 7138 GAGTCAGTCAGCGAGGAGCGGAGGAGCGCCCAATACGCAAAACCGCTCTCTCCCGCGCGGT 7197
Db 515 GAGTCAGTCAGCGAGGAGCGGAGGAGCGCCCAATACGCAAAACCGCTCTCTCCCGCGCGGT 456
QY 7198 TGCGCGGCTCATTAATGTCAGTCGCGCAGCAGCAGGTTTCCCGACCTGGAAGCGGCGCAGTGAG 7257
Db 455 TGCGCGGCTCATTAATGTCAGTCGCGCAGCAGCAGGTTTCCCGACCTGGAAGCGGCGCAGTGAG 396
QY 7258 CGCAACGCAATTAATGTCAGTCGCGCAGCAGCAGGTTTCCCGACCTGGAAGCGGCGCAGTGAG 7317
Db 395 CGCAACGCAATTAATGTCAGTCGCGCAGCAGCAGGTTTCCCGACCTGGAAGCGGCGCAGTGAG 336
QY 7318 CTTCGCGCTCTATGTTGTGTGGAATGTCAGCGGAGTAACAATTTTACACAGGAAACAGC 7377
Db 335 CTTCGCGCTCTATGTTGTGTGGAATGTCAGCGGAGTAACAATTTTACACAGGAAACAGC 276
QY 7378 TATGACCATGATTACGCCAAGCGCGCA 7404
Db 275 TATGACCATGATTACGCCAAGCTTGCA 249

RESULT 5

US-09-945-917-28/c
; Sequence 28, Application US/09945917
; Publication No. US20030042381A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; APPLICANT: Vandekerckhove, Joel
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/945,917
; CURRENT FILING DATE: 1998-09-21
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 10288
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc feature
; LOCATION: (8456)
; OTHER INFORMATION: "N is A, C, G, or T"
; OTHER INFORMATION: Description of Artificial Sequence: artificial
; OTHER INFORMATION: plasmid
US-09-945-917-28

Query Match 57.4%; Score 4492.6; DB 10; Length 10288;
Best Local Similarity 87.3%; Pred. No. 0;
Matches 5104; Conservative 0; Mismatches 629; Indels 114; Gaps 12;
QY 1559 TCATGTAATAGTATGTCAGCGCTACATTCAGCCCTCCGCCACATCGGCTCTAACCG 1618
Db 7878 TCATGTAATAGTATGTCAGCGCTACATTCAGCCCTCCGCCACATCGGCTCTAACCG 7819
QY 1619 AAAAGGAAGGAGTTAGACAACTGAACTGAGTCTAGGTCCTATTTATTTTATATGTTATGT 1678
Db 7818 AAAAGGAAGGAGTTAGACAACTGAACTGAGTCTAGGTCCTATTTATTTTATATGTTATGT 7759
QY 1679 TAGTATTAGAACGTTATTATATTATTTTCAATTTTCTTTTCTTTCTGTACAGCGGCTGT 1738
Db 7758 TAGTATTAGAACGTTATTATATTATTTTCAATTTTCTTTTCTTTCTGTACAGCGGCTGT 7699
QY 1739 AGCGATGTAACATTTATCTAGTAACCTTGCTTGAGAGGTTTGGGACGCTCGAGGCTT 1798
Db 7698 AGCGATGTAACATTTATCTAGTAACCTTGCTTGAGAGGTTTGGGACGCTCGAGGCTT 7639
QY 1799 TAATTTGCGCGGAGTACCAATTCGCCCTATAGTGAGTCGTATTACGCGGCTCACTGGC 1858

Db 7638 TAAATTTG-----CAAAGCTCGGATCTCGAGCTCGCGAAAGCTTGGACGACTGGC 7589
QY 1859 CGTCTGTTTACAAAGCTGTCGACCTGGGAAAACCTTCGCTTACCAACTTAATCGCCTTGC 1918
Db 7588 CGTCTGTTTACAAAGCTGTCGACCTGGGAAAACCTTCGCTTACCAACTTAATCGCCTTGC 7529
QY 1919 AGCACATCCCCCTTTTCGCGAGCTGGCGTAAATAGCGAAGAGGCCCGCACCGATCGCCCTTC 1978
Db 7528 AGCACATCCCCCTTTTCGCGAGCTGGCGTAAATAGCGAAGAGGCCCGCACCGATCGCCCTTC 7469
QY 1979 CCNACAGTTGCGCAGCTGAAATGGCGGAAATGGCGGAGCGCCCTGTAGCGGCGCATTAAG 2038
Db 7468 CCNACAGTTGCGCAGCTGAAATGGCGGAAATGGCGGAGCGCCCTGTAGCGGCGCATTAAG 7409
QY 2039 CGCGGCGGCTGTGCTGCTTACCGCAGCTGACCGCTACACTTGGCAGCGCCCTAGCGCC 2098
Db 7408 CGCGGCGGCTGTGCTGCTTACCGCAGCTGACCGCTACACTTGGCAGCGCCCTAGCGCC 7349
QY 2099 CGCTCCCTTTTCGCTTTCTTCCCTTCTCGCAGCTTCGCGGCTTTTCCCGTCAAGC 2158
Db 7348 CGCTCCCTTTTCGCTTTCTTCCCTTCTCGCAGCTTCGCGGCTTTTCCCGTCAAGC 7289
QY 2159 TCTAAATCGGGGCTCCCTTTTAGGGTTCCGATTTAGTGTCTTACGGCAGCTCGACCCCAA 2218
Db 7288 TCTAAATCGGGGCTCCCTTTTAGGGTTCCGATTTAGTGTCTTACGGCAGCTCGACCCCAA 7229
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Db 7228 AAAACTTGATAGGGTGATGTTTACAGTAGTGGCCCATCGCCCTGATAGACGGTTTTTCG 7169
QY 2279 CCCTTTGAGCTTGGAGTCCACGCTTCTTAAATAGTGGACTTCTTGTCCAAATCGAAACAAC 2338
Db 7168 CCCTTTGAGCTTGGAGTCCACGCTTCTTAAATAGTGGACTTCTTGTCCAAATCGAAACAAC 7109
QY 2339 ACTCAACCTTCTCGTCTATTTCTTTGATTTAAGGGAATTTTCGCGGATTTTCGGGCTA 2398
Db 7108 ACTCAACCTTCTCGTCTATTTCTTTTGAATTTAAGGGAATTTTCGCGGATTTTCGGGCTA 7049
QY 2399 TTGGTTAAAAAATGAGCTGATTTTAAACAAATTTTAAACGGAATTTTAAACAAATATTAAAC 2458
Db 7048 TTGGTTAAAAAATGAGCTGATTTTAAACAAATTTTAAACGGAATTTTAAACAAATATTAAAC 6989
QY 2459 GTTTACAAATTTCTGATGCGGTATTTTCTCTTACGATCTGTGCGGTATTTTACACCGC 2518
Db 6988 GTTTACAAATTTCTGATGCGGTATTTTCTCTTACGATCTGTGCGGTATTTTACACCGC 6929
QY 2519 ATAGGTAATACTGATATAATTAATGAACTCTAAATTTGAGTGTAGTATAGTATG 2578
Db 6928 ATAGATCGGCAAGTGCAACAATACTTAAATAAATACTACTCAGTAATAAATCTATTTTC 6869
QY 2579 ATTTACTTATAATACAGTTTATTTTGTGCGCGCATCTTCTCAATATGCTTCCCA 2638
Db 6868 TTAGCATTTTGTACGAAATTTGCTATTTTGTAGAGTCTTTTACACATTTTGTCTCACA 6809
QY 2639 GCGTCTTTCTGTAACTTACCGTTCACCTCTACTTAGCATCCCTTCCCTTTGCAATAGTCC 2698
Db 6808 CTTCCGCTTACATCAAC-----ACCAATTAACGC 6781
QY 2699 TCTTCCAAACAATAATATCTCAGATCTCTGAGAGCAATCAATCATCAAGGTTCTATAGT 2758
Db 6780 CATTTAATCTAAGCGCATCAACAATTTTCTGCGCTCAGTCCACGAGCTTAACATAAAT 6721
QY 2759 TTGACCAATGCTCTCCCTTGTCTATCTAAACCCACCGGCTGTATTAATCAACCAATC 2818
Db 6720 GTAAGCTTTGGGGGCTCTCTTGGCTT-----CAACCCAGTCAAGAAATCGAGTTCCAATC 6666
QY 2819 GTAACCTTCTCATCTCTTCCACCCATGCTCTTTGAGCAATAAAGCCGATCAACAAATCTTT 2878
Db 6665 CAAAAGTTTCACTGTCTCCAC-----CTGCTTCTGAATCAACAAGGAAATAACGAATG 6612
QY 2879 GTGCGCTTTCGCAATGTCACAGTACCTTATGATTTTCTCCAGTAGATAGGAGGCCCTT 2938

Db 6611 AGTTTCTGTGAAGCTGCACGTGAGTAGTATGTTGAGTCTTTTGGAAATACGAGTCTTTT 6552
Qy 2939 GCATGACAAATTCGTCTACATCAAAAGCCCTAGGTTCCCTTTGTTACTTCTTCTGCGC 2998
Db 6551 -----AATAACTGGCAAAACCGAGAACTCTTGGTATCTTGCCACGACTCAATCTCCA 6500
Qy 2999 CTGCTTTCAAACCGCTAAACAATACCTTGGGCCCAACACACACCGTGTGCATTCGTAAATGTCG 3058
Db 6499 TGCAGT-----TGGAGATATCAATGTCCTTAATCATTTGACGAGAGCCAAACATCCTC 6447
Qy 3059 CCAATTCGTCTATTCGTATATACCCGAGAGTACTGCAATTTGATTTGATATTAACCAATGTC 3118
Db 6446 CTTAGGTTGATTAAGAAACAGCCCAACCAAGTATTTGGAGTGGCTGAACTATTTTTATA 6387
Qy 3119 AGCAAAATTTCTGTCTTCGAGAGTGAAGAAATTTGATTTGGCGGATATGCTTTAGCGG 3178
Db 6386 TG-----CTTTTCAAGACTTTGAAATTTCTCTGCAATTAACCGGGTCAATTTGT 6339
Qy 3179 CTTAACTGTGCCCTCCATGGGAAATCAGTCAAGATATCCAATGTTGTTTTAGTAAACA 3238
Db 6338 TCTCTTTCTATTTGGGCACACATATAATACCAGCAAGTCAGCATCGGAACTAG--AGCA 6281
Qy 3239 AATTTGGAGCTAATGCTTCAACTTACTCCAGTAAATTCCTTGGTGTGAC-GAACAATCCA 3297
Db 6280 CATTCTCGGGCTCTGTCTCTGCAAGCGGCAAACTTTCAACAATGGACAGAACTACCT 6221
Qy 3298 ATGAAGCACACAAGTTTGTCTTTCGTCATGATATTAATAGCTTGGCAGCAACAG 3357
Db 6220 GTGAAATTAATAACAGACATACTCCAAGCTGCCCTTGTGTGCTTAATCAAGTATACTAC 6161
Qy 3358 GACTAGGATGAGTAGCAGCAGTTCCTTATATGATGCTTTCGACATGATTTATCTTCGTT 3417
Db 6160 GTGCTCAATAGTCACCAATGCCCTCCCTCTTGGCCCTCTCC-----TTTTCCTT 6112
Qy 3418 TCCTCAGGTTTGTCTGTGCAATTTGAAAGTGTGGTAAAGATPACTGGGCAATTCATGTTCTT 3477
Db 6111 TTTGACCGAATTAATTTCTTAATCGGCAAAAAAGAAAGCTCCGGA-----T 6064
Qy 3478 GAACACTACATATGCTATATATACCAATCTAAGTCTGTGCTCCTTCTTCTGTTCTTCT 3537
Db 6063 CAAGATTGACGAAGTGACAAAGTATATTTTCAATAAAGAAATATCTTCCACTACTGCCA 6004
Qy 3538 TCTGTTTCGGAGATTACCGAATCAAAAAATTTCAAAGAAACCGAAATCAAAAAAAGAAT 3597
Db 6003 TCTGGCGTCATAACTGCAAGTACACATATTA-----CGATGCTGTCTATTAAAT 5952
Qy 3598 AAAAAAATGATGAATTTGAATTTGAAAGTGTGGTATGTTGTCATCTCTCAGTACAATCT 3657
Db 5951 GCTTCTATATATATATATAGTATGTCGTTGATCTATGTTGCACTCTCAGTACAATCT 5892
Qy 3658 GCTCTGATGCCGATAGTTAGCCAGCCCGCACACCCGCCAACCCGCTGACCGGCCCT 3717
Db 5891 GCTCTGATGCCGATAGTTAAGCCAGCCCGCACACCCGCCAACCCGCTGACCGGCCCT 5832
Qy 3718 GACGGGCTTGTCTGCTCCGGCATCCGCTTACAGCAAGCTGTGACCGCTCTCCGGGAGCT 3777
Db 5831 GACGGGCTTGTCTGCTCCGGCATCCGCTTACAGCAAGCTGTGACCGCTCTCCGGGAGCT 5772
Qy 3778 GCATGTGTCAGAGTTTTCACCGTCAATCACCGAAACCGCGAGACGAAAGGGCTCTGTGA 3837
Db 5771 GCATGTGTCAGAGTTTTCACCGTCAATCACCGAAACCGCGAGACGAAAGGGCTCTGTGA 5712
Qy 3838 TAGGCTATTTTATAGTTAATGTCATGATATTAATGTTTCTTAGTATGATCCAATAT 3897
Db 5711 TAGGCTATTTTATAGTTAATGTCATGATATTAATGTTTCTTAGTATGATCCAATAT 5652
Qy 3898 CAAAGGAATGATAGCATTTGAAGATGAGACTTAATCCAAATTTGAGAGTGGCAGCATATAG 3957
Db 5651 CAAAGGAATGATAGCATTTGAAGATGAGACTTAATCCAAATTTGAGAGTGGCAGCATATAG 5592
Qy 3958 AACAGCTAAGGGTATGCTGAAGGAAGCATACGATACCCCGCATGGAAATGGGATATAT 4017
Db 5591 AACAGCTAAGGGTATGCTGAAGGAAGCATACGATACCCCGCATGGAAATGGGATATAT 5532

Qy 4018 CACAGGAGTACTAGACTACCTTTTCTTCCCTACATAAATAGACGCATATAAGTAGCAATTT 4077
Db 5531 CACAGGAGTACTAGACTACCTTTTCTTCCCTACATAAATAGACGCATATAAGTAGCAATTT 5472
Qy 4078 AAGCATAAACACGCACTATGTCGCTTCTTCTCATGTATATATATATACAGGCAACACGAG 4137
Db 5471 AAGCATAAACACGCACTATGTCGCTTCTTCTCATGTATATATATATACAGGCAACACGAG 5412
Qy 4138 ATATAGTGCAGCTGNAACAGTGAAGTGTATGTCGAGCTCGCGTTCGCAATTTTCGGAG 4197
Db 5411 ATATAGTGCAGCTGNAACAGTGAAGTGTATGTCGAGCTCGCGTTCGCAATTTTCGGAG 5352
Qy 4198 CGCTCGTTTTCGGAACCGCTTTCGAAGTTCCTATTTCCGAAGTTCCTATTTCTAGAAAAT 4257
Db 5351 CGCTCGTTTTCGGAACCGCTTTCGAAGTTCCTATTTCCGAAGTTCCTATTTCTAGAAAAT 5292
Qy 4258 TAGGAATCTCAGAGCGCTTTTGAACCAAAAGCGCTCTGAAGACGCACTTTTCAAAAAAC 4317
Db 5291 TAGGAATCTCAGAGCGCTTTTGAACCAAAAGCGCTCTGAAGACGCACTTTTCAAAAAAC 5232
Qy 4318 CAAAACGCAACGCACTGTAAACGAGCTACTAAATATTTGGAATACCGCTTCCACAAACA 4377
Db 5231 CAAAACGCAACGCACTGTAAACGAGCTACTAAATATTTGGAATACCGCTTCCACAAACA 5172
Qy 4378 TTGCTCAAAAAGTATCTTTTGTCTATATATCTCTGTGCTATATCTCTATATATAACCTACCCA 4437
Db 5171 TTGCTCAAAAAGTATCTTTTGTCTATATATCTCTGTGCTATATCTCTATATAACCTACCCA 5112
Qy 4438 TCACCTTTTCGCTCTTGAACCTTGCACTCTAAACCTCGACCTCTACATTTTATGTTATC 4497
Db 5111 TCACCTTTTCGCTCTTGAACCTTGCACTCTAAACCTCGACCTCTACATTTTATGTTATC 5052
Qy 4498 TCTAGTATTAATCTTTTAGACAAAATAATTTAGTAAAGCACTTTCATAGAGTGAATCGAA 4557
Db 5051 TCTAGTATTAATCTTTTAGACAAAATAATTTAGTAAAGCACTTTCATAGAGTGAATCGAA 4992
Qy 4558 AACAACTAGCAAAATGTAAACATTTCTTATAGTATATAGAGCAAAAATAGAGAANAAC 4617
Db 4991 AACAACTAGCAAAATGTAAACATTTCTTATAGTATATAGAGCAAAAATAGAGAANAAC 4932
Qy 4618 CGTTCATAATTTCTGACCAATGAAGAAATCATCAACGCTATCACTTTCTGTTCAAAAGT 4677
Db 4931 CGTTCATAATTTCTGACCAATGAAGAAATCATCAACGCTATCACTTTCTGTTCAAAAGT 4872
Qy 4678 ATGGCAATCCATCGGTATAGAAATATATCGGGATGCTTTATCTTTGAAAAATGCA 4737
Db 4871 ATGGCAATCCATCGGTATAGAAATATATCGGGATGCTTTATCTTTGAAAAATGCA 4812
Qy 4738 CCGGCACTTCGCTAGTAATCAGTAAACCGGGAGTGGAGTCAAGCTTTTATATGGA 4797
Db 4811 CCGGCACTTCGCTAGTAATCAGTAAACCGGGAGTGGAGTCAAGCTTTTATATGGA 4752
Qy 4798 GAGAAATAGACACAAAGTAGCCTTCTTAACTTAAACGCACTACAGTGCAAAAGT 4857
Db 4751 GAGAAATAGACACAAAGTAGCCTTCTTAACTTAAACGCACTACAGTGCAAAAGT 4692
Qy 4858 TATCAAGAGTGCATTTATAGCGCACAAAGAGAGAAAAGTAATCTTAGATGCTTTG 4917
Db 4691 TATCAAGAGTGCATTTATAGCGCACAAAGAGAGAAAAGTAATCTTAGATGCTTTG 4632
Qy 4918 TTAGAAAAATAGCGCTCTCGGGATGCAATTTTGTAGAACAAAAAGAGATATAGATTTCT 4977
Db 4631 TTAGAAAAATAGCGCTCTCGGGATGCAATTTTGTAGAACAAAAAGAGATATAGATTTCT 4572
Qy 4978 TGTGTTAAATAGCGCTCTCGCGTTGCAATTTCTGTTCTGTAAATAATCAGCTCAGATTC 5037
Db 4571 TGTGTTAAATAGCGCTCTCGCGTTGCAATTTCTGTTCTGTAAATAATCAGCTCAGATTC 4512
Qy 5038 TTTGTTGAAAAATTAGCGCTCTCGCGTTGCAATTTTCTGTTCTGTAAATAATCAGCTCAGATTC 5097
Db 4511 TTTGTTGAAAAATTAGCGCTCTCGCGTTGCAATTTTCTGTTCTGTAAATAATCAGCTCAGATTC 4452

Db 2291 CGCAACGCAATTAATGTGAGTTACCTCACTACTAGGACCCAGGCTTTTACATTTATG 2232
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Db 2231 CTTCCGGCTCTATCTGTGTGAAATGTGACGGGATTAACAATTTACACAGGAAACAGC 2172
Qy 7378 TATGACCATGATTACGCCAAGCGCGCA 7404
Db 2171 TATGACCATGATTACGCCAAGCTTGCA 2145

RESULT 6
US-09-845-917A-28/c
; Sequence 28, Application US/09845917A
; Publication No. US20030167538A1
; GENERAL INFORMATION:
; APPLICANT: Bogaert, Thierry
; INVENTOR: Vandekerckhove, Joël
; TITLE OF INVENTION: PROCESSES FOR THE IDENTIFICATION OF COMPOUNDS WHICH
; TITLE OF INVENTION: CONTROL CELL BEHAVIOUR, THE COMPOUNDS IDENTIFIED AND
; TITLE OF INVENTION: PHARMACEUTICAL COMPOSITIONS CONTAINING THEM AND THEIR
; TITLE OF INVENTION: USE IN THE CONTROL OF CELL BEHAVIOUR
; FILE REFERENCE: P/14-1
; CURRENT APPLICATION NUMBER: US/09/845,917A
; CURRENT FILING DATE: 2001-04-30
; NUMBER OF SEQ ID NOS: 58
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 28
; LENGTH: 10288
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; NAME/KEY: misc-feature
; LOCATION: (8456)
; OTHER INFORMATION: "N is A, C, G, or T"
; OTHER INFORMATION: Description of Artificial Sequence: artificial
; OTHER INFORMATION: plasmid
US-09-845-917A-28

Query Match 57.4%; Score 4492.6; DB 10; Length 10288;
Best Local Similarity 87.3%; Pred. No. 0;
Matches 5104; Conservative 0; Mismatches 629; Indels 114; Gaps 12;

Qy 1559 TCATCTAATAGTATGTCAGCTTACATTCACGCCCTCCGCCACATCCGCTCTAACCG 1618
Db 7878 TCATCTAATAGTATGTCAGCTTACATTCACGCCCTCCGCCACATCCGCTCTAACCG 7819
Qy 1619 AAAAGGAAGGATTAGACAACTGAGTCTAGGTCCTCTATTTATTTTATAGTTATGT 1678
Db 7818 AAAAGGAAGGATTAGACAACTGAGTCTAGGTCCTCTATTTATTTTATAGTTATGT 7759
Qy 1679 TAGTATTAGAACGTTATTTATTTTAAATTTTCTTTTCTTTTCTGTACAGACGGTGT 1738
Db 7758 TAGTATTAGAACGTTATTTATTTTAAATTTTCTTTTCTTTTCTGTACAGACGGTGT 7699
Qy 1739 AGCATGTACATTTATCTGAAACCTTCTGTGAGAGTTTGGAGCTCTGAGGCTT 1798
Db 7698 AGCATGTACATTTATCTGAAACCTTCTGTGAGAGTTTGGAGCTCTGAGGCTT 7639
Qy 1799 TAAATTGGCGCGGTACCAATTTCCGCTATAGTGTGAGTCTGATACGGCGCTCACTGGC 1858
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Qy 1859 CCGTCTTTTACAACTCGTGTGACTGGGAAACCTTGGCGTTTACCAACTTAATCGCCTTGC 1918
Db 7588 CCGTCTTTTACAACTCGTGTGACTGGGAAACCTTGGCGTTTACCAACTTAATCGCCTTGC 7529
Qy 1919 AGCATATCCCTTTTCCGCTGCTGAGTAAATAGAGAGCGCGCCGATCCGCTTTC 1978
Db 7528 AGCATATCCCTTTTCCGCTGCTGAGTAAATAGAGAGCGCGCCGATCCGCTTTC 7469
Qy 1979 CCAACAGTTGCGCAGCTGAATGGCGAATGGCGGACGCGCCCTGTAGCGGCGCATTAAG 2038

Db 7468 CCAACAGTTGCGCAGCTGAATGGCGAATGGCGGACGCGCCCTGTAGCGGCGCATTAAG 7409
Qy 2039 CGCGGCGGCTGTGTGTGTAGCGGACGCTGACCGCTACACTTTCGACGCGCTTAGCGCC 2098
Db 7408 CGCGGCGGCTGTGTGTGTGTAGCGGACGCTGACCGCTACACTTTCGACGCGCTTAGCGCC 7349
Qy 2099 CGCTCCTTTTCGCTTTTCTTCCCTTTCGCGCACGTTTCGCGCGCTTTTCCCGCTCAAGC 2158
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Qy 2159 TCTAAATCGGGGCTCCTCTTTAGGGTTCCGATTTAGTGTCTTTAGCGACCTCGACCCCAA 2218
Db 7288 TCTAAATCGGGGCTCCTCTTTAGGGTTCCGATTTAGTGTCTTTAGCGACCTCGACCCCAA 7229
Qy 2219 AAAAATTGATTAGGTTGATGTTCACTAGTGGGCCATCGCCCTGATAGAGCGTTTTCG 2278
Db 7228 AAAAATTGATTAGGTTGATGTTCACTAGTGGGCCATCGCCCTGATAGAGCGTTTTCG 7169
Qy 2279 CCCTTTCAGCTTGGAGTCCACGTTCTTTAATAGTGGACTTTGTTCCAAACCTGGAAACAC 2338
Db 7168 CCCTTTCAGCTTGGAGTCCACGTTCTTTAATAGTGGACTTTGTTCCAAACCTGGAAACAC 7109
Qy 2339 ACTCAACCTTATCTCGGTCTATTCTTTTGAATTTAAGGGAATTTTCCGATTTCCGCTTA 2398
Db 7108 ACTCAACCTTATCTCGGTCTATTCTTTTGAATTTAAGGGAATTTTCCGATTTCCGCTTA 7049
Qy 2399 TTGGTTAAAAATGAGCTGATTTAAACAAATTTTAAACGCGAATTTTAAACAAATTTAAC 2458
Db 7048 TTGGTTAAAAATGAGCTGATTTAAACAAATTTTAAACGCGAATTTTAAACAAATTTAAC 6989
Qy 2459 GTTTTACAAATTTCTGATGCGGTATTTCTCTTACGATCTGTGCGGTATTTTACACCGC 2518
Db 6988 GTTTTACAAATTTCTGATGCGGTATTTCTCTTACGATCTGTGCGGTATTTTACACCGC 6929
Qy 2519 ATAGGTPAATACTGATATTAATAATTAAGAGTCTTAATTTGTGAGTTTGTATGATG 2578
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Qy 2579 ATTTTACTTATAATACAGTTTGTAGTTTGTGCGCGCATCTTCTCAATATGCTTCCCA 2638
Db 6868 TTAGCATTTTGTAGGAAATTTGCTATTTTGTAGAGTCTTTTACACCATTTGTCTCCACA 6809
Qy 2639 GCCTGCTTTTCTGTAAGCTTTCACCTCTACCTTAGCATCCCTTCCCTTTGCAAAATAGTCC 2698
Db 6808 CCTCCGCTTACATCAAC-----ACCAATAACGC 6781
Qy 2699 TCTTCCAACTAATAATAGTCAGATCTCTGTAGAGACCATCATCTCCAGGTTCTATCTG 2758
Db 6780 CATTTAATCTAAGCGCATCAACCAATTTCTGCGGTGAGTCCACAGCTAATAAAT 6721
Qy 2759 TTGACCAATGCGTCTCCCTGTGATCTTAACCCACACCGGCTGTCTATAATCAACCAATC 2818
Db 6720 GTAAGCTTTTGGGGCTCTTTCGCTT-----CCAAACCCAGTCAAGAAATCGAGTCCAAATC 6666
Qy 2819 GTAACCTTCTCTTCCACCATGCTCTCTTTGAGCAATAAAGCCGATAAATAAATCTTT 2878
Db 6665 CAAAGTTTCACTGTCCAC-----CTGCTTCTGAATCAAAAGGGAATAAAGAAATG 6612
Qy 2879 GTGCTCTTTCCGAAATGCAACAGTACCTTTAGTATATTTCTCAAGTATAGAGAGGCTTT 2938
Db 6611 AGGTTTCTGTGAAGCTGACGTAGTATGTTGCACTCTTTTGGAAATACAGAGTCTTTT 6552
Qy 2939 GCATGCAATTTCTGCTAACAACGAGCTTCTAGGTTCTTCTTCTTCTTCTTCTTCTGCGC 2998
Db 6551 -----AATACTGGCAACCGAGGAATCTTTGGTATTTCTTGGCAGACTCATCTCCA 6500
Qy 2999 CTGCTTCAAAACCGCTAACAATACCTGGGCCCAACACACCGGTGTGATTCGTAATGTCTGC 3058
Db 6499 TGCAGT-----TGGAGGATATCAATGCGCGTAAATCATTTGACAGAGCCAAACATCTCTC 6447
Qy 3059 CCATTTCTGCTATTCTGTATACACCGGAGAGTACTGCAATTTGACTGTATTTACCAATGTC 3118

Db 6446 CTTAGGTTGATTACGAAACAGCCACCAAGTATTTTCGGAGTGCCTGAACTATTTTATA 6387
Qy 3119 AGCAAAATTTCTGTCTTGAAGAGTAAAAATTTGTACTTGGCGGATAATGCGCTTTAGCGG 3178
Db 6386 TG-----CTTTTACAAGACTTGAAATTTTCTTGTCAATAAACCGGGTCAATTGT 6339
Qy 3179 CTTAACTGTGCCCTCCATGGAAAAATCAGTCAAGATATCCACATGTGTTTTAGTAACA 3238
Db 6338 TCTCTTTCTATTGGGCACACATATAATACCAGCAAGTCAGCATCGGAATCTAG--AGCA 6281
Qy 3239 AATTTTGGGACCTAAATGCTTCAACTAACTCCAGTAATTCCTGGTGTAC-GAACAATCCA 3297
Db 6280 CATCTCGGGCTCTGTCTCTGCAAGCCGCAACTTTCACCAATGGACGAGAACTACCT 6221
Qy 3298 ATGAAGCACACAAGTTGTTGTTTTGTTGTCATGATATTAATATGCTTGGCAGCAACAG 3357
Db 6220 GTGAAATTAATAACAGACATACTCCAAAGTGCCTTTGTGTGCTTAATCAGTATACTAC 6161
Qy 3358 GACTAGATGAGTAGCAGCAGCTTCTTATATGTAGCTTTCGACATGATTTATCTCGTT 3417
Db 6160 GTGCTCAATAGTACCAAATGCCCTCCCTCTTGGCCCTCTCC-----TTTTCTTT 6112
Qy 3418 TCTGTGAGGTTTTGTTCTGTGAGTTGGTTAAGAAATCTGGGCAATTTTCATGTTTCTT 3477
Db 6111 TTTTCGACCAATTAATTTCTTAATCGGCAAAAAGAAAGCTCCGA-----T 6064
Qy 3478 CAACACTACATATGCGTATATATACCAATCTAAGTCTGTGCTCTTCTTCTGTTCTCT 3537
Db 6063 CAAGATTGTACGTAAGTGACAGCTATTTTCAATAAAGAAATATCTTCCACTACTGCCA 6004
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RESULT 7

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; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 27
; LENGTH: 13414
; TYPE: DNA
; ORGANISM: Artificial Sequence
; NAME/KEY: misc feature
; LOCATION: (11582)
; OTHER INFORMATION: "N is A, G, C or T"
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: artificial
; OTHER INFORMATION: plasmid
US-09-845-917A-27

Query Match      57.4%; Score 4492.6; DB 10; Length 13414;
Best Local Similarity 87.3%; Pred. No. 0;
Matches 5104; Conservative 0; Mismatches 629; Indels 114; Gaps 12;

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RESULT 9

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; Sequence 31, Application US/09758036

; Publication No. US20030190693A1

; GENERAL INFORMATION:

; APPLICANT: LEBERER, Ekkehard

; APPLICANT: LEEUW, Thomas

; APPLICANT: RITSCHER, Allegra

; TITLE OF INVENTION: POTASSIUM CHANNEL MUTANTS OF THE YEAST SACHAROMYCES CEREVISIAE

; TITLE OF INVENTION: USE FOR SCREENING EUKARYOTIC POTASSIUM CHANNELS

; FILE REFERENCE: 38005-0126

; CURRENT APPLICATION NUMBER: US/09/758,036

; CURRENT FILING DATE: 2001-01-11

; PRIOR APPLICATION NUMBER: DE 100 00 651.5

; NUMBER OF SEQ ID NOS: 31

; SOFTWARE: PatentIn version 3.0

; SEQ ID NO 31

; LENGTH: 7772

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-758-036-31

Query Match 46.1%; Score 3610.2; DB 10; Length 7772;

Best Local Similarity 99.8%; Pred. No. 0;

Matches 3626; Conservative 0; Mismatches 8; Indels 1; Gaps 1;

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Qy	CCTTTGTAGTGAATACCGCTCGCGCAGCGCAACGACCGAGCGCAGCGAGTCACTGA	7147
	CCTTTGTAGTGAATACCGCTCGCGCAGCGCAACGACCGAGCGCAGCGAGTCACTGA	8613
	GCGAGGAAGCGGAAGAGGGCCATAGCAAAACCGCTCTCTCCCGCGCGTTGGCCGATTC	7207
Db	GCGAGGAAGCGGAAGAGGGCCATAGCAAAACCGCTCTCTCCCGCGCGTTGGCCGATTC	8553
	ATTAAATCGAGCTGGCAACGACAGGTTTCCCGATCTGGAAAGCGGGCAGTGAGCGCAACGCA	7267
	ATTAAATCGAGCTGGCAACGACAGGTTTCCCGATCTGGAAAGCGGGCAGTGAGCGCAACGCA	8493

Qy	7268	TTAATGTGAGTTACCTCACTCATTAGGCACCCACAGGCTTTTACACTTTATGCTTTCCGGCTC	7327
Db	8492	TTAATGTGAGTTACCTCACTCATTAGGCACCCACAGGCTTTTACACTTTATGCTTTCCGGCTC	8433
Qy	7328	CTATGTTGTGTGGAATTGTGAGCGGATACCAATTTTCCACACAGGAACAGCTATGACCAATG	7387
Db	8432	GTATGTTGTGTGGAATTGTGAGCGGATACCAATTTTCCACACAGGAACAGCTATGACCAATG	8373
Qy	7388	ATTACGCCAAGCGCGCA	7404
Db	8372	ATTACGCCAAGCTTGCA	8356

RESULT 11
 US-10-228-785-9
 ; Sequence 9, Application US/10228785
 ; Publication No. US20030186443A1
 ; GENERAL INFORMATION:
 ; APPLICANT: ANDLID, THOMAS
 ; APPLICANT: VEIDE, JENNY
 ; APPLICANT: SANDBERG, ANN-SOFIE
 ; TITLE OF INVENTION: PHYTASE ACTIVE YEAST
 ; FILE REFERENCE: 6821
 ; CURRENT APPLICATION NUMBER: US/10/228,785
 ; CURRENT FILING DATE: 2002-08-26
 ; PRIOR APPLICATION NUMBER: SE 0200911-6
 ; PRIOR FILING DATE: 2002-03-22
 ; NUMBER OF SEQ ID NOS: 12
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 9
 ; LENGTH: 9210
 ; TYPE: DNA
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Synthetic plasmid
 ; OTHER INFORMATION: pYX212 nucleotide sequence
 US-10-228-785-9

Query Match	42.4%;	Score 3318.6;	DB 15;	Length 9210;	
Best Local Similarity	74.8%;	Pred. No. 0;			
Matches 4787;	Conservative	0;	Mismatches 769;	Indels 847;	Gaps 16;
QY	1851	TCAC	TGCGCGCTGCTTTTACAA	CGTCGTGACTGGGAAACCCCTCGCGTTACCCCAACTTAAT	1910
DB	1095	TCAC	TGCGCGCTGCTTTTACAA	CGTCGTGACTGGGAAACCCCTCGCGTTACCCCAACTTAAT	1154
QY	1911	CGCCTT	GACGACATCCCCCTTTT	CGCCAGCTGCGGTAAATAGCGAAGAGGCCCCGACCCGAT	1970
DB	1155	CGCCTT	GACGACATCCCCCTTTT	CGCCAGCTGCGGTAAATAGCGAAGAGGCCCCGACCCGAT	1214
QY	1971	GGCGCTT	CCCAAAGTGTGGCAGCCTGAAT	TGGCGAATGGCGACGGCCCTGTAGGGCC	2030
DB	1215	GGCGCTT	CCCAAAGTGTGGCAGCCTGAAT	TGGCGAATGGCGACGGCCCTGTAGGGCC	1274
QY	2031	GCATT	AAGCGCGCGGTGTGGTGT	TAGCGCAGCGGTGACCGCTACACTTGCACGGCC	2090
DB	1275	GCATT	AAGCGCGCGGTGTGGTGT	TAGCGCAGCGGTGACCGCTACACTTGCACGGCC	1334
QY	2091	CTAG	CGCGCCGCTCCTTTT	CGGCTTTCTTCCCTTCTTCTTCTGCGCACGTTGCGCGGCTTTCCC	2150
DB	1335	CTAG	CGCGCCGCTCCTTTT	CGGCTTTCTTCCCTTCTTCTTCTGCGCACGTTGCGCGGCTTTCCC	1394
QY	2151	CGTCA	AGCTCTAAATCGGGGGCTCCCTTT	TAGGGTTCCGATTTAGTGTGTTTACGGCACCTC	2210
DB	1395	CGTCA	AGCTCTAAATCGGGGGCTCCCTTT	TAGGGTTCCGATTTAGTGTGTTTACGGCACCTC	1454
QY	2211	GACCC	CAAAAACCTTCATTAGG	TGATGGTTTACAGTAGTGGGCATCGCCCTCATAGACG	2270
DB	1455	GACCC	CAAAAACCTTCATTAGG	TGATGGTTTACAGTAGTGGGCATCGCCCTCATAGACG	1514
QY	2271	GT	TTTTTTCGCCCTTTGAC	GTGTGGAGTCCACGTTCTTTTAATAGTGGACTCTTGTGTTCCAAACT	2330

1515	Db	GT	TTTTTCGCCCTTTGAGCTGGTGGAGTCA	CGTCTCTTTAAATAGTGGAC	CTCTTGTTCCAAACT	1574
2331	Qy	GG	AACAACTCAACCCATCTCGGTCTA	TTCTTTTGATTTATAAGGGA	TTTTTGC	2390
1575	Db	GG	AACAACACTCAACCCATCTCGGTCTA	TTCTTTTGATTTATAAGGGA	TTTTTGC	1634
2391	Qy	TC	GGCCTATTGGTTAAAAATGAGCTGAT	TTAAACAAAATTTAAACGGA	ATTTTAA	2450
1635	Db	TC	GGCCTATTGGTTAAAAATGAGCTGAT	TTAAACAAAATTTAAACGGA	ATTTTAA	1694
2451	Qy	AT	ATTAAAGGTTTAAATTTCTGATCGGT	ATATTTCTCTTACGCACTGTGCGGT	ATATTT	2510
1695	Db	AT	ATTAAAGGTTTAAATTTCTGATCGGT	ATATTTCTCTTACGCACTGTGCGGT	ATATTT	1754
2511	Qy	CACA	CCGATAGGGTAAATACTGATATAA	TTAAATTTGAAGCTCTAAATTTGT	AGATTTAGT	2570
1755	Db	CACA	CCGATAGGGTAAATACTGATATAA	TTAAATTTGAAGCTCTAAATTTGT	AGATTTAGT	1814
2571	Qy	AT	CATGCAATTTACTTTAATACAGTTTT	TTTTTTAGTTTTGCTGGCGG	CAATCTTCTCA	2630
1815	Db	AT	CATGCAATTTACTTTAATACAGTTTT	TTTTTTAGTTTTGCTGGCGG	CAATCTTCTCA	1874
2631	Qy	GC	TTCCAGCGCTCTTTTCTGTAACGTT	CAACCTCTACCTTTAGCAATCCCT	TTCCCTTTGCA	2690
1875	Db	GC	TTCCAGCGCTCTTTTCTGTAACGTT	CAACCTCTACCTTTAGCAATCCCT	TTCCCTTTGCA	1934
2691	Qy	AA	TAGTCTCTTCCAAATAAATAGTCAG	ATCCTGTAGAGACCAATCATCC	ACGGTT	2750
1935	Db	AA	TAGTCTCTTCCAAATAAATAGTCAG	ATCCTGTAGAGACCAATCATCC	ACGGTT	1994
2751	Qy	CT	ATCTGTTGACCCAAATGGTCTCCT	GTGCATCTAAACCCACACGGGT	GTCTAATC	2810
1995	Db	CT	ATCTGTTGACCCAAATGGTCTCCT	GTGCATCTAAACCCACACGGGT	GTCTAATC	2054
2811	Qy	AA	CCAATCGTAACCTTTCATCTCTTCC	ACCACTGTCTTTGAGCAATAAGC	CGATAACA	2870
2055	Db	AA	CCAATCGTAACCTTTCATCTCTTCC	ACCACTGTCTTTGAGCAATAAGC	CGATAACA	2114
2871	Qy	AA	ATCTTTGTGCTCTTCGCAATGTCAA	AGTAGTACCTTACTATTTCTCC	AGTAGATAGG	2930
2115	Db	AA	ATCTTTGTGCTCTTCGCAATGTCAA	AGTAGTACCTTACTATTTCTCC	AGTAGATAGG	2174
2931	Qy	GAG	CCCTTGATGACAAATCTGCTAA	CATCAAAAGGCCTCTAGGTTCT	TTGTTACTTCT	2990
2175	Db	GAG	CCCTTGATGACAAATCTGCTAA	CATCAAAAGGCCTCTAGGTTCT	TTGTTACTTCT	2234
2991	Qy	TC	TGCGCGCTCTTCAACCGCTTAACA	ATACCTGGGCCCAACACGGGTG	CAATTCGTA	3050
2235	Db	TC	TGCGCGCTCTTCAACCGCTTAACA	ATACCTGGGCCCAACACGGGTG	CAATTCGTA	2294
3051	Qy	AT	GTCTGCCAATCTGCTATTCTGTATA	CACCGCAGAGTACTGCAATTTG	ACTGTATTA	3110
2295	Db	AT	GTCTGCCAATCTGCTATTCTGTATA	CACCGCAGAGTACTGCAATTTG	ACTGTATTA	2354
3111	Qy	CCA	ATGTCAGCAAAATTTTCTGTCTT	CGAAGATAAAAATTTGACTTGG	CGGATAATGCC	3170
2355	Db	CCA	ATGTCAGCAAAATTTTCTGTCTT	CGAAGATAAAAATTTGACTTGG	CGGATAATGCC	2414
3171	Qy	TT	TAGCGGCTTAATGTGCGCCCTC	CAATGGAATAATCAGTCAAG	ATATCCCATGTGTTTTT	3230
2415	Db	TT	TAGCGGCTTAATGTGCGCCCTC	CAATGGAATAATCAGTCAAG	ATATCCCATGTGTTTTT	2474
3231	Qy	AG	TAAACAAAATTTTGGGACCTTA	ATGCTTCAACTAACTCAGTA	ATATTTCTTGGTGSTACGA	3290
2475	Db	AG	TAAACAAAATTTTGGGACCTTA	ATGCTTCAACTAACTCAGTA	ATATTTCTTGGTGSTACGA	2534
3291	Qy	AC	ATCCAATGAAGCACACAAGTT	TTGTTGCTTTTCTGTCATG	ATATTTAAATAGCTTGGCA	3350
2535	Db	AC	ATCCAATGAAGCACACAAGTT	TTGTTGCTTTTCTGTCATG	ATATTTAAATAGCTTGGCA	2594
3351	Qy	GC	AACAGGACTAGGATGAGTAGAC	GACGTTCTCTTATATAGCTTT	TCGACATGATTTAT	3410
2595	Db	GC	AACAGGACTAGGATGAGTAGAC	GACGTTCTCTTATATAGCTTT	TCGACATGATTTAT	2654

Qy	3411	CTTCGTTTCTCGAGGTTTTTGTGTCGAGTTGGGTTAAGAATACTGGGCAATTTTCAT	3470
Db	2655	CTTCGTTTCTCGAGGTTTTTGTGTCGAGTTGGGTTAAGAATACTGGGCAATTTTCAT	2714
Qy	3471	GTTCCTTCAACACTACATATGCGGTATATACCAATCTAAGTCTGTGCTCCTTCCCTTCGT	3530
Db	2715	GTTCCTTCAACACTACATATGCGGTATATACCAATCTAAGTCTGTGCTCCTTCCCTTCGT	2774
Qy	3531	TCTTCTTCTGTTCCGGAGATTACCGAATCAAAAAATTTCAAGAAACCGAAATCAAAA	3590
Db	2775	TCCTTCTTCTGTTCCGGAGATTACCGAATCAAAAATTTCAAGAAACCGAAATCAAAA	2834
Qy	3591	AAAGATAAAAAAATAATGATGAATTGAATTGAAAGCTGTGTGATGTGGTGCACTCTCAGT	3650
Db	2835	AAAGATAAAAAAATAATGATGAATTGAATTGAAAGCTGTGTGATGTGGTGCACTCTCAGT	2894
Qy	3651	ACAATCTGCTCTGATCGCGCATAGTTTAAGCCGCGCCGACACCCGCCAACACACCGCTGAC	3710
Db	2895	ACAATCTGCTCTGATCGCGCATAGTTTAAGCCGCGCCGACACCCGCCAACACACCGCTGAC	2954
Qy	3711	GCGCCCTGACCGGCTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGCTCC	3770
Db	2955	GCGCCCTGACCGGCTGTCTGCTCCCGGCATCCGCTTACAGACAAGCTGTGACCGCTCC	3014
Qy	3771	GGGAGCTGCATGTGTACAGAGTTTTTCAACCGTCATCACCGAAACCGCGACGAAAGGGC	3830
Db	3015	GGGAGCTGCATGTGTACAGAGTTTTTCAACCGTCATCACCGAAACCGCGACGAAAGGGC	3074
Qy	3831	CTCGTGATACGCCCTATTTTTATAGTTTAATGTGCATGATTAATATGTTTTCTTAA	3883
Db	3075	CTCGTGATACGCCCTATTTTTATAGTTTAATGTGCATGATTAATATGTTTTCTTAA	3134
Qy	3884	-----	3883
Db	3135	GCGCGCTCTAGAACTAGTGGATCAATTCACGGACTATAGACTATAGTACTAGTACTCCGT	3194
Qy	3884	-----GTATGATCCAAATATCAAAAGAAATGATAGCAATTGAAGGATG-----	3924
Db	3195	CTACTGTACGATACACTTCCGCTCAGGTCCTTGTCTCTTTAAACGAGGCTTACCACTCTTT	3254
Qy	3925	-----AGCTAATCCAAATTGAGGAGTGGCAGCATATAGAACAGCTAAAGGGTAGTCT	3977
Db	3255	TGTTACTCTATTGATCCAGCTCAGCAAAAGCAGTGTGATCTAAGATTCTATCTTCGCGAT	3314
Qy	3978	GAAGGAGCATACGATACCCCGCATGGATGGGATTAATATCACAGAGGTACTAGACTAC	4037
Db	3315	GTAGTAAACTAGCTAGACCAGAAAGAGACTAGAATGCAAAAGGCATCTTCTACAAATG	3374
Qy	4038	CTTTCATCCT-----ACATAAATAGAGCGCATATAAGTACGCATT	4076
Db	3375	CTGCCATATTATTATCCGATGTGACGCTGCAGTCTCTCAATGATTTCCGAATACGCTTT	3434
Qy	4077	TAGCATAAACAGCACTATGC-----CGTCTCTCTCAT	4110
Db	3435	GAGGAGATACAGCTTAATATCCGACAAATGTTTTACAGATTTTACGATCTGTGTTAC	3494
Qy	4111	GTATATATATACAGCAACACGAGATATAGTGGAGCTGAAACAGTCAGCTGTATGT	4170
Db	3495	CCATCATTTGAATTTTGAACATCCGAACCTGGAGTTTTCCCTGAAACAGATGATATTT	3554
Qy	4171	GCGCAGCTCGGTTGCATTTTCGGAAGCGCTCGTTTTTCGAAACGCTTTTGAAGTTCCTAT	4230
Db	3555	GAACCTGTATTAATATATAGTCTAGCGCTTTTACGGAAGCAATGATGATTTCCGTT	3614
Qy	4231	TCCGAAGTTCCTATCTCTAGAAAGTATAGGAACCTTCAGACG-----	4273
Db	3615	CCTGGAAACTATTGCACTTATTGTCATAGGTAATCTTTCGACGTCGCATCCCGGTTTCAT	3674
Qy	4274	-----	4273
Db	3675	TTTCTCGGTTTCCACTTTGCACTTCAATAGCATATCTTTGTTAAACGAAGATCTGTGCTT	3734

QY 4274 -CTTTTGAACCAAAAGCGCTCTGAAGCGCACT----- 4307
Db 3735 CATTTTGTAGAACAAAATGCAACGCGAGCGCTAAATTTTCAAACAAGAACTGAGC 3794
QY 4308 -----TTCAAAAACCAAAAGCGCTCTGAAGCGCACT----- 4354
Db 3795 TCGAATTTTACAGACAGAAATGCAACGCGAGCGCTAAATTTTCAAACAAGAACTG 3854
QY 4355 TCGAATTTTACAGACAGAAATGCAACGCGAGCGCTAAATTTTCAAACAAGAACTG 4409
Db 3855 GCTTCATTTTGTAAAAAAGAAATGCAACGCGAGCGCTAAATTTTCAAACAAGAACTG 3914
QY 4410 TGTGCTATATCCCTATATACCTAC-----COATCACTT 4445
Db 3915 TGAAGTTCATTTTACAGAACAGAAATGCAACGCGAGCGCTAAATTTTCAAACAAGAA 3974
QY 4446 TCGCTCTTGAACCTTGCATCTAAA-----CTCGACCTCTA 4480
Db 3975 TCTATACCTTTTGTCTTCAAAAATGCAACGCGAGCGCTAAATTTTCAAACAAG 4034
QY 4481 CATTTTGTATGTTATCTCTAGTATTTACTCTTTAGACAAAATAATGTAGTAAGAACTAT 4540
Db 4035 CATCTTAGATTTACTTTTTTCTCTTTGCGCTCTAATGCGAGTCTCTTGAATACCTT 4094
QY 4541 TCATAGAGTGAATCGAAAAACAATACGAAAAATGTAAACAATTTCTATACGTAGTATAGA 4600
Db 4095 TTGCACTGTAGTCCGTTAAGGTAGAGAGGCTACTTTTGTGTCTATTTTCTCTTCCA 4154
QY 4601 GACAAA-----TAGAAGAAACCGTTTCATAATTTT 4630
Db 4155 TAAAAAAGCCTGACTCCACTTTCCGCGGTTTACTGATTTACTAGCGAAGCTCGGGTGCA 4214
QY 4631 CTGACCAATGAAGAAATCATCAAGCTATCACTTTCTGTTCAAAAAGTATGCGCAATCCAC 4690
Db 4215 TTTTTCAGATTAAGGCATCCCGATTTATATCTTAACCGATGTGGATGCGCATCTTT 4274
QY 4691 ATCGGTATAGAATAAATCGGGGATGCCCTTATCTTG-----AAAAATGCACT 4739
Db 4275 GTGAACAGAAAGTATAGCGGTTGATGATTTCTTCAATTTGTCAGAAAAATATGACGGTTTC 4334
QY 4740 CGGAGCTTCGTAGTAATCAAGTAAGCGGGAAGTGGAGTCAGGCTTTTTTTTATGGAAGA 4799
Db 4335 TTCTATTTTGTCTCTATATACCTATACGTATAGGAATGTTTACATTTTCGTATTTGTTTGA 4394
QY 4800 GAAAAATAGACCAAGTAGCTCTCTTCACTTAAACGGACCTACAGTGCAGAAAGTTA 4859
Db 4395 TTCACCTATGATAGTCTTCTACTCAATTTTTTTTGTCTAAGAGTAATACCTAGATAA 4454
QY 4860 TCAAGAGACTGCATTTATAGAGCGCAAAAGGAGAAAAAGTAATCTAAGATGCTTTGTT 4919
Db 4455 ACATAAAAAATGTAGAGTTCAGATTTAGATGCAAGTTCAGAGGCGAAAGTGGATGGT 4514
QY 4920 AGAAAAATAGCGCTCTCGGATGCAATTTTGTGAGAACAA----- 4959
Db 4515 AGTTATATAGGATATAGCACAGATATATAGCAAGAGATACTTTTGAAGCAATGTTT 4574
QY 4960 ---AAGAGATATAGTCTTTGTTGTAATAAGCGCTCTCGGTTGCAATTTCTGTTCT 5016
Db 4575 GTGGAAGCGGTATTCGCAATATTTTAGTAGCTCGTTACAGTCCGCTGCGTTTGGTTT 4634
QY 5017 GTAAAAATCGAGCTCAGATTTCTTTGTTTGAATAATAGCGCTCTCGGTTGCAATTTTGG 5075
Db 4635 TTGGAAGTCCGCTCTCAGAGCGCTTTTGGTTTCAAAAGCGCTCTGAAGTTCCTATACTT 4694
QY 5076 TTTTCAAAAAATGAAGCAAGAT----- 5099
Db 4695 TCTAGAGAAATAGGAACCTTCGGAATAGGAACCTTCAAGCGTTTCCGAAAAACGAGCGCTTCC 4754
QY 5100 -----CTTCGTTGGTAAATAGCG 5118
Db 4755 GAAAAATGCAACGCGAGCTGCGCACTACAGCTCACTGTTACGTGCGACCTATATCTGCG 4814
QY 5119 CTTTGGCGTTGCAATTTCTGTTCTGTAAAAATGCACTCAGATTTCTTTGTTG----- 5170

Db 4815 TGTGCTGTATATATATATATATACATGAGAGAAACGGCATAGTGCCTGTTTATGCTTTAAATG 4874
QY 5171 ----- 5170
Db 4875 CGTACTTATATGCGTCTATTTATGTAGATGAAAGGTAGTCTAGTACCTCCTGTGATATT 4934
QY 5171 ----- 5170
Db 4935 ATCCCAATTCATGCGGGGTATCGTATGCTTCTCAGCACTACCCCTTAGCTGTTCTATA 4994
QY 5171 ----- 5170
Db 4995 TGTGCGCACTCTCAATTTGATTTAGTCTCATTTCAATGCTATCATTTTCTTTGATATT 5054
QY 5171 ----- 5170
Db 5055 GGATCATATGCTATAGTACCGAGAAAACTAGTCCGAAGTAGTATGCTGCTTTATGCTGTTATC 5114
QY 5171 -----AA 5172
Db 5115 TGATGACTATACGTTGTCCTGGCCACGCGAGAACGCTTATCGCTCCAATTTCCACCA 5174
QY 5173 AAATTAGCGCTCTGCGGTTGCAATTTTGTCTTCAAAAATGAAGCACAGATGCTTCTG 5229
Db 5175 ACATTTAGTCAACTCCGTTAGGCCCTTCATTTGAAAGAAATGAGGTCAATCAAAATGCTTCCA 5234
QY 5230 ----- 5229
Db 5235 ATGTGAGATTTTGGGCCAATTTTATATAGCAAAAGATTGAATAAGGCGCAATTTTCTTCAA 5294
QY 5230 -----TCAGTGGCACTTTTTCGGGGAATGTGCGCGGAA 5263
Db 5295 GCTGCGGCCGCACTCTCACTAGTACGTCAGTGGCACTTTTCGGGGAATGTGCGCGGAA 5354
QY 5264 CCGCTATTTGTTTATTTTCTTAAATAATTTCAAAATATGATTCGCTCATAGACAAATAC 5323
Db 5355 CCGCTATTTGTTTATTTTCTTAAATAATTTCAAAATATGATTCGCTCATAGACAAATAC 5414
QY 5324 CCTGATAAATGCTTCAATAATTTTGAAGAAAGGAGATGATGAGTATTTCAAAATTTCCG 5383
Db 5415 CGTATAAATGCTTCAATAATTTTGAAGAAAGGAGATGATGAGTATTTCAAAATTTCCG 5474
QY 5384 TCGCCCTTATTTCCCTTTTTCGGGCAATTTTGCCTTCTGTTTTCCTCACCAGAAACGC 5443
Db 5475 TCGCCCTTATTTCCCTTTTTCGGGCAATTTTGCCTTCTGTTTTCCTCACCAGAAACGC 5534
QY 5444 TGTGGAAGTAAAGATGCTGAAGATCAGTTTGGGTGCAACGAGTGGTTTACATCGAACTGG 5503
Db 5535 TGTGGAAGTAAAGATGCTGAAGATCAGTTTGGGTGCAACGAGTGGTTTACATCGAACTGG 5594
QY 5504 ATCTCAACGCGGTAAAGATCCTTGAAGATTTTCCGCCGAGAACGTTTCCAAATGATCA 5563
Db 5595 ATCTCAACGCGGTAAAGATCCTTGAAGATTTTCCGCCGAGAACGTTTCCAAATGATCA 5654
QY 5564 GCATTTTAAAGTTCCTCTATGTCGCGGCTTATTTATCCGCTTATGACCGCGGCAAGAGC 5623
Db 5655 GCATTTTAAAGTTCCTCTATGTCGCGGCTTATTTATCCGCTTATGACCGCGGCAAGAGC 5714
QY 5624 AACTCGGTTCGCGCATACCTATTTCTCAGAAATGATCTTGGTTGAGTACTCAACAGTCAAG 5683
Db 5715 AACTCGGTTCGCGCATACCTATTTCTCAGAAATGATCTTGGTTGAGTACTCAACAGTCAAG 5774
QY 5684 AAAAGCATCTTACGGATGGCATGACAGTAAGAGAAATTTATGAGTGTCTGCCATAACATGA 5743
Db 5775 AAAAGCATCTTACGGATGGCATGACAGTAAGAGAAATTTATGAGTGTCTGCCATAACATGA 5834
QY 5744 GTGATAACACTTCGCGCAACTTACTCTGACAAAGTCGAGGACCGAAGAGCTTAAACCG 5803
Db 5835 GTGATAACACTTCGCGCAACTTACTCTGACAAAGTCGAGGACCGAAGAGCTTAAACCG 5894
QY 5804 CTTTGTGCAACAATCGGGGATCATGTAATTCGCTTGTATCTGTTGGGAAACCGGAGCTGA 5863

5895 CTTTTTGGACAACATGGGGGATCATGTAACTCGCCTTGATCGTTGGGAACCGAGCTGA 5954
5864 ATGAAGCCATACCAACGAGAGCGTGACACCAAGATGCTGTAGCAATGGCAACAACTGT 5923
5955 ATGAAGCCATACCAACGAGAGCGTGACACCAAGATGCTGTAGCAATGGCAACAACTGT 6014
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6015 TGGCGCAAACTATTAACTGGGGAACCTACTTACTTACTTACTTCCCGGCAACAACTAATAGACT 6074
5984 GGAATGAGGCGGATAAAGTTGACGAGCACTCTCTGCGCTCGGCGCTTCCGGCTGGCTGGT 6043
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6195 GGCAGATGGTAAGCCCTCCGCTATCGTAGTTATCTACAGGAGCGGAGTCAAGCAACTA 6254
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6255 TGGATCAACGAAATAGACAGATCGCTGAGATAGTGCCTCACTGATTTAAGCATTTGTAAC 6314
6224 TGTGAGCAACCAAGTTTACTCATATATATCTTTAGATGATTTAAACTTCAATTTTAAATTA 6283
6315 TGTGAGCAACCAAGTTTACTCATATATATCTTTAGATGATTTAAACTTCAATTTTAAATTA 6374
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6584 TAGCACCGCTACATACCTCGCTCTGCTAATCTGTTTACCAGTGGCTGCTGCCAGTGGCG 6643
6675 TAGCACCGCTACATACCTCGCTCTGCTAATCTGTTTACCAGTGGCTGCTGCCAGTGGCG 6734
6644 ATAAGTCTGCTTCTTACCGGTTGGACTCAAGACGATAGTTTACCGGATAAGGCGCAGCGT 6703
6735 ATAAGTCTGCTTCTTACCGGTTGGACTCAAGACGATAGTTTACCGGATAAGGCGCAGCGT 6794
6704 CGGGCTGAACCGGGGTTTCTGCAACAGCCGAGTGTGGAGCGAAACGACCTACACCGAAC 6763
6795 CGGGCTGAACCGGGGTTTCTGCAACAGCCGAGTGTGGAGCGAAACGACCTACACCGAAC 6854
6764 TGAGATACCTTACAGCTGAGCTATGAGAGCGCCACGCTTCCGGAAGGAGAGAGCGCG 6823
6855 TGAGATACCTTACAGCTGAGCTATGAGAGCGCCACGCTTCCGGAAGGAGAGAGCGCG 6914
6824 ACAGGTATCCGGTAAGCGGCGAGGCTCGGAACAGGAGAGCGCAAGGAGCTTCCAGGGG 6883
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6884 GAAACGCTGGTATCTTTATGCTCTGTGGGTTTCGCCACTCTGACTTGAAGCGTGCAT 6943
6975 GAAACGCTGGTATCTTTATGCTCTGTGGGTTTCGCCACTCTGACTTGAAGCGTGCAT 7034

6944 TTTTGTGATGCTCGTTCAGGGGGCGGAGCCTATGGAATAAACGCAAGACGCGGCTTTT 7003
7035 TTTTGTGATGCTCGTTCAGGGGGCGGAGCCTATGGAATAAACGCAAGACGCGGCTTTT 7094
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7095 TAGGTTCTCGGCTTTTGTCTGCGCTTTTGTCTCACATGTTCTTCTCGGTATCCCTG 7154
7064 ATTCTGTGATAAACCGTATTACCGCTTTGAGTGAGCTGATACCGCTCGCGCGAGCGAA 7123
7155 ATTCTGTGATAAACCGTATTACCGCTTTGAGTGAGCTGATACCGCTCGCGCGAGCGAA 7214
7124 CGACGAGCGCAGCGAGTCACTGAGCGAGGAAGCGGAAGCGCCCAATAACGAAACCGC 7183
7215 CGACGAGCGCAGCGAGTCACTGAGCGAGGAAGCGGAAGCGCCCAATAACGAAACCGC 7274
7184 CTCTCCCGCGGCTTGGCGGATTCATTAATGAGCTGCGACGACAGGTTTCCGACTGGA 7243
7275 CTCTCCCGCGGCTTGGCGGATTCATTAATGAGCTGCGACGACAGGTTTCCGACTGGA 7334
7244 AAGCGGCGAGTCAAGCGCAACGCAATTAATGAGTACCTCACTCACTAGGCAACCCAGG 7303
7335 AAGCGGCGAGTCAAGCGCAACGCAATTAATGAGTACCTCACTCACTAGGCAACCCAGG 7394
7304 CTTTACACTTTATGCTTCCGGCTCTCTATGTTGTGGAATTTGTAGCGGATAACTTTTC 7363
7395 CTTTACACTTTATGCTTCCGGCTCTCTATGTTGTGGAATTTGTAGCGGATAACTTTTC 7454
7364 ACACAGGAACAGCTATGACCATGATTACGCCAGCGCGCAAT 7406
7455 ACACAGGAACAGCTATGACCATGATTACGCCAGCGCTCGAAAT 7497

RESULT 12

US-10-228-785-3
; Sequence 3, Application US/10228785
; Publication No. US20030186443A1
; GENERAL INFORMATION:
; APPLICANT: ANDLID, THOMAS
; APPLICANT: VEIDE, JENNY
; APPLICANT: SANDBERG, ANN-SOFIE
; TITLE OF INVENTION: PHYTASE ACTIVE YEAST
; FILE REFERENCE: 6821
; CURRENT APPLICATION NUMBER: US/10/228,785
; CURRENT FILING DATE: 2002-08-26
; PRIOR APPLICATION NUMBER: SE 0200911-6
; PRIOR FILING DATE: 2002-03-22
; NUMBER OF SEQ ID NOS: 12
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 3
; LENGTH: 9715
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Description of Artificial Sequence: Synthetic plasmid
; OTHER INFORMATION: pYX212 nucleotide sequence
US-10-228-785-3

Query Match 42.4%; Score 3318.6; DB 15; Length 9715;
Best Local Similarity 74.8%; Pred. No. 0;
Matches 4787; Conservative 0; Mismatches 769; Indels 847; Gaps 16;
1851 TCACTGGCGCTCGTTTACAACTCGTGTGAGTGGGAACCCCTGGCTTACCCAACTTAAT 1910
1599 TCACTGGCGCTCGTTTACAACTCGTGTGAGTGGGAACCCCTGGCTTACCCAACTTAAT 1658
1911 CGCTTTCAGCAGCATCTCCCTTTTCCGAGCTGGCGTAATAGCAAGAGCGCCGACCGAT 1970
1659 CGCTTTCAGCAGCATCTCCCTTTTCCGAGCTGGCGTAATAGCAAGAGCGCCGACCGAT 1718
1971 CGCCCTTCCCAACAGTTGCGCAGCTGAATGGCGAATGGCGGACGCGCCCTGTAGCGG 2030

QY 4077 TAAGCATAAACAGCGACTATGC-----CGTCTCTTCAT 4110
Db 3939 GAGGAGATACAGCGCTAATATCCGACAAACCTGTTTACAGATTACGATCGTACTGTGTAC 3998
QY 4111 GTATATATATATACAGCAACAGCAGATATAGTGCAGCTGAAACAGTGCAGCTGTATGT 4170
Db 3999 CCATCATTTGATTTTGAACATCCGACCTGGAGTTTCCCTGAAACAGATAGTATATTT 4058
QY 4171 GCGCAGCTCGCGTGTCAATTTTCGGAAGCGCTCGTTTTTCGGAACAGCTTTGGAAGTTCCTAT 4230
Db 4059 GAACCTGTATAAATAATATATAGTCTAGCGCTTTACGGAAGACAATGTATGTATTTCCGTT 4118
QY 4231 TCCGAAGTTCCTATTCTTAGAAGTATAGGAACCTTCAGAGCG----- 4273
Db 4119 CTTGGAAGAACTATTGCATCTATTGATAGGTAATCTTGACGTCGCATCCCGGTTTCAT 4178
QY 4274 ----- 4273
Db 4179 TTTCTCGGTTTCCATCTTGCACTTCAATAGCATATCTTTGTTAAAGCAATCTGTGCTT 4238
QY 4274 -CTTTTGAACCAACAAAGCGCTCTGAAGCGCACT----- 4307
Db 4239 CATTTTGTAGAACAAATAATGCAACGCGAGAGCGCTAATTTTCAAACAAAGATCTGAGC 4298
QY 4308 -----TTCAAAAAACCAAAACGCAACCGGACGTGTAAACGAGCTACTAAATAT 4354
Db 4299 TGCATTTTTCAGAACAGAAATGCAACGCGAAGCGCTATTTTACCACGAAGAACTGT 4358
QY 4355 TCGGAATACCGCTTCCACAAACATTTGCTCAAAAG-----TATCTCTTTGCTATATATCTC 4409
Db 4359 GCTTCATTTTGTAAACAAATAATGCAACGCGAGAGCGCTAATTTTCAAACAAAGAAATC 4418
QY 4410 TGTGCTATATCCCTATATACCTAC-----CCATCCACCTT 4445
Db 4419 TGAGCTGCAATTTTACAGAACAGAAATGCAACGCGAGAGCGCTATTTTACCACAAAGAA 4478
QY 4446 TCGCTCCTTGAACTTGCAATCTAAA-----CTCGACCTCTA 4480
Db 4479 TCTATACTCTTTTGTGTTTGTACAAAAATGCAATCCGAGAGCGCTATTTTCTAACAAAG 4538
QY 4481 CATTTTATGTTTATCTCTAGTATTTACTCTTTAGACAAATAATTTGTAGTAACTAT 4540
Db 4539 CATCTTAGATTACTTTTCTCTCTGCGCTCTATATATGAGTCTCTTGATACTTT 4598
QY 4541 TCATAGAGTGAATCGAAAAACAATACGAAATGTAAACATTTCTATACGTAAGTATATAGA 4600
Db 4599 TTGCATGTAGTCCGTTAGGTTAGAGAGGCTACTTTGGTGTCTATTTCTCTTCCA 4658
QY 4601 GACAAA-----TAGAAGAAACCGTTCAATTTT 4630
Db 4659 TAAAAAAGCGCTGACTCCACTTCCGCGTTTACTGTATTTACTAGCAAGCTGCGGTGCAT 4718
QY 4631 CTGACCAATGAAGAAATCATCAAGCTATCACTTCTGTTTCAAAAGTATGCGCAATCCAC 4690
Db 4719 TTTTCAAGATAAAGGCATCCCGATTTATTTATACCGAATGGAATGCGCATCTTT 4778
QY 4691 ATCGGTATAGAAATATATCGGGATGCTTTTATCTTG-----AAAAATGCACC 4739
Db 4779 GTGAACGAAGATGATAGCGTTGATGATCTTCATTTGGTCAGAAAAATATGAACGGTTTC 4838
QY 4740 CGCAGCTTCGCTAGTAATCAGTAACCGCGGAAGTGGAGTCAAGCTTTTTTTTATGAAGA 4799
Db 4839 TTTCTATTTTCTCTATATACTAGTATAGGAATGTTTACAATTTTCGTATGTTTTTGA 4898
QY 4800 GAAAAATAGACCAAGTAGCTCTTCTTAACTTAAACCGACCTACAGTGCAAAAAGTTA 4859
Db 4899 TTTCACTCTATGAATAGTCTTACTACAAATTTTTTGTCTAAAGAGTAATACTAGAGATAA 4958
QY 4860 TCAAGAGACTGCATTAATAGAGCGCACAAAGGAGAAAAAGTAATCTTAAGATGCTTTGTT 4919
Db 4959 ACATAAAAATGTAGAGGTGAGTTTAGATGCAAGTTCAAGGAGCGAAGGTGGTGGT 5018
QY 4920 AGAAAAATAGCGCTCTCGGATGCAATTTTGTAGAACAA----- 4959

Db 5019 AGTTATATAGGATATAGCACAGAGATATATAGCAAGAGATACTTTTTGAGCAATGTTT 5078
QY 4960 ---AAAGAAAGTATAGATTCTTTTGTGTAATAATAGCGCTCTCGGTTCATTTCTCTGTTCT 5016
Db 5079 GTGGAAGCGGTATTCGCAATATTTTAGTAGCTCGTTACAGTCGGTGGTTTTTGGTTTT 5138
QY 5017 GTAAAAATCGAGC-TCAGATTCTTTTGTGTTGAAAAATAGCGCTCTCGGTTCGATTTTGG 5075
Db 5139 TTAGAAGTCCGCTCTTCAGAGCGCTTTTGGTTTTTCAAAGCGCTCTGAAGTTCTTACTATT 5198
QY 5076 TTTTACAAAAATGAAGCACAGATT----- 5099
Db 5199 TCTAGAGAATAGAACTTCGSAATAGAACTTCAAAGCGTTTCCGAAAAACGAGCGTCTC 5258
QY 5100 -----CTTCGTTGTAATAATAGCG 5118
Db 5259 GAAATGCAACGCGAGCTGCGCACATACAGCTCAGTTCAGCTCGCACCTATATCTGCG 5318
QY 5119 CTTTCGCGTTGCAATTTCTGTTCTGTAATAATGCAGCTCAGATTCTTTGTTTGG----- 5170
Db 5319 TGTTCCTGTATATATATATACATGAGAAGACGGCATAGTGGTGTGTTATGCTTAAATG 5378
QY 5171 ----- 5170
Db 5379 CGTACTTATATCGTCTATTTATGTAGGATGAAGGTAGTCTAGTAGTACCTCTCTGTGATAT 5438
QY 5171 ----- 5170
Db 5439 ATCCCATTCCTCCATTCGCGGTATCGTATGCTTCCTTCAGCACTACCTTTAGCTGTTCTATA 5498
QY 5171 ----- 5170
Db 5499 TGTGCGCACTCCTCAATTCGATTGATGCTCATCTTCATGCTATCATTTCTTTTGATATT 5558
QY 5171 ----- 5170
Db 5559 GGATCATATGCATAGTACCGAGAAACTAGTGGAGTAGTGTATGATTCAGGTATTTGTTATC 5618
QY 5171 -----AA 5172
Db 5619 TGATGATATACGTTGCTCTGCGCCAGGAGACAGCTTATCGCTCCAAATTTCCACACA 5678
QY 5173 AAATTAGCGCTCTCGGTTGCAATTTTGTCTACAAAATGAAGACAGATGCTTCGT--- 5229
Db 5679 ACATTAGTCAACTCCGTTAGGCCCTTCAATTGAAAGAAATGAGGTCAATCAATGCTCTCCA 5738
QY 5230 ----- 5229
Db 5739 ATGTGAGATTTTGGGCCAATTTTATAGCAAGATTTGAATAAGCGCATTTTCTTCAAA 5798
QY 5230 -----TCAGGTGGCACTTTTTCGGGGAATATGTCGCGGAA 5263
Db 5799 GCTGCGCGCGCACTCTCACTAGTACGTCAGGTGGCACTTTTCGGGGAATATGTCGCGGAA 5858
QY 5264 CCCTATTTGTTTATTTTCTAAATACATTTCAATATGATATCGCTCATGAGCAATAAC 5323
Db 5859 CCCTATTTGTTTATTTTCTAAATACATTTCAATATGATATCGCTCATGAGCAATAAC 5918
QY 5324 CTTGATAAATGCTTCAATATATTTGAAAAAGGAGATGATGATTTCAACATTTCCGTG 5383
Db 5919 CTTGATAAATGCTTCAATATATTTGAAAAAGGAGATGATGATTTCAACATTTCCGTG 5978
QY 5384 TCGCCCTTATCCCTTTTTCGGGCATTTTTCCTCTCTGTTTTCCTCAGCCCAAGAACGC 5443
Db 5979 TCGCCCTTATCCCTTTTTCGGGCATTTTTCCTCTCTGTTTTCCTCAGCCCAAGAACGC 6038
QY 5444 TGGTGAAGTAAAGATGCTGAAGTCACTTGGGTGCAGAGTGGGTATCATCGAACTGG 5503
Db 6039 TGGTGAAGTAAAGATGCTGAAGTCACTTGGGTGCAGAGTGGGTATCATCGAACTGG 6098
QY 5504 ATCTCAACAGCGGTAAAGATCTTTGAGAGTTTTCGCCCGGAGAACGTTTTCATGATGATA 5563

; TYPE: DNA									
; ORGANISM: Artificial									
; FEATURE:									
; OTHER INFORMATION: Nucleotide Sequence of p416 GPD-Edges									
US-10-340-447-3									
Query Match 29.0%; Score 2273; DB 16; Length 6831;									
Best Local Similarity 100.0%; Pred. No. 0;									
Matches 2273; Conservative 0; Mismatches 0; Indels 0; Gaps 0;									
Qy	1547	GTCCACCTCGAGTCATGTAATAGTATATGTCACCGTTACATTCACGCCCTCCGCCACAT	1606						
Db	2273	GTCCACCTCGAGTCATGTAATAGTATATGTCACCGTTACATTCACGCCCTCCGCCACAT	2214						
Qy	1607	CCGCTCTAAACCGAAAGAGGAGTATAGACAACTGAAGTCTAGGTCCCTATTATTTT	1666						
Db	2213	CCGCTCTAAACCGAAAGAGGAGTATAGACAACTGAAGTCTAGGTCCCTATTATTTT	2154						
Qy	1667	TTATAGTTATGTTAGTATTAAGAACGTTATTTATTTTCAAATTTTTTTTTTCTGT	1726						
Db	2153	TTATAGTTATGTTAGTATTAAGAACGTTATTTATTTTCAAATTTTTTTTTTCTGT	2094						
Qy	1727	ACGACCGGTGTCGCATGTAACTATATCTGAACAACTTGCTGTGAGAGTTTTGGAC	1786						
Db	2093	ACGACCGGTGTCGCATGTAACTATATCTGAACAACTTGCTGTGAGAGTTTTGGAC	2034						
Qy	1787	GCTCGAAGGCTTTAAATTTGCGGCCGTTACCCAAATTCGCCCTATAGTCAGTCGTATTACG	1846						
Db	2033	GCTCGAAGGCTTTAAATTTGCGGCCGTTACCCAAATTCGCCCTATAGTCAGTCGTATTACG	1974						
Qy	1847	GGCTCTCACTGGCCGTGTTTTTACAACGTCTGTGACTGGGAAACCCCTGGCGTTACCCAAC	1906						
Db	1973	GGCTCTCACTGGCCGTGTTTTTACAACGTCTGTGACTGGGAAACCCCTGGCGTTACCCAAC	1914						
Qy	1907	TAATCGCCTTGCAGCACATCCCCCTTTGCCAGCTGGCGTAATAGCGAAGAGGCCGAC	1866						
Db	1913	TAATCGCCTTGCAGCACATCCCCCTTTGCCAGCTGGCGTAATAGCGAAGAGGCCGAC	1854						
Qy	1967	CGATCGCCCTTCCCAACAGTTGCGCAGCTGAATGCGCAATGGCGCAGCGCCCTGTAG	2026						
Db	1853	CGATCGCCCTTCCCAACAGTTGCGCAGCTGAATGCGCAATGGCGCAGCGCCCTGTAG	1794						
Qy	2027	CGCGCATTAAGCGCGCGGTGTGGTGTACGCGAGCGTGACCGCTACACTTGCAG	2086						
Db	1793	CGCGCATTAAGCGCGCGGTGTGGTGTACGCGAGCGTGACCGCTACACTTGCAG	1734						
Qy	2087	CGCCCTAGCGCCGCTCCTTTGCGCTTTCTTCCCTTCTTCTCGCAGTTCGCGCGCTT	2146						
Db	1733	CGCCCTAGCGCCGCTCCTTTGCGCTTTCTTCCCTTCTTCTCGCAGTTCGCGCGCTT	1674						
Qy	2147	TCCCGTCAAGCTCTAAATCGGGGGTCCCTTTTAGGGTTCCGATTTAGTCTTTACGGCA	2206						
Db	1673	TCCCGTCAAGCTCTAAATCGGGGGTCCCTTTTAGGGTTCCGATTTAGTCTTTACGGCA	1614						
Qy	2207	CCTCGACCCCAAAAACTTGATTAGGGTGATGTTTCACTAGTGGGCCATCGCCCTGATA	2266						
Db	1613	CCTCGACCCCAAAAACTTGATTAGGGTGATGTTTCACTAGTGGGCCATCGCCCTGATA	1554						
Qy	2267	GACGGTTTTTCGCCCTTTGAGTTGGAGTCCACGTTCTTTAAATAGTGGATCTTTGCCA	2326						
Db	1553	GACGGTTTTTCGCCCTTTGAGTTGGAGTCCACGTTCTTTAAATAGTGGATCTTTGCCA	1494						
Qy	2327	AACGTGAACAACACTCAACCTATCTCGGTCTATCTTTTGAATTAAGGGATTTTGGC	2386						
Db	1493	AACGTGAACAACACTCAACCTATCTCGGTCTATCTTTTGAATTAAGGGATTTTGGC	1434						
Qy	2387	GATTTTGGCCCTATTGGTTAAAAAATGAGCTGATTTTAAACAAAAATTTAACCGGAATTTAA	2446						
Db	1433	GATTTTGGCCCTATTGGTTAAAAAATGAGCTGATTTTAAACAAAAATTTAACCGGAATTTAA	1374						
Qy	2447	CAAAAATATTAACTTTTCAATTTCTGTAGACGGTATTTTCTCTCTTACGATCTGTGCGGT	2506						
Db	1373	CAAAAATATTAACTTTTCAATTTCTGTAGACGGTATTTTCTCTCTTACGATCTGTGCGGT	1314						

Qy	2507	ATTTCACACCGCATAGGGTAATAAATCTGATATAAATTAATAATTGAAGCTCTAAATTTGTGAGTT	2506
Db	1313	ATTTTCACACCGCATAGGGTAATAAATCTGATATAAATTAATAATTGAAGCTCTAAATTTGTGAGTT	1254
Qy	2567	TAGTATACATGCATTTACTTATAATAACAGTTTTTTTAGTTTTGTCTGGCGCGATCTTCTCAA	2628
Db	1253	TAGTATACATGCATTTACTTATAATAACAGTTTTTTTAGTTTTGTCTGGCGCGATCTTCTCAA	1194
Qy	2627	ATATGCTTCCAGCGCTGCTTTCTGTAAAGGTTCAACCTCTACCTTTAGCATCCCTTCCCTT	2686
Db	1193	ATATGCTTCCAGCGCTGCTTTCTGTAAAGGTTCAACCTCTACCTTTAGCATCCCTTCCCTT	1134
Qy	2687	TGCAAAATAGTCTCTTCCAAACAATAAATATGTCHAGATCTCTGTAGAGACCAATCATCCAC	2746
Db	1133	TGCAAAATAGTCTCTTCCAAACAATAAATATGTCHAGATCTCTGTAGAGACCAATCATCCAC	1074
Qy	2747	GGTTCTATACTGTTGACCCGAATGGGTCTCCGTTGTGTATCTAAACCCACACCGGGTGTAT	2806
Db	1073	GGTTCTATACTGTTGACCCGAATGGGTCTCCGTTGTGTATCTAAACCCACACCGGGTGTAT	1014
Qy	2807	AATCAACAATCGTAACCTTCATCTCTTCCACCCATGTCTCTTTGAGCAATAAAGCCGAT	2866
Db	1013	AATCAACAATCGTAACCTTCATCTCTTCCACCCATGTCTCTTTGAGCAATAAAGCCGAT	954
Qy	2867	AACAAAATCTTTGTGCGTCTTTCCGAAATGTCAAACAGTAGCCCTTAGTATATTTCCAGTAGA	2926
Db	953	AACAAAATCTTTGTGCGTCTTTCCGAAATGTCAAACAGTAGCCCTTAGTATATTTCCAGTAGA	894
Qy	2927	TAGGGAGCCCTTGCAATGACAAATTTCTGCTAAATCAATAAAGGCTCTAGGTTCTTTTGTATC	2986
Db	893	TAGGGAGCCCTTGCAATGACAAATTTCTGCTAAATCAATAAAGGCTCTAGGTTCTTTTGTATC	834
Qy	2987	TTCTTCTGCGCGCTTCAAACGGCTAAACAAATACCTTGGGCGCCACCAACGGTGTGCATT	3046
Db	833	TTCTTCTGCGCGCTTCAAACGGCTTCAAACAAATACCTTGGGCGCCACCAACGGTGTGCATT	774
Qy	3047	CGTAATGCTGCGCCATTCTGCTATTTCTGTATACACCCGCGAGAGTACTGCAATTTGACTGT	3106
Db	773	CGTAAATGCTGCGCCATTCTGCTATTTCTGTATACACCCGCGAGAGTACTGCAATTTGACTGT	714
Qy	3107	ATTACCAATGTGACGAAATTTTCTGCTTTCGAGAGTAAAAAATGTACTTTGGCGGATAA	3166
Db	713	ATTACCAATGTGACGAAATTTTCTGCTTTCGAGAGTAAAAAATGTACTTTGGCGGATAA	654
Qy	3167	TGCTTTTAGCGGCTTAACGTGCGCTCCATGGAAATAATCAGTCAAGATATCCACATGCT	3226
Db	653	TGCTTTTAGCGGCTTAACGTGCGCTCCATGGAAATAATCAGTCAAGATATCCACATGCT	594
Qy	3227	TTTTAGTAAACAAATTTTGGGACCTAATGCTTCAACTAACTCCAGTAAATTTCTTTGGTGGT	3286
Db	593	TTTTAGTAAACAAATTTTGGGACCTAATGCTTCAACTAACTCCAGTAAATTTCTTTGGTGGT	534
Qy	3287	ACGAACATCCAATGGAAGCACACAAGTTTGTCTTTTGTGCAATGATATTAATAAGCTT	3346
Db	533	ACGAACATCCAATGGAAGCACACAAGTTTGTCTTTTGTGCAATGATATTAATAAGCTT	474
Qy	3347	GGCAGCAACGAGGACTAGGATGAGTAGCAGCACGTTCTCTTATATGTAGCTTTCGACATGAT	3406
Db	473	GGCAGCAACGAGGACTAGGATGAGTAGCAGCACGTTCTCTTATATGTAGCTTTCGACATGAT	414
Qy	3407	TTATCTCGTTTCTCGCAGGTTTTTGTCTGTGTCAGTTGGGTTAAGAAATACTGGGCAATT	3466
Db	413	TTATCTCGTTTCTCGCAGGTTTTTGTCTGTGTCAGTTGGGTTAAGAAATACTGGGCAATT	354
Qy	3467	TCATGTTTCTTCAACACTACATATGCGTATATATACCAATCTAAGTCTGTGCTCTTCTCT	3526
Db	353	TCATGTTTCTTCAACACTACATATGCGTATATATACCAATCTAAGTCTGTGCTCTTCTCT	294
Qy	3527	TCGTTCTTCTCTGTTTCGAGATATACCGAATCAAAAAAATTTTCAAGAAACCGAAATCA	3586
Db	293	TCGTTCTTCTCTGTTTCGAGATATACCGAATCAAAAAAATTTTCAAGAAACCGAAATCA	234

6791 AAAGCGCCAGCTTCCCGAAGGAGGAAAGCGGACAGGTATCCGGTAAGCGGAGGGTGG 6850
1561 AAAGCGCCAGCTTCCCGAAGGAGGAAAGCGGACAGGTATCCGGTAAGCGGAGGGTGG 1620
6851 GAACAGAGAGCGCACAGAGGAGCTTCCAGGGGAAACGCGCTGGTATCTTTATAGTCCTG 6910
1621 GAACAGAGAGCGCACAGAGGAGCTTCCAGGGGAAACGCGCTGGTATCTTTATAGTCCTG 1680
6911 TCGGGTTTCGCCACCTCTGACTTGTAGCGTCAATTTTGTGATGCTCGTCAAGGGGGCGGA 6970
1681 TCGGGTTTCGCCACCTCTGACTTGTAGCGTCAATTTTGTGATGCTCGTCAAGGGGGCGGA 1740
6971 GCCTATGGRAAAGCGCAGCAACGCGCTTTTACGGTTCTCGGCTTTTGTGCGCTT 7030
1741 GCCTATGGRAAAGCGCAGCAACGCGCTTTTACGGTTCTCGGCTTTTGTGCGCTT 1800
7031 TTGCTCACATGTTCTTTCCTCGGTTATCCCTGATCTGTGGATTAACCGTATTACGCGCT 7090
1801 TTGCTCACATGTTCTTTCCTCGGTTATCCCTGATCTGTGGATTAACCGTATTACGCGCT 1860
7091 TTGAGTGAGTGATACCGCTCGCGCAGCGCAACGACCGAGCGAGTCAAGTGAGCG 7150
1861 TTGAGTGAGTGATACCGCTCGCGCAGCGCAACGACCGAGCGAGTCAAGTGAGCG 1920
7151 AGAAGCGGAAGAGCGCCCAATAGCAACCGCTCTCCCGCGCGTGTGCGCGATTCATT 7210
1921 AGAAGCGGAAGAGCGCCCAATAGCAACCGCTCTCCCGCGCGTGTGCGCGATTCATT 1980
7211 AATGCACTGCGCAGCAGAGTTCGCGACTGGAAGCGGCGAGTGAGCGCAACGCAATTA 7270
1981 AATGCACTGCGCAGCAGAGTTCGCGACTGGAAGCGGCGAGTGAGCGCAACGCAATTA 2040
7271 ATGTGAGTTACCTCACTATTAGGCAACCGAGGCTTTTACACTTTATGCTTCCGGCTCCTA 7330
2041 ATGTGAGTTAGCTCACTATTAGGCAACCGAGGCTTTTACACTTTATGCTTCCGGCTCGTA 2100
7331 TGTGTGTGAATTTGAGCGGATTAACAATTCACAGAAACAGCTATGACCATGATT 7390
2101 TGTGTGTGAATTTGAGCGGATTAACAATTCACAGAAACAGCTATGACCATGATT 2160
7391 ACCCAAGCGCGCAATTAACCTCACTAAAGGGAACAAAGCTGGAGCTCGTAG 7444
2161 ACCCAAGCGCGCAATTAACCTCACTAAAGGGAACAAAGCTGGAGCTCGAAG 2214

RESULT 15

US-10-343-303-1
; Sequence 1, Application US/10343303
; Publication No. US20040038394A1
; GENERAL INFORMATION:
; APPLICANT: Mogen Biotechnology Research Institute
; APPLICANT: Pan-Gen Biotech Laboratories Inc.
; TITLE OF INVENTION: Expression vector for animal cell
; FILE REFERENCE: opp010629kr
; CURRENT APPLICATION NUMBER: US/10/343,303
; CURRENT FILING DATE: 2003-08-04
; PRIOR APPLICATION NUMBER: KR10-2000-43996
; PRIOR FILING DATE: 2000-07-29
; NUMBER OF SEQ ID NOS: 24
; SOFTWARE: KopatentIn 1.55
; SEQ ID NO 1
; LENGTH: 6287
; TYPE: DNA
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: pMS vector sequence
; FEATURE:
; NAME/KEY: promoter
; LOCATION: (1)..(419)
; OTHER INFORMATION: SV40virus
; FEATURE:
; NAME/KEY: gene
; LOCATION: (3305)..(6269)

; OTHER INFORMATION: Human beta globin MAR element
US-10-343-303-1

Query Match 28.2%; Score 2204.6; DB 13; Length 6287;
Best Local Similarity 99.8%; Pred. No. 0;
Matches 2207; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 5230 TCAGGTGGCACTTTTCGGGAAATGTGCGGAAACCCCTATTTTGTATTTTCTAAATA 5289
DB 1080 TCAGGTGGCACTTTTCGGGAAATGTGCGGAAACCCCTATTTTGTATTTTCTAAATA 1139
QY 5290 CATTCAAATATGATCGCTCATGAGCAATTAACCTGATAAATGCTCAATAATTTGA 5349
DB 1140 CATTCAAATATGATCGCTCATGAGCAATTAACCTGATAAATGCTCAATAATTTGA 1199
QY 5350 AAAAGAAAGATGATGATTTCAACATTTCCGTGTGCGCCCTATTCCTTTTTCGGGCA 5409
DB 1200 AAAAGAAAGATGATGATTTCAACATTTCCGTGTGCGCCCTATTCCTTTTTCGGGCA 1259
QY 5410 TTTTGCCTTCTGTTTTGCTCACCCAGAAACGCTGCTGAAAGCTAAAAGATGCTGAAGAT 5469
DB 1260 TTTTGCCTTCTGTTTTGCTCACCCAGAAACGCTGCTGAAAGCTAAAAGATGCTGAAGAT 1319
QY 5470 CAGTTGGGTGCACGAGTGGGTTACATCGAATCTCAACAGCGGTAAAGATCCTTGAG 5529
DB 1320 CAGTTGGGTGCACGAGTGGGTTACATCGAATCTCAACAGCGGTAAAGATCCTTGAG 1379
QY 5530 AGTTTTGCGCCCGCAAGAGCTTTTCCATGATGAGCACTTTTAAAGTTCTGCTATGTGGC 5589
DB 1380 AGTTTTGCGCCCGCAAGAGCTTTTCCATGATGAGCACTTTTAAAGTTCTGCTATGTGGC 1439
QY 5590 GCGGTATTATCCCGTATTGACGCGCGGCAAGAGCAACTCGGTCCGCGCATACATTTCT 5649
DB 1440 GCGGTATTATCCCGTATTGACGCGCGGCAAGAGCAACTCGGTCCGCGCATACATTTCT 1499
QY 5650 CAGAAATGACTTGTGTGAGTACTCACCAGTCAAGAAAGCATCTTACGGATGCGATGACA 5709
DB 1500 CAGAAATGACTTGTGTGAGTACTCACCAGTCAAGAAAGCATCTTACGGATGCGATGACA 1559
QY 5710 GTAAGAGAAATTATGCAAGTCTGCTCAATACCAGTGAATAACACTGCGGCAACTTACTT 5769
DB 1560 GTAAGAGAAATTATGCAAGTCTGCTCAATACCAGTGAATAACACTGCGGCAACTTACTT 1619
QY 5770 CTGACAAACGATCGGAGGACCGAAGAGCTAAACCGCTTTTTCGACAAACATGGGGGATCAT 5829
DB 1620 CTGACAAACGATCGGAGGACCGAAGAGCTAAACCGCTTTTTCGACAAACATGGGGGATCAT 1679
QY 5830 GTHAATCGGCTTGTGATCGTGGGAAACCGGAGCTGAAATGAAGCCATACCAACGAGCGGT 5889
DB 1680 GTHAATCGGCTTGTGATCGTGGGAAACCGGAGCTGAAATGAAGCCATACCAACGAGCGGT 1739
QY 5890 GACACCAACGATGCTGTAGCAATGGCAACAAACGCTGCGGCAAACTATTAACTGGCGAACTA 5949
DB 1740 GACACCAACGATGCTGTAGCAATGGCAACAAACGCTGCGGCAAACTATTAACTGGCGAACTA 1799
QY 5950 CTTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGGATGGAGCGGATTAAGTTTCAGGA 6009
DB 1800 CTTTACTCTAGCTTCCCGGCAACAAATTAATAGACTGGATGGAGCGGATTAAGTTTCAGGA 1859
QY 6010 CCACTTCTGCGCTCGGCGCTTCCGGCTGGCTGTTTATGCTGATTAATCTGGAGCGGCT 6069
DB 1860 CCACTTCTGCGCTCGGCGCTTCCGGCTGGCTGTTTATGCTGATTAATCTGGAGCGGCT 1919
QY 6070 GAGCGTGGGTCTGCGGCTATCATTTGAGCACTCGGGGCGAGATGTAAGCCCTCCCGTATC 6129
DB 1920 GAGCGTGGGTCTGCGGCTATCATTTGAGCACTCGGGGCGAGATGTAAGCCCTCCCGTATC 1979
QY 6130 GTAGTTATCTACAGCGGGGAGTCAAGCAACTATATGATGAACGAAATAGACAGATCGCT 6189
DB 1980 GTAGTTATCTACAGCGGGGAGTCAAGCAACTATATGATGAACGAAATAGACAGATCGCT 2039
QY 6190 GAGATAGGTGCTCTCACTGATTAAGCAATTTGATTAATCTGTACAGCAAGTTTACTATATATA 6249

Db 2040 GAGATAGTGCCTCTACTGATTAAAGCATTTGGTAACGTCTCAGACCAAGTTTACTCATATATA 2099
Qy 6250 CTTTAGATTGATTTAAACTCTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTTT 6309
Db 2100 CTTTAGATTGATTTAAACTCTCATTTTAAATTTAAAGGATCTAGGTGAAGATCCTTTTT 2159
Qy 6310 GATAATCTCATGACCAAAATCCCTTAACTGAGTTTTCGTTCCACTGAGCGTCAAGCCCC 6369
Db 2160 GATAATCTCATGACCAAAATCCCTTAACTGAGTTTTCGTTCCACTGAGCGTCAAGCCCC 2219
Qy 6370 GTAGAAAGATCAAGGATCTCTTGATGATCCTTTTTTTTTCGCGGTAATCTGCTGCTTG 6429
Db 2220 GTAGAAAGATCAAGGATCTCTTGATGATCCTTTTTTTTTCGCGGTAATCTGCTGCTTG 2279
Qy 6430 CAAACAAAACCAACACCGCTACACGCGTGGTTGTTGCCGGATCAAGAGCTACCAACT 6489
Db 2280 CAAACAAAACCAACACCGCTACACGCGTGGTTGTTGCCGGATCAAGAGCTACCAACT 2339
Qy 6490 CTTTTTCCGAAGGTAACCTGGCTTACGACAGCGCAGATACCAAAATACCTCTCTTAGTG 6549
Db 2340 CTTTTTCCGAAGGTAACCTGGCTTACGACAGCGCAGATACCAAAATACCTCTCTTAGTG 2399
Qy 6550 TAGCCGTAGTTAGGCGACCACTTCAAGAACTCTGTAGCACCGCCTACATACCTCGCTCTG 6609
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Db 2460 CTAATCCTGTTACCAAGTGGCTGCTGCCAGTGGCGGATAGTCTGTCTTTACCGGGTTGGAC 2519
Qy 6670 TCAAGACGATAGTTACCGGATAAGCGCAGCGGTCGGGCTGAAACGGGGGTTCTGTGCACA 6729
Db 2520 TCAAGACGATAGTTACCGGATAAGCGCAGCGGTCGGGCTGAAACGGGGGTTCTGTGCACA 2579
Qy 6730 CAGCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGA 6789
Db 2580 CAGCCAGCTTGGAGCGAACGACCTACACCGAACTGAGATACCTACAGCGTGAGCTATGA 2639
Qy 6790 GAAAGCGCACCTTCCGAGGGAGAAAGCGGACAGTATCCGGTAAGCGCGAGGGTC 6849
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Qy 6850 GGAACAGGAGAGCGCACGAGGGAGCTTCCAGGGGAAACGGCTGTGTATCTTTATAGTCT 6909
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Qy 6910 GTCCGGTTTCGGCACCTCTGACTGAGCGTCGATTTTGTGATGCTCGTAGGGGGGGGG 6969
Db 2760 GTCCGGTTTCGGCACCTCTGACTGAGCGTCGATTTTGTGATGCTCGTAGGGGGGGGG 2819
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Qy 7090 TTTGAGTGAGCTGATACCGCTCGCCGCGACCGCAACGAGCGGAGCGAGTCAAGTGAAC 7149
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Qy 7150 GAGGAAGCGGAAGAGCGCCCAATAGCAAAACCGCTCTCCCGCGGCTTGGCCGATTCCAT 7209
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Qy 7210 TAATGAGCTGGCACACAGGTTTCCCGACTGGAAGCGGGCAGTGAGCGCAACGCAATT 7269
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Qy 7330 ATGTTGTGTGGAATTTGTAGCGGATAACAATTTTCAACAGGAAACAGCTATGACCATGAT 7389
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Db 3240 TAGCCCAAGCTCGAAATTAACCTCTACTAAGGGAAACAAAAGCTGGAGCTC 3290

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